

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
14 September 2006 (14.09.2006)

PCT

(10) International Publication Number
WO 2006/096527 A2

(51) International Patent Classification:
C12Q 1/68 (2006.01)

(21) International Application Number:
PCT/US2006/007642

(22) International Filing Date: 3 March 2006 (03.03.2006)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/658,984 4 March 2005 (04.03.2005) US

(71) Applicant (for all designated States except US): DI-
VERSA CORPORATION [US/US]; 4955 Directors
Place, San Diego, California 92121 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): MATHUR, Eric
[US/US]; 2654 Galicia Way, Carlsbad, California 92009
(US). CHANG, Cathy [US/US]; 1318 Shadow Hills
Drive, San Marcos, California 92069 (US).

(74) Agents: EINHORN, Gregory et al.; MORRISON & FO-
ERSTER LLP, 12531 High Bluff Drive, Suite 100, San
Diego, California 92130-2040 (US).

(81) Designated States (unless otherwise indicated, for every
kind of national protection available): AE, AG, AL, AM,
AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI,
GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE,
KG, KM, KN, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV,
LY, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI,
NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG,
SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US,
UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every
kind of regional protection available): ARIPO (BW, GH,
GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM,
ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI,
FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT,
RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA,
GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished
upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: NUCLEIC ACIDS AND PROTEINS AND METHODS FOR MAKING AND USING THEM

(57) Abstract: The invention provides polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. Polypeptides, including enzymes and antibodies, and nucleic acids of the invention can be used in industrial, experimental, food and feed processing, nutritional and pharmaceutical applications, e.g., for food and feed supplements, colorants, nutraceuticals, cosmetic and pharmaceutical needs.

WO 2006/096527 A2

NUCLEIC ACIDS AND PROTEINS AND METHODS FOR MAKING AND USING THEM

REFERENCE TO SEQUENCE LISTING SUBMITTED ON A COMPACT DISC

The content of the following submissions on compact discs are incorporated herein by reference in their entirety: A computer readable form (CRF) of the Sequence Listing (file name: 564462014340 SEQUENCE LISTING.txt, date recorded: March 4, 2005, size: 36,463,033 bytes); a duplicate compact disc copy (COPY 1) of the Sequence Listing (file name: 564462014340 SEQUENCE LISTING.txt, date recorded: March 4, 2005, size: 36,463,033 bytes); and a duplicate compact disc copy (COPY 2) of the Sequence Listing (file name: 564462014340 SEQUENCE LISTING.txt, date recorded: March 4, 2005, size: 36,463,033 bytes).

FIELD OF THE INVENTION

This invention relates to molecular and cellular biology and biochemistry. In one aspect, the invention provides polypeptides, including enzymes, structural proteins and binding proteins (e.g., ligands, receptors), polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, structural proteins and binding proteins, including thermostable and thermotolerant activity, and polynucleotides encoding these enzymes, structural proteins and binding proteins and making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used in a variety of pharmaceutical, agricultural and industrial contexts, including the manufacture of cosmetics and nutraceuticals.

Additionally, the polypeptides of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in the photographic industry, medical treatment, silk degumming, biofilm degradation, biomass conversion to ethanol, biodefense, antimicrobial agents and disinfectants, personal care and cosmetics, biotech reagents, in corn wet milling and pharmaceuticals such as digestive aids and anti-inflammatory (anti-phlogistic) agents.

BACKGROUND

The invention provides isolated and recombinant polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. The polypeptides of the invention, and the polynucleotides encoding the polypeptides of the invention, encompass many classes of enzymes, structural proteins and binding proteins. In one aspect, the enzymes and proteins of the invention include, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases. The invention also provides isolated and recombinant polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, having the activities described in Table 1, Table 2 or Table 3, below. The enzymes and proteins of the invention have utility in a variety of applications.

SUMMARY

The invention provides isolated or recombinant nucleic acids comprising a nucleic acid sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention, e.g., including SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2200, 2250, 2300, 2350, 2400, 2450, 2500, or more residues, encodes at least one polypeptide having an enzyme, structural or binding activity, and the sequence identities are determined by analysis with

a sequence comparison algorithm or by a visual inspection. In one aspect, the enzymes and proteins of the invention include, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases. In another aspect, the isolated and recombinant polypeptides of the invention, including enzymes, structural proteins and binding proteins, and polynucleotides encoding these polypeptides, of the invention have activity as described in Table 1, Table 2 or Table 3, below.

In one aspect, the invention also provides isolated or recombinant nucleic acids with a common novelty in that they are all derived from a common source, e.g., an environmental source, mixed environmental sources or mixed cultures. The invention provides isolated or recombinant nucleic acids isolated from a common source, e.g. an environmental source, mixed environmental sources or mixed cultures comprising a polynucleotide of the invention, e.g., an exemplary sequence of the invention, including SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2200, 2250, 2300, 2350, 2400, 2450, 2500, or more residues, encodes at least one polypeptide having an enzyme, structural or binding activity, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection. In one aspect, the enzymes and proteins of the invention include, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases. In another aspect, the isolated and recombinant polypeptides of the invention, including enzymes, structural proteins and binding proteins, and polynucleotides

encoding these polypeptides, of the invention have activity as described in Table 1, Table 2 or Table 3, below.

In alternative aspects, the isolated or recombinant nucleic acid encodes a polypeptide comprising an exemplary sequence of the invention, e.g., including sequences as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO: 26,898. In one aspect these polypeptides have an enzyme, structural or binding activity. In one aspect, the enzymes and proteins of the invention include, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases. In another aspect, the isolated and recombinant polypeptides of the invention, including enzymes, structural proteins and binding proteins, and polynucleotides encoding these polypeptides, of the invention have activity as described in Table 1, Table 2 or Table 3, below.

In alternative aspects, the enzyme, structural or binding activity comprises a recombinase activity, a helicase activity, a DNA replication activity, a DNA recombination activity, an isomerase, a trans-isomerase activity or topoisomerase activity, a methyl transferase activity, an aminotransferase activity, a uracil-5- methyl transferase activity, a cysteinyl tRNA synthetase activity, a hydrolase, an esterase activity, a phosphoesterase activity, an acetylmuramyl pentapeptide phosphotransferase activity, a glycosyltransferase activity, an acetyltransferase activity, an acetylglucosamine phosphate transferase activity, a centromere binding activity, a telomerase activity or a transcriptional regulatory activity, a heat shock protein activity, a protease activity, a proteinase activity, a peptidase activity, a carboxypeptidase activity, an endonuclease activity, an exonuclease activity, a RecB family exonuclease activity, a polymerase activity, a carbamoyl phosphate synthetase activity, a methyl-thioadenine synthetase activity, an oxidoreductase activity, an Fe-S oxidoreductase activity, a flavodoxin reductase activity, a permease activity, a thymidylate activity, a dehydrogenase activity, a pyrophosphorylase activity, a coenzyme metabolism activity, a dinucleotide-utilizing enzyme activity, a molybdopterin or thiamine biosynthesis activity, a beta-lactamase

activity, a ligand binding activity, an ion transport activity, an ion metabolism activity, a tellurite resistance protein activity, an inorganic ion transport activity, a nucleotide transport activity, a nucleotide metabolism activity, an actin or myosin activity, a lipase activity or a lipid acyl hydrolase (LAH) activity, a cell envelop biogenesis activity, an outer membrane synthesis activity, a ribosomal structure synthesis activity, a translational processing activity, a transcriptional initiation activity, a TATA-binding activity, a signal transduction activity, an energy metabolism activity, an ATPase activity, an information storage and/or processing activity, and/or any of the polypeptides activities as set forth in Table 1, Table 2 or Table 3, below.

In one aspect, the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

Another aspect of the invention is an isolated or recombinant nucleic acid including at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2200, 2250, 2300, 2350, 2400, 2450, 2500, or more consecutive bases of a nucleic acid sequence of the invention, sequences substantially identical thereto, and the sequences complementary thereto.

In one aspect, the isolated or recombinant nucleic acid encodes a polypeptide having a enzyme, structural or binding activity, that is thermostable. The polypeptide can retain activity under conditions comprising a temperature range of between about 37°C to about 95°C; between about 55°C to about 85°C, between about 70°C to about 95°C, or, between about 90°C to about 95°C.

In another aspect, the isolated or recombinant nucleic acid encodes a polypeptide having an enzyme, structural or binding activity, which is thermotolerant. The polypeptide can retain activity after exposure to a temperature in the range from greater than 37°C to about 95°C or anywhere in the range from greater than 55°C to about 85°C. The polypeptide can retain activity after exposure to a temperature in the range between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more. In one aspect, the polypeptide retains activity after exposure to a temperature in the range from greater than 90°C to about 95°C at about pH 4.5.

The invention provides isolated or recombinant nucleic acids comprising a sequence that hybridizes under stringent conditions to a nucleic acid comprising a sequence of the invention, e.g., an exemplary sequence of the invention, including SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, or fragments or subsequences thereof. In one aspect, the nucleic acid encodes a polypeptide having a enzyme, structural or binding activity. The nucleic acid can be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200 or more residues in length or the full length of the gene or transcript. In one aspect, the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

The invention provides a nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a enzyme, structural or binding activity, wherein the probe comprises at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 or more, consecutive bases of a sequence comprising a sequence of the invention, or fragments or subsequences thereof, wherein the probe identifies the nucleic acid by binding or hybridization. The probe can comprise an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of a sequence comprising a sequence of the invention, or fragments or subsequences thereof.

The invention provides a nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a enzyme, structural or binding activity, wherein the probe comprises a nucleic acid comprising a sequence at least about 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 or more residues having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to a nucleic acid of the invention. In one aspect, the sequence identities are determined by analysis with a sequence comparison

algorithm or by visual inspection. In alternative aspects, the probe can comprise an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of a nucleic acid sequence of the invention, or a subsequence thereof.

The invention provides an amplification primer pair for amplifying a nucleic acid encoding a polypeptide having a enzyme, structural or binding activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence of the invention, or fragments or subsequences thereof. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising at least about 10 to 50, or more, consecutive bases of the sequence, or about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

The invention provides amplification primer pairs, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36 or more residues of a nucleic acid of the invention, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36 or more residues of the complementary strand of the first member.

The invention provides polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding nucleic acids generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding nucleic acids generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides methods of making a polypeptide, enzyme, protein, e.g. structural or binding protein, by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. In one aspect, the amplification primer pair amplifies a nucleic acid from a library, e.g., a gene library, such as an environmental library.

The invention provides methods of amplifying a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity, comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence of the invention, or fragments or subsequences thereof.

The invention provides expression cassettes comprising a nucleic acid of the invention or a subsequence thereof. In one aspect, the expression cassette can comprise the nucleic acid that is operably linked to a promoter. The promoter can be a viral, bacterial, mammalian or plant promoter. In one aspect, the plant promoter can be a potato, rice, corn, wheat, tobacco or barley promoter. The promoter can be a constitutive promoter. The constitutive promoter can comprise CaMV35S. In another aspect, the promoter can be an inducible promoter. In one aspect, the promoter can be a tissue-specific promoter or an environmentally regulated or a developmentally regulated promoter. Thus, the promoter can be, e.g., a seed-specific, a leaf-specific, a root-specific, a stem-specific or an abscission-induced promoter. In one aspect, the expression cassette can further comprise a plant or plant virus expression vector.

The invention provides cloning vehicles comprising an expression cassette (e.g., a vector) of the invention or a nucleic acid of the invention. The cloning vehicle can be a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome. The viral vector can comprise an adenovirus vector, a retroviral vector or an adeno-associated viral vector. The cloning vehicle can comprise a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

The invention provides transformed cell comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention, or a cloning vehicle of the invention. In one aspect, the transformed cell can be a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell. In one aspect, the plant cell can be a cereal, a potato, wheat, rice, corn, tobacco or barley cell.

The invention provides transgenic non-human animals comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. In one aspect, the animal is a mouse, a rat, a pig, a goat or a sheep.

The invention provides transgenic plants comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. The transgenic plant can be a cereal plant, a corn plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant or a tobacco plant.

The invention provides transgenic seeds comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. The transgenic seed

can be a cereal plant, a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a peanut or a tobacco plant seed.

The invention provides an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. The invention provides methods of inhibiting the translation of a polypeptide, enzyme, protein, e.g. structural or binding protein message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. In one aspect, the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length, e.g., 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more bases in length.

The invention provides methods of inhibiting the translation of a polypeptide, enzyme, protein, e.g. structural or binding protein message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. The invention provides double-stranded inhibitory RNA (RNAi, or RNA interference) molecules (including small interfering RNA, or siRNAs, for inhibiting transcription, and microRNAs, or miRNAs, for inhibiting translation) comprising a subsequence of a sequence of the invention. In one aspect, the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more duplex nucleotides in length. The invention provides methods of inhibiting the expression of a polypeptide, enzyme, protein, peptide, e.g. structural or binding protein in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA, including small interfering RNA, or siRNAs, for inhibiting transcription, and microRNAs, or miRNAs, for inhibiting translation), wherein the RNA comprises a subsequence of a sequence of the invention.

The invention provides isolated or recombinant polypeptides encoded by a nucleic acid of the invention. In alternative aspects, the polypeptide can have a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898 (the exemplary sequences of the invention), or subsequences thereof, including fragments having

enzymatic and/or substrate binding activity. The polypeptide can have an enzyme, structural or binding activity.

In alternative aspects, the enzyme, structural or binding activity comprises a recombinase activity, a helicase activity, a DNA replication activity, a DNA recombination activity, an isomerase, a trans-isomerase activity or topoisomerase activity, a methyl transferase activity, an aminotransferase activity, a uracil-5- methyl transferase activity, a cysteinyl tRNA synthetase activity, a hydrolase, an esterase activity, a phosphoesterase activity, an acetylmuramyl pentapeptide phosphotransferase activity, a glycosyltransferase activity, an acetyltransferase activity, an acetylglucosamine phosphate transferase activity, a centromere binding activity, a telomerase activity or a transcriptional regulatory activity, a heat shock protein activity, a protease activity, a proteinase activity, a peptidase activity, a carboxypeptidase activity, an endonuclease activity, an exonuclease activity, a RecB family exonuclease activity, a polymerase activity, a carbamoyl phosphate synthetase activity, a methyl-thioadenine synthetase activity, an oxidoreductase activity, an Fe-S oxidoreductase activity, a flavodoxin reductase activity, a permease activity, a thymidylate activity, a dehydrogenase activity, a pyrophosphorylase activity, a coenzyme metabolism activity, a dinucleotide-utilizing enzyme activity, a molybdopterin or thiamine biosynthesis activity, a beta-lactamase activity, a ligand binding activity, an ion transport activity, an ion metabolism activity, a tellurite resistance protein activity, an inorganic ion transport activity, a nucleotide transport activity, a nucleotide metabolism activity, an actin or myosin activity, a lipase activity or a lipid acyl hydrolase (LAH) activity, a cell envelop biogenesis activity, an outer membrane synthesis activity, a ribosomal structure synthesis activity, a translational processing activity, a transcriptional initiation activity, a TATA-binding activity, a signal transduction activity, an energy metabolism activity, an ATPase activity, an information storage and/or processing activity, and/or any of the polypeptides activities as set forth in Table 1, Table 2 or Table 3, below.

Exemplary polypeptide or peptide sequences of the invention include SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898, and subsequences thereof and variants thereof. Exemplary polypeptides also include fragments of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600 or more residues in length, or over the full length of an enzyme. Exemplary

polypeptide or peptide sequences of the invention include sequence encoded by a nucleic acid of the invention. Exemplary polypeptide or peptide sequences of the invention include polypeptides or peptides specifically bound by an antibody of the invention.

In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein, is thermostable. The polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more. In another aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can be thermotolerant. The polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity after exposure to a temperature in the range from greater than 37°C to about 95°C, or in the range from greater than 55°C to about 85°C. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity after exposure to a temperature in the range from greater than 90°C to about 95°C at pH 4.5.

Another aspect of the invention provides an isolated or recombinant polypeptide or peptide including at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 or more consecutive bases of a polypeptide or peptide sequence of the invention, sequences substantially identical thereto, and the sequences complementary thereto. The peptide can be, e.g., an immunogenic fragment, a motif (e.g., a binding site), a signal sequence, a prepro sequence or an active site.

The invention provides isolated or recombinant nucleic acids comprising a sequence encoding a polypeptide, enzyme, protein, e.g. structural or binding protein having any of the activities as set forth in Tables 1, 2 or 3, and a signal sequence, wherein the nucleic acid comprises a sequence of the invention. In one aspect, the isolated or recombinant polypeptide can comprise the polypeptide of the invention comprising a heterologous signal sequence or a heterologous preprosequence, such as a heterologous enzyme or non-enzyme signal sequence. The invention provides isolated or recombinant nucleic acids comprising a sequence encoding a polypeptide, enzyme, protein, e.g. structural or binding protein having any of the activities as set forth in Tables 1, 2 or 3, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence of the invention. In one aspect, the invention provides an isolated or

recombinant polypeptide comprising a polypeptide of the invention lacking all or part of a signal sequence.

In one aspect, the invention provides chimeric proteins comprising a first domain comprising a signal sequence of the invention and at least a second domain. The protein can be a fusion protein. The second domain can comprise an enzyme. The enzyme can be a non-enzyme.

The invention provides chimeric polypeptides comprising at least a first domain comprising signal peptide (SP), a prepro sequence and/or a catalytic domain (CD) of the invention and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP), prepro sequence and/or catalytic domain (CD). In one aspect, the heterologous polypeptide or peptide is not an enzyme. The heterologous polypeptide or peptide can be amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP), prepro sequence and/or catalytic domain (CD).

The invention provides isolated or recombinant nucleic acids encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP), a prepro domain and/or a catalytic domain (CD) of the invention and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP), prepro domain and/or catalytic domain (CD).

The invention provides isolated or recombinant signal sequences (e.g., signal peptides) consisting of or comprising a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44, 1 to 45, 1 to 46 or 1 to 47, of a polypeptide of the invention, including the exemplary polypeptides of the invention (including SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898). In one aspect, the invention provides signal sequences comprising the first 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70 or more amino terminal residues of a polypeptide of the invention.

In one aspect, the enzyme, structural or binding activity comprises a specific activity at about 37°C in the range from about 1 to about 1200 units per milligram of protein, or, about 100 to about 1000 units per milligram of protein. In another aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein activity comprises a specific activity from about 100 to about 1000 units per milligram of protein, or, from about 500 to about 750 units per milligram of protein. Alternatively, the enzyme, structural or binding activity comprises a specific activity at 37°C in the range from about 1 to about 750 units per milligram of protein, or, from about 500 to about 1200 units per milligram of protein. In one aspect, the enzyme, structural or binding activity comprises a specific activity at 37°C in the range from about 1 to about 500 units per milligram of protein, or, from about 750 to about 1000 units per milligram of protein. In another aspect, the enzyme, structural or binding activity comprises a specific activity at 37°C in the range from about 1 to about 250 units per milligram of protein. Alternatively, the enzyme, structural or binding activity comprises a specific activity at 37°C in the range from about 1 to about 100 units per milligram of protein.

In another aspect, thermotolerance comprises retention of at least half of the specific activity of the enzyme, structural or binding protein at 37°C after being heated to the elevated temperature. Alternatively, thermotolerance can comprise retention of specific activity at 37°C in the range from about 1 to about 1200 units per milligram of protein, or, from about 500 to about 1000 units per milligram of protein, after being heated to the elevated temperature. In another aspect, thermotolerance can comprise retention of specific activity at 37°C in the range from about 1 to about 500 units per milligram of protein after being heated to the elevated temperature.

The invention provides the isolated or recombinant polypeptide of the invention, wherein the polypeptide comprises at least one glycosylation site. In one aspect, glycosylation can be an N-linked glycosylation. In one aspect, the polypeptide can be glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity under conditions comprising about pH 6.5, pH 6, pH 5.5, pH 5, pH 4.5 or pH 4. In another aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity under conditions comprising about pH 7, pH 7.5 pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5 or pH 11. In one aspect, the polypeptide can retain an enzyme, structural or binding activity after exposure to conditions comprising about pH 6.5, pH 6, pH 5.5, pH 5, pH 4.5 or pH 4. In another aspect, the polypeptide can retain

enzyme, structural or binding activity after exposure to conditions comprising about pH 7, pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5 or pH 11.

In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein of the invention has activity at under alkaline conditions, e.g., the alkaline conditions of the gut, e.g., the small intestine. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity after exposure to the acidic pH of the stomach.

The invention provides protein preparations comprising a polypeptide of the invention, wherein the protein preparation comprises a liquid, a solid or a gel.

The invention provides heterodimers comprising a polypeptide of the invention and a second protein or domain. The second member of the heterodimer can be a different enzyme, a different enzyme or another protein. In one aspect, the second domain can be a polypeptide and the heterodimer can be a fusion protein. In one aspect, the second domain can be an epitope or a tag. In one aspect, the invention provides homodimers comprising a polypeptide of the invention.

The invention provides immobilized polypeptides having enzyme, structural or binding activity, wherein the polypeptide comprises a polypeptide of the invention, a polypeptide encoded by a nucleic acid of the invention, or a polypeptide comprising a polypeptide of the invention and a second domain. In one aspect, the polypeptide can be immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

The invention provides arrays comprising an immobilized nucleic acid of the invention. The invention provides arrays comprising an antibody of the invention.

The invention provides isolated or recombinant antibodies that specifically bind to a polypeptide of the invention or to a polypeptide encoded by a nucleic acid of the invention. These antibodies of the invention can be a monoclonal or a polyclonal antibody. The invention provides hybridomas comprising an antibody of the invention, e.g., an antibody that specifically binds to a polypeptide of the invention or to a polypeptide encoded by a nucleic acid of the invention. The invention provides nucleic acids encoding these antibodies.

The invention provides method of isolating or identifying a polypeptide having enzyme, structural or binding activity comprising the steps of: (a) providing an antibody of the invention; (b) providing a sample comprising polypeptides; and (c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can

specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having an enzyme, structural or binding activity.

The invention provides methods of making an anti-polypeptide, anti-enzyme, or anti-protein, e.g. anti-structural or anti-binding protein, antibody comprising administering to a non-human animal a nucleic acid of the invention or a polypeptide of the invention or subsequences thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-polypeptide, anti-enzyme, or anti-protein, e.g. anti-structural or anti-binding protein, antibody. The invention provides methods of making an anti-polypeptide, anti-enzyme, or anti-protein, e.g. anti-structural or anti-binding protein, immune comprising administering to a non-human animal a nucleic acid of the invention or a polypeptide of the invention or subsequences thereof in an amount sufficient to generate an immune response.

The invention provides methods of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid of the invention operably linked to a promoter; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide. In one aspect, the method can further comprise transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

The invention provides methods for identifying a polypeptide having enzyme, structural or binding activity comprising the following steps: (a) providing a polypeptide of the invention; or a polypeptide encoded by a nucleic acid of the invention; (b) providing an enzyme, structural or binding activity substrate; and (c) contacting the polypeptide or a fragment or variant thereof of step (a) with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a enzyme, structural or binding activity.

The invention provides methods for identifying a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate comprising the following steps: (a) providing a polypeptide of the invention; or a polypeptide encoded by a nucleic acid of the invention; (b) providing a test substrate; and (c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an

increase in the amount of a reaction product identifies the test substrate as a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate.

The invention provides methods of determining whether a test compound specifically binds to a polypeptide comprising the following steps: (a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid comprises a nucleic acid of the invention, or, providing a polypeptide of the invention; (b) providing a test compound; (c) contacting the polypeptide with the test compound; and (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

The invention provides methods for identifying a modulator of a enzyme, structural or binding activity comprising the following steps: (a) providing a polypeptide of the invention or a polypeptide encoded by a nucleic acid of the invention; (b) providing a test compound; (c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the polypeptide, enzyme, protein, e.g. structural or binding protein, wherein a change in the enzyme, structural or binding activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the enzyme, structural or binding activity. In one aspect, the enzyme, structural or binding activity can be measured by providing a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product. A decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of enzyme, structural or binding activity. An increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of enzyme, structural or binding activity.

The invention provides computer systems comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence of the invention (e.g., a polypeptide encoded by a nucleic acid of the invention). In one aspect, the computer system can further comprise a sequence comparison algorithm and a data storage device having at least one reference sequence

stored thereon. In another aspect, the sequence comparison algorithm comprises a computer program that indicates polymorphisms. In one aspect, the computer system can further comprise an identifier that identifies one or more features in said sequence. The invention provides computer readable media having stored thereon a polypeptide sequence or a nucleic acid sequence of the invention. The invention provides methods for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence of the invention; and (b) identifying one or more features in the sequence with the computer program. The invention provides methods for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence of the invention; and (b) determining differences between the first sequence and the second sequence with the computer program. The step of determining differences between the first sequence and the second sequence can further comprise the step of identifying polymorphisms. In one aspect, the method can further comprise an identifier that identifies one or more features in a sequence. In another aspect, the method can comprise reading the first sequence using a computer program and identifying one or more features in the sequence.

The invention provides methods for isolating or recovering a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, from an environmental sample comprising the steps of: (a) providing an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, wherein the primer pair is capable of amplifying a nucleic acid of the invention; (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and, (c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein from an environmental sample. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising an amplification primer sequence pair of the invention, e.g., having at least about 10 to 50 consecutive bases of a sequence of the invention.

The invention provides methods for isolating or recovering a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein from an environmental sample comprising the steps of: (a) providing a polynucleotide probe comprising a nucleic acid of the invention or a subsequence thereof; (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a); (c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and (d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein from an environmental sample. The environmental sample can comprise a water sample, a liquid sample, a soil sample, an air sample or a biological sample. In one aspect, the biological sample can be derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

The invention provides methods of generating a variant of a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity comprising the steps of: (a) providing a template nucleic acid comprising a nucleic acid of the invention; and (b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid. In one aspect, the method can further comprise expressing the variant nucleic acid to generate a variant the polypeptide, enzyme, protein, e.g. structural or binding protein. The modifications, additions or deletions can be introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR) or a combination thereof. In another aspect, the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

In one aspect, the method can be iteratively repeated until a polypeptide, enzyme, protein, e.g. structural or binding protein having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced. In one aspect, the variant the polypeptide, enzyme, protein, e.g. structural or binding protein is thermotolerant, and retains some activity after being exposed to an elevated temperature. In another aspect, the variant the polypeptide, enzyme, protein, e.g. structural or binding protein has increased glycosylation as compared to the polypeptide, enzyme, protein, e.g. structural or binding protein encoded by a template nucleic acid. Alternatively, the variant the polypeptide, enzyme, protein, e.g. structural or binding protein has an enzyme, structural or binding activity under a high temperature, wherein the polypeptide, enzyme, protein, e.g. structural or binding protein encoded by the template nucleic acid is not active under the high temperature. In one aspect, the method can be iteratively repeated until a polypeptide, enzyme, protein, e.g. structural or binding protein coding sequence having an altered codon usage from that of the template nucleic acid is produced. In another aspect, the method can be iteratively repeated until a polypeptide, enzyme, protein, e.g. structural or binding protein gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity to increase its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention encoding a polypeptide having an enzyme, structural or binding activity; and, (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity; the method comprising the following steps: (a) providing a nucleic acid of the invention; and, (b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity to increase its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, polypeptide; and, (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

The invention provides methods for modifying a codon in a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity to decrease its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention; and (b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell. In one aspect, the host cell can be a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

The invention provides methods for producing a library of nucleic acids encoding a plurality of modified polypeptides, enzymes, proteins, e.g. structural or binding proteins, active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps: (a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a nucleic acid of the invention, and the nucleic acid encodes a polypeptide, enzyme, protein, e.g. structural or binding protein, active site or a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate binding site; (b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and, (c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or

substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified the polypeptide, enzyme, protein, e.g. structural or binding protein, active sites or substrate binding sites. In one aspect, the method comprises mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, and a combination thereof. In another aspect, the method comprises mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

The invention provides methods for making a small molecule comprising the steps of: (a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises an enzyme encoded by a nucleic acid of the invention; (b) providing a substrate for at least one of the enzymes of step (a); and, (c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

The invention provides methods for modifying a small molecule comprising the steps: (a) providing a enzyme encoded by a nucleic acid of the invention; (b) providing a small molecule; and, (c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the enzyme, thereby modifying a small molecule by an enzymatic reaction. In one aspect, the method comprises providing a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the enzyme. In one aspect, the method further comprises a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the

plurality of enzymatic reactions. In one aspect, the method further comprises the step of testing the library to determine if a particular modified small molecule that exhibits a desired activity is present within the library. The step of testing the library can further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

The invention provides methods for determining a functional fragment of a polypeptide, enzyme, protein, e.g. structural or binding protein, comprising the steps of: (a) providing a polypeptide, enzyme, protein, e.g. structural or binding protein, wherein the enzyme comprises a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, or a subsequence thereof; and (b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for an enzyme, structural or binding activity, thereby determining a functional fragment of a polypeptide, enzyme, protein, e.g. structural or binding protein. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein activity is measured by providing a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

The invention provides methods for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps: (a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid of the invention; (b) culturing the modified cell to generate a plurality of modified cells; (c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and, (d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis. In one aspect, the genetic composition of the cell can be modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene. In one aspect, the method can further comprise selecting a cell comprising a newly engineered phenotype. In another aspect,

the method can comprise culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

The invention provides methods of increasing thermotolerance or thermostability of a polypeptide, enzyme, protein, e.g. structural or binding protein, polypeptide, the method comprising glycosylating a polypeptide, enzyme, protein, e.g. structural or binding protein, wherein the polypeptide, enzyme, protein, e.g. structural or binding protein comprises at least thirty contiguous amino acids of a polypeptide of the invention; or a polypeptide encoded by a nucleic acid sequence of the invention, thereby increasing thermotolerance or thermostability of the polypeptide, enzyme, protein, e.g. structural or binding protein. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein specific activity can be thermostable or thermotolerant at a temperature in the range from greater than about 37°C to about 95°C.

The invention provides methods for overexpressing a recombinant polypeptide, enzyme, protein, e.g. structural or binding protein, in a cell comprising expressing a vector comprising a nucleic acid comprising a nucleic acid of the invention or a nucleic acid sequence of the invention, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

The invention provides methods of making a transgenic plant comprising the following steps: (a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a nucleic acid sequence of the invention, thereby producing a transformed plant cell; and (b) producing a transgenic plant from the transformed cell. In one aspect, the step (a) can further comprise introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts. In another aspect, the step (a) can further comprise introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment. Alternatively, the step (a) can further comprise introducing the heterologous nucleic acid sequence into the plant cell DNA using an *Agrobacterium tumefaciens* host. In one aspect, the plant cell can be a potato, corn, rice, wheat, tobacco, or barley cell.

The invention provides methods of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps: (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the

heterologous nucleic sequence comprises a nucleic acid of the invention; (b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell. The invention provides methods of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps: (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence of the invention; (b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

The invention provides feeds or foods comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention. In one aspect, the invention provides a food, feed, a liquid, e.g., a beverage (such as a fruit juice or a beer), a bread or a dough or a bread product, or a beverage precursor (e.g., a wort), comprising a polypeptide of the invention. The invention provides food or nutritional supplements for an animal comprising a polypeptide of the invention, e.g., a polypeptide encoded by the nucleic acid of the invention.

In one aspect, the polypeptide in the food or nutritional supplement can be glycosylated. The invention provides edible enzyme delivery matrices comprising a polypeptide of the invention, e.g., a polypeptide encoded by the nucleic acid of the invention. In one aspect, the delivery matrix comprises a pellet. In one aspect, the polypeptide can be glycosylated. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein activity is thermotolerant. In another aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein activity is thermostable.

The invention provides a food, a feed or a nutritional supplement comprising a polypeptide of the invention. The invention provides methods for utilizing a polypeptide, enzyme, protein, e.g. structural or binding protein, as a nutritional supplement in an animal diet, the method comprising: preparing a nutritional supplement containing a polypeptide, enzyme, protein, e.g. structural or binding protein, comprising at least thirty contiguous amino acids of a polypeptide of the invention; and administering the nutritional supplement to an animal. The animal can be a human, a ruminant or a monogastric animal. The polypeptide, enzyme, protein, e.g. structural or binding protein can be prepared by expression of a polynucleotide encoding the polypeptide, enzyme, protein, e.g. structural or binding protein in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal. The

organism can be selected from the group consisting of an *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

The invention provides edible enzyme delivery matrix comprising thermostable recombinant polypeptide, enzyme, protein, e.g. structural or binding protein of the invention. The invention provides methods for delivering a polypeptide, enzyme, protein, e.g. structural or binding protein, supplement to an animal, the method comprising: preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and thermostable recombinant polypeptide, enzyme, protein, e.g. structural or binding protein, wherein the pellets readily disperse the polypeptide, enzyme, protein, e.g. structural or binding protein contained therein into aqueous media, and administering the edible enzyme delivery matrix to the animal. The recombinant polypeptide, enzyme, protein, e.g. structural or binding protein can comprise a polypeptide of the invention. The polypeptide, enzyme, protein, e.g. structural or binding protein can be glycosylated to provide thermostability at pelletizing conditions. The delivery matrix can be formed by pelletizing a mixture comprising a grain germ and a polypeptide, enzyme, protein, e.g. structural or binding protein. The pelletizing conditions can include application of steam. The pelletizing conditions can comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

In one aspect, invention provides a pharmaceutical composition comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, or a polypeptide encoded by a nucleic acid of the invention. In one aspect, the pharmaceutical composition acts as a digestive aid.

The details of one or more aspects of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

All publications, patents, patent applications, GenBank sequences and ATCC deposits, cited herein are hereby expressly incorporated by reference for all purposes.

BRIEF DESCRIPTION OF DRAWINGS

The following drawings are illustrative of aspects of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

Figure 1 is a block diagram of a computer system.

Figure 2 is a flow diagram illustrating one aspect of a process for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database.

Figure 3 is a flow diagram illustrating one aspect of a process in a computer for determining whether two sequences are homologous.

Figure 4 is a flow diagram illustrating one aspect of an identifier process 300 for detecting the presence of a feature in a sequence.

Like reference symbols in the various drawings indicate like elements.

DETAILED DESCRIPTION

The invention provides isolated and recombinant polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. The polypeptides of the invention, and the polynucleotides encoding the polypeptides of the invention, encompass many classes of enzymes, structural proteins and binding proteins. In one aspect, the enzymes and proteins of the invention comprise, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases, which are more specifically described below. The invention also provides isolated and recombinant polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, having the activities described in Table 1, Table 2 or Table 3, below.

Aldolases

In one aspect, the invention provides aldolases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an aldolase activity, including thermostable and thermotolerant aldolase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. In one aspect, the aldolase activity comprises catalysis of the formation of a carbon-carbon bond. In one aspect, the aldolase activity comprises an aldol condensation. The aldol condensation can have an aldol donor substrate comprising an acetaldehyde and an aldol acceptor substrate comprising an aldehyde. The aldol condensation can yield a

product of a single chirality. In one aspect, the aldolase activity is enantioselective. The aldolase activity can comprise a 2-deoxyribose-5-phosphate aldolase (DERA) activity. The aldolase activity can comprise catalysis of the condensation of acetaldehyde as donor and a 2(R)-hydroxy-3-(hydroxy or mercapto)-propionaldehyde derivative to form a 2-deoxysugar. The aldolase activity can comprise catalysis of the condensation of acetaldehyde as donor and a 2-substituted acetaldehyde acceptor to form a 2,4,6-trideoxyhexose via a 4-substituted-3-hydroxybutanal intermediate. The aldolase activity can comprise catalysis of the generation of chiral aldehydes using two acetaldehydes as substrates. The aldolase activity can comprises enantioselective assembling of chiral β,δ -dihydroxyheptanoic acid side chains. The aldolase activity can comprise enantioselective assembling of the core of [R-(R*,R*)]-2-(4-fluorophenyl)-b,d-dihydroxy-5-(1-methylethyl)-3-phenyl-4-(phenylamino)-carbonyl]-1H-pyrrole-1-heptanoic acid (Atorvastatin, or LIPITOR™), rosuvastatin (CRESTOR™) and/or fluvastatin (LESCOL™). The aldolase activity can comprise, with an oxidation step, synthesis of a 3R,5S-6-chloro-2,4,6-trideoxy-erythro-hexonolactone.

Alpha-galactosidases

In one aspect, the invention provides alpha-galactosidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an alpha-galactosidase activity, including thermostable and thermotolerant alpha-galactosidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

An alpha galactosidase hydrolyses the non-reducing terminal alpha 1-3,4,6 linked galactose from poly- and oligosaccharides. These saccharides are commonly found in legumes and are difficult to digest. As such, alpha-galactosidases can be used as a digestive aid to break down raffinose, stachyose, and verbascose, found in such foods as beans and other gassy foods.

Amidases

In one aspect, the invention provides amidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an amidase activity, including thermostable and thermotolerant amidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the amidases of the invention are used in the removal of arginine, phenylalanine or methionine from the N-terminal end of peptides in peptide or peptidomimetic synthesis. In one aspect, the enzyme of the invention, e.g. an amidase, is selective for the L, or "natural" enantiomer of the amino acid derivatives and is therefore useful for the production of optically active compounds. These reactions can be performed in the presence of the chemically more reactive ester functionality, a step which is very difficult to achieve with nonenzymatic methods. The enzyme is also able to tolerate high temperatures (at least 70° C), and high concentrations of organic solvents (>40% DMSO), both of which cause a disruption of secondary structure in peptides, which enables cleavage of otherwise resistant bonds.

Secondary amidases

In one aspect, the invention provides secondary amidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a secondary amidase activity, including thermostable and thermotolerant secondary amidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Secondary amidases include a variety of useful enzymes including peptidases, proteases, and hydantoinases. This class of enzymes can be used in a range of commercial applications. For example, secondary amidases can be used to: 1) increase flavor in food, in particular cheese (known as enzyme ripened cheese); 2) promote bacterial and fungal killing; 3) modify and de-protect fine chemical intermediates 4) synthesize peptide bonds; 5) and carry out chiral resolutions. Particularly, there is a need in the art for an enzyme capable of hydrolyzing Cephalosporin C.

Amylases

In one aspect, the invention provides amylases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an amylase activity, including thermostable and thermotolerant amylase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the polypeptides of the invention can be used as amylases, for example, alpha amylases or glucoamylases, to catalyze the hydrolysis of starch into sugars. In one aspect, the invention is directed to polypeptides having thermostable

amylase activity, such as alpha amylases or glucoamylase activity, e.g., a 1,4-alpha-D-glucan glucohydrolase activity. In one aspect, the polypeptides of the invention can be used as amylases, for example, alpha amylases or glucoamylases, to catalyze the hydrolysis of starch into sugars, such as glucose. The invention is also directed to nucleic acid constructs, vectors, and host cells comprising the nucleic acid sequences of the invention as well as recombinant methods for producing the polypeptides of the invention. The invention is also directed to the use of amylases of the invention in starch conversion processes, including production of high fructose corn syrup (HFCS), ethanol, dextrose, and dextrose syrups.

Commercially, glucoamylases are used to further hydrolyze cornstarch, which has already been partially hydrolyzed with an alpha-amylase. The glucose produced in this reaction may then be converted to a mixture of glucose and fructose by a glucose isomerase enzyme. This mixture, or one enriched with fructose, is the high fructose corn syrup commercialized throughout the world. In general, starch to fructose processing consists of four steps: liquefaction of granular starch, saccharification of the liquefied starch into dextrose, purification, and isomerization to fructose. The object of a starch liquefaction process is to convert a concentrated suspension of starch polymer granules into a solution of soluble shorter chain length dextrans of low viscosity.

The amylases of the invention can be used in automatic dish wash (ADW) products and laundry detergent. In ADW products, the amylase will function at pH 10-11 and at 45-60°C in the presence of calcium chelators and oxidative conditions. For laundry, activity at pH 9-10 and 40°C in the appropriate detergent matrix will be required. Amylases are also useful in textile desizing, brewing processes, starch modification in the paper and pulp industry and other processes described in the art.

Amylases can be used commercially in the initial stages (liquefaction) of starch processing; in wet corn milling; in alcohol production; as cleaning agents in detergent matrices; in the textile industry for starch desizing; in baking applications; in the beverage industry; in oilfields in drilling processes; in inking of recycled paper and in animal feed. Amylases are also useful in textile desizing, brewing processes, starch modification in the paper and pulp industry and other processes.

Carotenoid pathway enzymes

The invention provides novel enzymes, and the polynucleotides encoding them, involved in carotenoid (such as lycopenes and luteins), astaxanthin and/or isoprenoid synthesis. The invention also provides novel genes in the carotenoid, astaxanthin and

isoprenoid biosynthetic pathways comprising at least one enzyme of the invention. For example, alternative aspects, the invention provides one or more nucleic acid coding sequences (CDSs, or ORFs) encoding all, or at least one, enzyme(s) involved in a desired biosynthetic pathway for carotenoids, astaxanthins and/or isoprenoids. The nucleic acid coding sequence(s) can be expressed through an expression plasmid, vector, engineered virus or any episomal expression system, or, can be integrated into the genome of the host cell. In one aspect, the enzyme(s) involved in the biosynthetic pathway system comprise a novel combination of enzymes. In another aspect, the enzyme(s) involved in the biosynthetic pathway system comprise at least one novel enzyme of the invention – where nucleic acids used in the system encode a novel enzyme of the invention.

Carotenoids are natural pigments which have antioxidant and anti-carcinogenic activity. They are free radical scavengers, and as such, strong antioxidants. Carotenoids have a conjugated backbone structure and are very rigid molecules, having a backbone consisting of 9 to 11 alternating single/double bonds and have very similar electro-optical properties as polyacetylene. Astaxanthins are abundant naturally occurring carotenoids. They contain an internal unit similar to beta-carotene but have two terminal carbonyl and hydroxyl functionalities. These compounds are useful for food and feed supplements, colorants, nutraceuticals, cosmetic and pharmaceutical needs. Isoprenoids are compounds biosynthesized from or containing isoprene (unsaturated branched chain five-carbon hydrocarbon) units, including terpenes, carotenoids, fat soluble vitamins, ubiquinone, rubber, and some steroids. Biosynthetic pathways for carotenoids, astaxanthins and isoprenoids are known; most of these published pathways are derived from one organism or a combination of genes from a few species.

Catalases

In one aspect, the invention provides catalases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a catalase activity, including thermostable and thermotolerant catalase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In processes where hydrogen peroxide is a by-product, catalases of the invention can be used to destroy or detect hydrogen peroxide, e.g., in production of glyoxylic acid and in glucose sensors. Also, in processes where hydrogen peroxide is used as a bleaching or antibacterial agent, catalases of the invention can be used to destroy residual hydrogen peroxide, e.g. in contact lens cleaning, in bleaching steps in pulp and paper

production, and in the pasteurization of dairy products. Further, such catalases of the invention can be used as catalysts for oxidation reactions, e.g. epoxidation and hydroxylation.

Dehalogenases

In one aspect, the invention provides dehalogenases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a dehalogenase activity, including thermostable and thermotolerant dehalogenase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Environmental pollutants consist of a large quantity and variety of chemicals; many of these are toxic, environmental hazards that were designated in 1979 as priority pollutants by the U.S. Environmental Protection Agency. Microbial and enzymatic biodegradation is one method for the elimination of these pollutants. Accordingly, methods have been designed to treat commercial wastes and to bioremediate polluted environments via microbial and related enzymatic processes. Unfortunately, many chemical pollutants are either resistant to microbial degradation or are toxic to potential microbial-degraders when present in high concentrations and certain combinations.

Dehalogenases, e.g. haloalkane dehalogenases, of the invention can cleave carbon-halogen bonds in haloalkanes and halocarboxylic acids by hydrolysis, thus converting them to their corresponding alcohols. This reaction can be used for detoxification involving haloalkanes, such as ethylchloride, methylchloride, and 1,2-dichloroethane (e.g., detoxification of toxic composition, e.g., pesticides, poisons, chemical warfare agents and the like comprising haloalkanes).

The present invention provides a number of dehalogenase enzymes useful in bioremediation having improved enzymatic characteristics. The polynucleotides and polynucleotide products of the invention are useful in, for example, groundwater treatment involving transformed host cells containing a polynucleotide or polypeptide of the invention (e.g., the bacteria *Xanthobacter autotrophicus*) and the haloalkane 1,2-dichloroethane as well as removal of polychlorinated biphenyls (PCB's) from soil sediment.

The haloalkane dehalogenase of the invention are useful in carbon-halide reduction efforts. The enzymes of the invention initiate the degradation of haloalkanes.

Alternatively, host cells containing a dehalogenase polynucleotide or polypeptide of the invention can feed on the haloalkanes and produce the detoxifying enzyme.

Endoglucanases

In one aspect, the invention provides endoglucanases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an endoglucanase activity, including thermostable and thermotolerant endoglucanase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the enzymes of the invention have a glucanase, e.g., an endoglucanase, activity, e.g., catalyzing hydrolysis of internal endo- β -1,4- and/or β -1,3-glucanase linkages. In one aspect, the endoglucanase activity (e.g., endo-1,4-beta-D-glucan 4-glucano hydrolase activity) comprises hydrolysis of 1,4- and/or β -1,3- beta-D-glycosidic linkages in cellulose, cellulose derivatives (e.g., carboxy methyl cellulose and hydroxy ethyl cellulose) lichenin, beta-1,4 bonds in mixed beta-1,3 glucans, such as cereal beta-D-glucans or xyloglucans and other plant material containing cellulosic parts.

Endoglucanases of the invention (e.g., endo-beta-1,4-glucanases, EC 3.2.1.4; endo-beta-1,3(1)-glucanases, EC 3.2.1.6; endo-beta-1,3-glucanases, EC 3.2.1.39) can hydrolyze internal β -1,4- and/or β -1,3- glucosidic linkages in cellulose and glucan to produce smaller molecular weight glucose and glucose oligomers. Glucans are polysaccharides formed from 1,4- β - and/or 1,3-glycoside-linked D-glucopyranose. Endoglucanases of the invention can be used in the food industry, for baking and fruit and vegetable processing, breakdown of agricultural waste, in the manufacture of animal feed, in pulp and paper production, textile manufacture and household and industrial cleaning agents. Endoglucanases are produced by fungi and bacteria.

Beta-glucans are major non-starch polysaccharides of cereals. The glucan content can vary significantly depending on variety and growth conditions. The physicochemical properties of this polysaccharide are such that it gives rise to viscous solutions or even gels under oxidative conditions. In addition glucans have high water-binding capacity. All of these characteristics present problems for several industries including brewing, baking, animal nutrition. In brewing applications, the presence of glucan results in wort filterability and haze formation issues. In baking applications (especially for cookies and crackers), glucans can create sticky doughs that are difficult to machine and reduce biscuit size. In addition, this carbohydrate is implicated in rapid rehydration of the baked

product resulting in loss of crispiness and reduced shelf-life. For monogastric animal feed applications with cereal diets, beta-glucan is a contributing factor to viscosity of gut contents and thereby adversely affects the digestibility of the feed and animal growth rate. For ruminant animals, these beta-glucans represent substantial components of fiber intake and more complete digestion of glucans would facilitate higher feed conversion efficiencies. It is desirable for animal feed endoglucanases to be active in the animal stomach.

Endoglucanases of the invention can be used in the digestion of cellulose, a beta-1,4-linked glucan found in all plant material. Cellulose is the most abundant polysaccharide in nature. Enzymes of the invention that digest cellulose have utility in the pulp and paper industry, in textile manufacture and in household and industrial cleaning agents.

Epoxide hydrolases

In one aspect, the invention provides epoxide hydrolases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an epoxide hydrolase activity, including thermostable and thermotolerant epoxide hydrolase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used as epoxide hydrolases to catalyze the hydrolysis of epoxides and arene oxides to their corresponding diols.

Epoxide hydrolases catalyze the hydrolysis of epoxides and arene oxides to their corresponding diols. Epoxide hydrolases from microbial sources are highly versatile biocatalysts for the asymmetric hydrolysis of epoxides on a preparative scale. Besides kinetic resolution, which furnishes the corresponding vicinal diol and remaining non-hydrolyzed epoxide in nonracemic form, enantioconvergent processes are possible. These are highly attractive as they lead to the formation of a single enantiomeric diol from a racemic oxirane.

Microsomal epoxide hydrolases are biotransformation enzymes that catalyze the conversion of a broad array of xenobiotic epoxide substrates to more polar diol metabolites, see, e.g., Omiecinski (2000) *Toxicol. Lett.* 112-113:365-370. Microsomal epoxide hydrolases catalyze the addition of water to epoxides in a two-step reaction involving initial attack of an active site carboxylate on the oxirane to give an ester

intermediate followed by hydrolysis of the ester. Soluble epoxide hydrolase play a role in the biosynthesis of inflammation mediators.

Epoxide hydrolases of the invention can be used in the detoxification of epoxides or in the biosynthesis of hormones. Additionally, epoxide hydrolases of the invention can efficiently process several substrates, leading to enantiomerically enriched-epoxides (the unreacted enantiomer) and/or to the corresponding vicinal diols.

Esterases

In one aspect, the invention provides esterases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an esterase activity, including thermostable and thermotolerant esterase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Many esterases are known and have been discovered in a broad variety of organisms, including bacteria, yeast and higher animals and plants. A principal example of esterases are the lipases, which are used in the hydrolysis of lipids, acidolysis (replacement of an esterified fatty acid with a free fatty acid) reactions, transesterification (exchange of fatty acids between triglycerides) reactions, and in ester synthesis. The major industrial applications for lipases include: the detergent industry, where they are employed to decompose fatty materials in laundry stains into easily removable hydrophilic substances; the food and beverage industry where they are used in the manufacture of cheese, the ripening and flavoring of cheese, as antistaling agents for bakery products, and in the production of margarine and other spreads with natural butter flavors; in waste systems; and in the pharmaceutical industry where they are used as digestive aids.

Alternatively, esterases of the invention can be used in detergent compositions. In one aspect, the esterase can be a nonsurface-active esterase. In another aspect, the esterase can be a surface-active esterase. The esterase can be formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel form, a paste or a slurry form.

In another aspect, the invention provides fabrics or clothing comprising an esterase of the invention. In another aspect, esterases of the invention are used to treat a lipid-containing fabric.

In another aspect, the invention provides foods and drinks comprising an esterase of the invention. The invention also provides cheeses comprising an esterase of the

invention. Additionally, the invention provides methods for the manufacture of cheese comprising the following steps: (a) providing a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention; (b) providing a cheese precursor; and (c) contacting the polypeptide of step (a) with the precursor of step (b) under condition wherein the esterase can catalyze cheese manufacturing processes. In one aspect, the method can comprise the process of ripening and flavoring of cheese.

In another aspect, the invention provides margarines and spreads comprising an enzyme of the invention. The invention provides methods for production of margarine or other spreads with natural butter flavors comprising the following steps: (a) providing a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention; (b) providing a margarine or a spread precursor; and (c) contacting the polypeptide of step (a) with the precursor of step (b) under condition wherein the esterase can catalyze processes involved in margarine or spread production.

The invention provides methods for treating solid or liquid waste products comprising the following steps: (a) providing a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention; (b) providing a solid or a liquid waste; and (c) contacting the polypeptide of step (a) and the waste of step (b) under conditions wherein the polypeptide can treat the waste. The invention provides solid or liquid waste products comprising a polypeptide of the invention.

The invention provides methods for aiding digestion in a mammal comprising (a) providing a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention; (b) providing a composition comprising a substrate for the polypeptide of step (a); (c) feeding or administering to the mammal the polypeptide of step (a) with a feed or food comprising a substrate for the polypeptide of step (a), thereby helping digestion in the mammal. In one aspect, the mammal is a human.

The invention provides pharmaceutical compositions comprising a polypeptide and/or a nucleic acid of the invention, e.g., a pharmaceutical composition for use as a digestive aid in a mammal comprising a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a

nucleic acid of the invention. In one aspect, the mammal comprises a human. The enzymes of the invention are used in the manufacture of medicaments.

The invention provides bakery products comprising a polypeptide of the invention. The invention provides antistaling agents for bakery products comprising a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention.

The invention provides methods for hydrolyzing, breaking up or disrupting a ester-comprising composition comprising the following steps: (a) providing a polypeptide of the invention having an esterase activity, or a polypeptide encoded by a nucleic acid of the invention; (b) providing a composition comprising a protein; and (c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the esterase hydrolyzes, breaks up or disrupts the ester-comprising composition.

Alternatively, the invention provides methods for liquefying or removing ester-comprising compositions comprising the following steps: (a) providing a polypeptide of the invention having an esterase activity, or a polypeptide encoded by a nucleic acid of the invention; (b) providing a composition comprising a protein; and (c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein esterase removes or liquefies the ester-comprising compositions.

Hydrolases

In one aspect, the invention provides hydrolases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a hydrolase activity, e.g., an esterase, acylase, lipase, phospholipase or protease activity, including thermostable and thermotolerant hydrolase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. The hydrolase activities of the polypeptides and peptides of the invention include esterase activity, lipase activity (hydrolysis of lipids), acidolysis reactions (to replace an esterified fatty acid with a free fatty acid), transesterification reactions (exchange of fatty acids between triglycerides), ester synthesis, ester interchange reactions, phospholipase activity (e.g., phospholipase A, B, C and D activity, patatin activity, lipid acyl hydrolase (LAH) activity) and protease activity (hydrolysis of peptide bonds). The polypeptides of the invention can be used in a variety of pharmaceutical, agricultural and industrial contexts, including the manufacture of cosmetics and nutraceuticals.

In one aspect, the polypeptides of the invention are used in the biocatalytic synthesis of structured lipids (lipids that contain a defined set of fatty acids distributed in a defined manner on the glycerol backbone), including cocoa butter alternatives (CBA), lipids containing poly-unsaturated fatty acids (PUFAs), diacylglycerides, e.g., 1,3-diacylglycerides (DAGs), monoglycerides, e.g., 2-monoglycerides (MAGs) and triacylglycerides (TAGs). In one aspect, the polypeptides of the invention are used to modify oils, such as fish, animal and vegetable oils, and lipids, such as poly-unsaturated fatty acids. The hydrolases of the invention having lipase activity can modify oils by hydrolysis, alcoholysis, esterification, transesterification and/or interesterification. The methods of the invention can use lipases with defined regio-specificity or defined chemoselectivity in biocatalytic synthetic reactions. In another aspect, the polypeptides of the invention are used to synthesize enantiomerically pure chiral products.

Additionally, the polypeptides of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in the photographic industry, medical treatment, silk degumming, biofilm degradation, biomass conversion to ethanol, biodefense, antimicrobial agents and disinfectants, personal care and cosmetics, biotech reagents, in increasing starch yield from corn wet milling and pharmaceuticals such as digestive aids and anti-inflammatory (anti-phlogistic) agents.

The major industrial applications for hydrolases, e.g., esterases, lipases, phospholipases and proteases, include the detergent industry, where they are employed to decompose fatty materials in laundry stains into easily removable hydrophilic substances; the food and beverage industry where they are used in the manufacture of cheese, the ripening and flavoring of cheese, as antistaling agents for bakery products, and in the production of margarine and other spreads with natural butter flavors; in waste systems; and in the pharmaceutical industry where they are used as digestive aids.

Oils and fats are an important renewable raw material for the chemical industry. They are available in large quantities from the processing of oilseeds from plants like rice bran oil, rapeseed (canola), sunflower, olive, palm or soy. Other sources of valuable oils and fats include fish, restaurant waste, and rendered animal fats. These fats and oils are a mixture of triglycerides or lipids, i.e. fatty acids (FAs) esterified on a glycerol scaffold. Each oil or fat contains a wide variety of different lipid structures, defined by the FA content and their regiochemical distribution on the glycerol backbone. These properties of

the individual lipids determine the physical properties of the pure triglyceride. Hence, the triglyceride content of a fat or oil to a large extent determines the physical, chemical and biological properties of the oil. The value of lipids increases greatly as a function of their purity. High purity can be achieved by fractional chromatography or distillation, separating the desired triglyceride from the mixed background of the fat or oil source. However, this is costly and yields are often limited by the low levels at which the triglyceride occurs naturally. In addition, the purity of the product is often compromised by the presence of many structurally and physically or chemically similar triglycerides in the oil.

An alternative to purifying triglycerides or other lipids from a natural source is to synthesize the lipids. The products of such processes are called structured lipids because they contain a defined set of fatty acids distributed in a defined manner on the glycerol backbone. The value of lipids also increases greatly by controlling the fatty acid content and distribution within the lipid. Lipases can be used to affect such control.

Phospholipases are enzymes that hydrolyze the ester bonds of phospholipids. Corresponding to their importance in the metabolism of phospholipids, these enzymes are widespread among prokaryotes and eukaryotes. The phospholipases affect the metabolism, construction and reorganization of biological membranes and are involved in signal cascades. Several types of phospholipases are known which differ in their specificity according to the position of the bond attacked in the phospholipid molecule. Phospholipase A1 (PLA1) removes the 1-position fatty acid to produce free fatty acid and 1-lyso-2-acylphospholipid. Phospholipase A2 (PLA2) removes the 2-position fatty acid to produce free fatty acid and 1-acyl-2-lysophospholipid. PLA1 and PLA2 enzymes can be intra- or extra-cellular, membrane-bound or soluble. Intracellular PLA2 is found in almost every mammalian cell. Phospholipase C (PLC) removes the phosphate moiety to produce 1,2 diacylglycerol and phospho base. Phospholipase D (PLD) produces 1,2-diacylglycerophosphate and base group. PLC and PLD are important in cell function and signaling. Patatins are another type of phospholipase thought to work as a PLA.

In general, enzymes, including hydrolases such as esterases, lipases and proteases, are active over a narrow range of environmental conditions (temperature, pH, etc.), and many are highly specific for particular substrates. The narrow range of activity for a given enzyme limits its applicability and creates a need for a selection of enzymes that (a) have similar activities but are active under different conditions or (b) have different substrates. For instance, an enzyme capable of catalyzing a reaction at 50°C may be so

inefficient at 35°C, that its use at the lower temperature will not be feasible. For this reason, laundry detergents generally contain a selection of proteolytic enzymes (e.g., polypeptides of the invention), allowing the detergent to be used over a broad range of wash temperature and pH. In view of the specificity of enzymes and the growing use of hydrolases in industry, research, and medicine, there is an ongoing need in the art for new enzymes and new enzyme inhibitors.

Glucosidases

In one aspect, the invention provides glucosidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a glucosidase activity, including thermostable and thermotolerant glucosidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Alpha-glucosidases of the invention can catalyze the hydrolysis of starches into sugars. Alpha-glucosidases can hydrolyze terminal non-reducing 1,4 or 1,6 linked α -D-glucose residues in starch, with release of α -D-glucose.

Alpha-glucosidases of the invention can be used commercially in the stages liquefaction and saccharification of starch processing; in wet corn milling; in alcohol production; as cleaning agents in detergent matrices; in the textile industry for starch desizing; in baking applications; in the beverage industry; in oilfields in drilling processes; in inking of recycled paper and in animal feed. Alpha-glucosidases of the invention are also useful in textile desizing, brewing processes, starch modification in the paper and pulp industry and other processes.

Glycosidases

In one aspect, the invention provides glycosidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a glycosidase activity, including thermostable and thermotolerant glycosidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. Glycosidase enzymes of the invention can have more specific activity as glucosidases, α -galactosidases, β -galactosidases, β -mannosidases, β -mannanases, endoglucanases, and pullulanases.

α -galactosidases of the invention can catalyze the hydrolysis of galactose groups on a polysaccharide backbone or hydrolyze the cleavage of di- or oligosaccharides comprising galactose. β -mannanases of the invention can catalyze the hydrolysis of mannose groups internally on a polysaccharide backbone or hydrolyze the cleavage of di- or oligosaccharides comprising mannose groups. β -mannosidases of the invention can hydrolyze non-reducing, terminal mannose residues on a mannose-containing polysaccharide and the cleavage of di- or oligosaccharides comprising mannose groups.

Guar gum is a branched galactomannan polysaccharide composed of β -1, 4 linked mannose backbone with α -1, 6 linked galactose sidechains. The enzymes required for the degradation of guar are β -mannanase, β -mannosidase and α -galactosidase. β -mannanase hydrolyses the mannose backbone internally and β -mannosidase hydrolyses non-reducing, terminal mannose residues. α -galactosidase hydrolyses α -linked galactose groups.

Galactomannan polysaccharides and the enzymes of the invention that degrade them have a variety of applications. Guar is commonly used as a thickening agent in food and is utilized in hydraulic fracturing in oil and gas recovery. Consequently, galactomannanases are industrially relevant for the degradation and modification of guar. Furthermore, a need exists for thermostable galactomannanases that are active in extreme conditions associated with oil drilling and well stimulation.

There are other applications for these enzymes in various industries, such as in the beet sugar industry. 20-30% of the domestic U.S. sucrose consumption is sucrose from sugar beets. Raw beet sugar can contain a small amount of raffinose when the sugar beets are stored before processing and rotting begins to set in. Raffinose inhibits the crystallization of sucrose and also constitutes a hidden quantity of sucrose. Thus, there is merit to eliminating raffinose from raw beet sugar. α -Galactosidase has also been used as a digestive aid to break down raffinose, stachyose, and verbascose in such foods as beans and other gassy foods.

β -Galactosidases of the invention can be used for the production of lactose-free dietary milk products. Additionally, β -galactosidases of the invention can be used for the enzymatic synthesis of oligosaccharides via transglycosylation reactions.

Pullulanase is well known as a debranching enzyme of pullulan and starch. The enzyme of the invention can hydrolyze α -1, 6-glucosidic linkages on these polymers. Starch degradation for the production of sweeteners (glucose or maltose) is a very

important industrial application of this enzyme. The degradation of starch is developed in two stages. The first stage involves the liquefaction of the substrate with α -amylase, and the second stage, or saccharification stage, is performed by β -amylase with pullulanase added as a debranching enzyme, to obtain better yields.

Endoglucanases of the invention can be used in a variety of industrial applications. For instance, the endoglucanases of the invention can hydrolyze the internal β -1, 4-glycosidic bonds in cellulose, which may be used for the conversion of plant biomass into fuels and chemicals. Endoglucanases of the invention also have applications in detergent formulations, the textile industry, in animal feed, in waste treatment, oil drilling and well stimulation, and in the fruit juice and brewing industry for the clarification and extraction of juices.

Inteins

In one aspect, the invention provides inteins, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In another aspect, the invention provides a chimeric protein comprising at least three domains, wherein the first domain comprises at least one enzyme domain or a binding protein domain, the second domain comprises at least one intein domain and a third domain comprising a detectable moiety domain, at least one intein domain is positioned between at least one enzyme or binding protein and at least one detectable moiety domain, and the intein domain has at least one cleavage or splicing activity.

In one aspect, the detectable moiety domain comprises a detectable peptide or polypeptide. The detectable peptide or a polypeptide can be a fluorescent peptide or polypeptide. The detectable peptide or a polypeptide can be a bioluminescent or a chemiluminescent peptide or polypeptide. In one aspect, the bioluminescent or chemiluminescent polypeptide comprises a green fluorescent protein (GFP), an aequorin, an obelin, a mnemiopsin or a berovin. In one aspect, the detectable moiety domain comprises an enzyme that generates a detectable signal. The enzyme that generates a detectable signal can comprise an alpha-galactosidase, an antibiotic (e.g., chloramphenicol acetyltransferase) or a kinase. The detectable moiety domain can comprise a radioactive isotope.

In one aspect, the chimeric protein is a recombinant fusion protein. In one aspect, the intein domain splicing activity results in cleavage of the enzyme domain from the intein domain and detectable domain. The intein domain splicing activity can result in cleavage of the enzyme domain from the intein domain and detectable domain and

cleavage of the detectable domain from the intein domain. In one aspect, the intein domain splicing activity results in cleavage of the detectable domain from the intein domain. In one aspect, the intein domain has only splicing activity. The intein domain can have only cleaving activity.

In one aspect, at least one domain is separated from another domain by a linker. The linker can be a flexible linker. The intein domain can be separated from the detectable moiety domain and the enzyme domain by a linker.

Isomerases

In one aspect, the invention provides isomerases, e.g. xylose isomerases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an isomerase activity, e.g. xylose isomerase activity, including thermostable and thermotolerant isomerase activity, e.g. xylose isomerase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the invention provides xylose isomerase enzymes, polynucleotides encoding the enzymes, methods of making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used in a variety of agricultural and industrial contexts. For example, the polypeptides of the invention can be used for converting glucose to fructose or for manufacturing high content fructose syrups in large quantities. Other examples include use of the polypeptides of the invention in confectionary, brewing, alcohol and soft drinks production, and in diabetic foods and sweeteners.

Laccases

In one aspect, the invention provides laccases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a laccase activity, including thermostable and thermotolerant laccase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the invention provides methods of depolymerizing lignin, e.g., in a pulp or paper manufacturing process, using a polypeptide of the invention. In another aspect, the invention provides methods for oxidizing products that can be mediators of laccase-catalyzed oxidation reactions, e.g., 2,2-azinobis-(3-ethylbenzthiazoline-6-

sulfonate) (ABTS), 1- hydroxybenzotriazole (HBT), 2,2,6,6-tetramethylpiperidin-1-yloxy (TEMPO), dimethoxyphenol, dihydroxyfumaric acid (DHF) and the like.

Laccases are a subclass of the multicopper oxidase super family of enzymes, which includes ascorbate oxidases and the mammalian protein, ceruloplasmin. Laccases are one of the oldest known enzymes and were first implicated in the oxidation of urushiol and laccol. In one aspect, reactions catalyzed by laccases of the invention comprises the oxidation of phenolic substrates. The major target application has been in the delignification of wood fibers during the preparation of pulp.

Lipases

In one aspect, the invention provides lipases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a lipase activity, including thermostable and thermotolerant lipase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the lipases of the invention can be used in a variety of pharmaceutical, agricultural and industrial contexts, including the manufacture of cosmetics and nutraceuticals. In one aspect, the lipases of the invention are used in the biocatalytic synthesis of structured lipids (lipids that contain a defined set of fatty acids distributed in a defined manner on the glycerol backbone), including cocoa butter alternatives (CBA), lipids containing poly-unsaturated fatty acids (PUFAs), diacylglycerides, e.g., 1,3-diacyl glycerides (DAGs), monoglycerides, e.g., 2-monoglycerides (MAGs) and triacylglycerides (TAGs). In one aspect, the polypeptides of the invention are used to modify oils, such as fish, animal and vegetable oils, and lipids, such as poly-unsaturated fatty acids. The lipases of the invention can modify oils by hydrolysis, alcoholysis, esterification, transesterification and/or interesterification. The methods of the invention use lipases with defined regio-specificity or defined chemoselectivity in biocatalytic synthetic reactions. In another aspect, the polypeptides of the invention are used to synthesize enantiomerically pure chiral products.

The invention provides lipase enzymes, polynucleotides encoding the enzymes, methods of making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used in a variety of pharmaceutical, agricultural and industrial contexts, including the manufacture of cosmetics and nutraceuticals. In one aspect, the polypeptides of the invention are used in the biocatalytic synthesis of structured lipids (lipids that contain a defined set of fatty acids distributed in a defined

manner on the glycerol backbone), including cocoa butter alternatives, poly-unsaturated fatty acids (PUFAs), 1,3-diacyl glycerides (DAGs), 2-monoglycerides (MAGs) and triacylglycerides (TAGs), such as 1,3-dipalmitoyl-2-oleoylglycerol (POP), 1,3-distearoyl-2-oleoylglycerol (SOS), 1-palmitoyl-2-oleoyl-3-stearoylglycerol (POS) or 1-oleoyl-2,3-dimyristoylglycerol (OMM), long chain polyunsaturated fatty acids such as arachidonic acid, docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA).

In one aspect, the invention provides synthesis (using lipases of the invention) of a triglyceride mixture composed of POS (Palmitic-Oleic-Stearic), POP (Palmitic-Oleic-Palmitic) and SOS (Stearic-Oleic-Stearic) from glycerol. This synthesis uses free fatty acids versus fatty acid esters. In one aspect, this reaction can be performed in one pot with sequential addition of fatty acids using crude glycerol and free fatty acids and fatty acid esters. In one aspect, stearate and palmitate are mixed together to generate mixtures of DAGs. In one aspect, the diacylglycerides are subsequently acylated with oleate to give components of cocoa butter equivalents. In alternative aspects, the proportions of POS, POP and SOS can be varied according to: stearate to palmitate ratio; selectivity of enzyme for palmitate versus stearate; or enzyme enantioselectivity (could alter levels of POS/SOP). One-pot synthesis of cocoa butter equivalents or other cocoa butter alternatives is possible using this aspect of the invention.

In one aspect, lipases that exhibit regioselectivity and/or chemoselectivity are used in the structure synthesis of lipids or in the processing of lipids. Thus, the methods of the invention use lipases with defined regio-specificity or defined chemoselectivity (e.g., a fatty acid specificity) in a biocatalytic synthetic reaction. For example, the methods of the invention can use lipases with SN1, SN2 and/or SN3 regio-specificity, or combinations thereof. In one aspect, the methods of the invention use lipases that exhibit regioselectivity for the 2-position of a triacylglyceride (TAG). This SN2 regioselectivity can be used in the synthesis of a variety of structured lipids, e.g., triacylglycerides (TAGs), including 1,3-DAGs and components of cocoa butter.

The methods and compositions (lipases) of the invention can be used in the biocatalytic synthesis of structured lipids, and the production of nutraceuticals (e.g., polyunsaturated fatty acids and oils), various foods and food additives (e.g., emulsifiers, fat replacers, margarines and spreads), cosmetics (e.g., emulsifiers, creams), pharmaceuticals and drug delivery agents (e.g., liposomes, tablets, formulations), and animal feed additives (e.g., polyunsaturated fatty acids, such as linoleic acids) comprising

lipids made by the structured synthesis methods of the invention or processed by the methods of the invention

In one aspect, lipases of the invention can act on fluorogenic fatty acid (FA) esters, e.g., umbelliferyl FA esters. In one aspect, profiles of FA specificities of lipases made or modified by the methods of the invention can be obtained by measuring their relative activities on a series of umbelliferyl FA esters, such as palmitate, stearate, oleate, laurate, PUFA, butyrate.

The methods and compositions (lipases) of the invention can be used to synthesize enantiomerically pure chiral products. In one aspect, the methods and compositions (lipases) of the invention can be used to prepare a D-amino acid and corresponding esters from a racemic mix. For example, D-aspartic acid can be prepared from racemic aspartic acid. In one aspect, optically active D-homophenylalanine and/or its esters are prepared. The enantioselectively synthesized D-homophenylalanine can be starting material for many drugs, such as Enalapril, Lisinopril, and Quinapril, used in the treatment of hypertension and congestive heart failure. The D-aspartic acid and its derivatives made by the methods and compositions of the invention can be used in pharmaceuticals, e.g., for the inhibition of argininosuccinate synthetase to prevent or treat sepsis or cytokine-induced systemic hypotension or as immunosuppressive agents. The D-aspartic acid and its derivatives made by the methods and compositions of the invention can be used as taste modifying compositions for foods, e.g., as sweeteners (e.g., ALITAME™). For example, the methods and compositions (lipases) of the invention can be used to synthesize an optical isomer S(+) of 2-(6-methoxy-2-naphthyl) propionic acid from a racemic (R,S) ester of 2-(6-methoxy-2-naphthyl) propionic acid.

In one aspect, the methods and compositions (lipases) of the invention can be used to for stereoselectively hydrolyzing racemic mixtures of esters of 2-substituted acids, e.g., 2-aryloxy substituted acids, such as R-2-(4-hydroxyphenoxy)propionic acid, 2-arylpropionic acid, ketoprofen to synthesize enantiomerically pure chiral products.

The methods and compositions (lipases) of the invention can be used to hydrolyze oils, such as fish, animal and vegetable oils, and lipids, such as poly-unsaturated fatty acids. In one aspect, the polypeptides of the invention are used process fatty acids (such as poly-unsaturated fatty acids), e.g., fish oil fatty acids, for use in or as a feed additive. Addition of poly-unsaturated fatty acids PUFAs to feed for dairy cattle has been demonstrated to result in improved fertility and milk yields. Fish oil contains a high level of PUFAs and therefore is a potentially inexpensive source for PUFAs as a starting

material for the methods of the invention. The biocatalytic methods of the invention can process fish oil under mild conditions, thus avoiding harsh conditions utilized in some processes. Harsh conditions may promote unwanted isomerization, polymerization and oxidation of the PUFAs. In one aspect, the methods of the invention comprise lipase-catalyzed total hydrolysis of fish-oil or selective hydrolysis of PUFAs from fish oil to provide a mild alternative that would leave the high-value PUFAs intact. In one aspect, the methods further comprise hydrolysis of lipids by chemical or physical splitting of the fat.

In one aspect, the lipases and methods of the invention are used for the total hydrolysis of fish oil. Lipases can be screened for their ability to catalyze the total hydrolysis of fish oil under different conditions using. In alternative aspects, a single or multiple lipases are used to catalyze the total splitting of the fish oil. Several lipases of the invention may need to be used, owing to the presence of the PUFAs. In one aspect, a PUFA-specific lipase of the invention is combined with a general lipase to achieve the desired effect.

The methods and compositions (lipases) of the invention can be used to catalyze the partial or total hydrolysis of other oils, e.g. olive oils, that do not contain PUFAs.

The methods and compositions (lipases) of the invention can be used to catalyze the hydrolysis of PUFA glycerol esters. These methods can be used to make feed additives. In one aspect, lipases of the invention catalyze the release of PUFAs from simple esters and fish oil. Standard assays and analytical methods can be utilized.

The methods and compositions (lipases) of the invention can be used to selectively hydrolyze saturated esters over unsaturated esters into acids or alcohols. The methods and compositions (lipases) of the invention can be used to treat latexes for a variety of purposes, e.g., to treat latexes used in hair fixative compositions to remove unpleasant odors. The methods and compositions (lipases) of the invention can be used in the treatment of a lipase deficiency in an animal, e.g., a mammal, such as a human. The methods and compositions (lipases) of the invention can be used to prepare lubricants, such as hydraulic oils. The methods and compositions (lipases) of the invention can be used in making and using detergents. The methods and compositions (lipases) of the invention can be used in processes for the chemical finishing of fabrics, fibers or yarns. In one aspect, the methods and compositions (lipases) of the invention can be used for obtaining flame retardancy in a fabric using, e.g., a halogen-substituted

carboxylic acid or an ester thereof, i.e. a fluorinated, chlorinated or bromated carboxylic acid or an ester thereof.

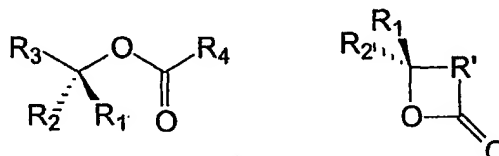
Monooxygenases

In one aspect, the invention provides monooxygenases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a monooxygenase activity, including thermostable and thermotolerant monooxygenase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the monooxygenases of the invention have commercial utility as biocatalysts for use in the synthesis of aromatic and aliphatic esters and their derivatives, such as acids and alcohols. In one aspect, the monooxygenases of the invention are used in the catalysis of sulfoxidation reactions. In one aspect, the invention provides Baeyer-Villiger monooxygenases, polynucleotides encoding the Baeyer-Villiger monooxygenases, and methods of using these Baeyer-Villiger monooxygenases and polynucleotides. In one aspect, the invention provides methods of producing chiral synthetic intermediates using Baeyer-Villiger monooxygenases.

In one aspect, the monooxygenase activity comprises catalysis of sulfoxidation reactions. The monooxygenase activity can comprise an asymmetric sulfoxidation reaction. The monooxygenase activity can be enantiospecific. In one aspect, it can generate a substantially chiral product.

In one aspect, the monooxygenase activity comprises generation of an ester or a lactone having at least one of the following structures:



wherein: R₁, R₂, R₃ and R₄ are each independently selected from -H, substituted or unsubstituted alkyl, alkenyl, alkynyl, aryl, heteroaryl, cycloalkyl, and heterocyclic; wherein the substituted groups are substituted with one or more of lower alkyl, hydroxy, alkoxy, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, and halogen, or two or more of R₁, R₂, R₃ and R₄ may together form cyclic moieties, and, R' is selected from substituted or unsubstituted alkylene, alkenylene, alkynylene, arylene, heteroarylene, cycloalkylene, and heterocyclic; wherein the substitutions are substituted

with one or more of lower alkyl, hydroxy, alkoxy, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, and halogen.

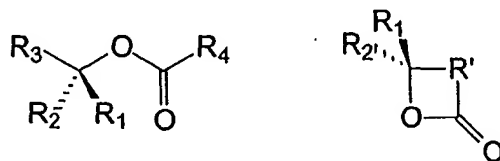
In one aspect, the monooxygenase activity comprises oxidation of a cycloalkanone to produce a chiral lactone. The cycloalkanone can comprise a cyclobutanone, a cyclopentanone, a cyclohexanone, a 2-methylcyclopentanone, a 2-methylcyclohexanone, a cyclohex-2-ene-1-one, a 2-(cyclohex-1-enyl)cyclohexanone, a 1,2-cyclohexanedione, a 1,3-cyclohexanedione or a 1,4-cyclohexanedione.

In one aspect, the monooxygenase activity comprises a chlorophenol 4-monooxygenase activity or a xylene monooxygenase activity.

The invention provides a pharmaceutical composition comprising a polypeptide of the invention.

The invention provides a method for converting a ketone to its corresponding ester comprising contacting the ketone with a polypeptide of the invention under conditions wherein the polypeptide catalyzes the conversion of the ketone to its corresponding ester. In one aspect, the polypeptide has an monooxygenase activity that is enantiospecific to generate a substantially chiral product. In one aspect, the ester is an aromatic or an aliphatic ester.

The invention provides a method for converting a cycloaliphatic ketone to its corresponding lactone comprising contacting the cycloaliphatic ketone with a polypeptide of the invention under conditions wherein the polypeptide catalyzes the conversion of the cycloaliphatic ketone to its corresponding lactone. In one aspect, the polypeptide has an monooxygenase activity that is enantiospecific to generate a substantially chiral product. In one aspect, the ester or lactone has at least one of the following structures:



wherein: R_1 , R_2 , R_3 and R_4 are each independently selected from -H, substituted or unsubstituted alkyl, alkenyl, alkynyl, aryl, heteroaryl, cycloalkyl, and heterocyclic; wherein the substituted groups are substituted with one or more of lower alkyl, hydroxy, alkoxy, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, and halogen, or two or more of R_1 , R_2 , R_3 and R_4 may together form cyclic moieties, and, R' is selected from substituted or unsubstituted alkylene, alkenylene, alkynylene, arylene,

heteroarylene, cycloalkylene, and heterocyclic; wherein the substitutions are substituted with one or more of lower alkyl, hydroxy, alkoxy, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, and halogen.

Nitroreductases

In one aspect, the invention provides nitroreductases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a nitroreductase activity, including thermostable and thermotolerant nitroreductase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Nitroreductases can catalyze the six-electron reduction of nitro compounds to the corresponding amines. Amines have a variety of applications as synthons and advanced pharmaceutical intermediates. There are markets for both aromatic amines and chiral aliphatic amines.

Nitroreductases of the invention fall in to two main classes. These are the oxygen-sensitive and oxygen-insensitive nitroreductases. The oxygen-sensitive enzyme can catalyze nitroreduction only under anaerobic conditions. A nitro anion radical is formed by a one-electron transfer and is immediately reoxidized in the presence of oxygen thus generating a futile cycle whereby reducing equivalents are consumed without nitroreduction. On the other hand the oxygen-insensitive nitroreductases catalyze nitroreduction in a series of two electron transfers, first via the nitroso and then the hydroxylamine intermediates before forming the amine.

Nitrilases

In one aspect, the invention provides nitrilases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a nitrilase activity, including thermostable and thermotolerant nitrilase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Nitrilases of the invention can be used for hydrolyzing a nitrile to a carboxylic acid. In one embodiment, the conditions of the reaction comprise aqueous conditions. In another embodiment, the conditions comprise a pH of about 8.0 and/or a temperature from about 37° C to about 45° C. Nitrilases of the invention can also be used for hydrolyzing a cyanohydrin moiety or an aminonitrile moiety of a molecule.

Alternatively, the nitrilases of the invention can be used for making a chiral α -hydroxy acid molecule, a chiral amino acid molecule, a chiral β -hydroxy acid molecule, or a chiral gamma-hydroxy acid molecule. In one embodiment, the chiral molecule is an (*R*)-enantiomer. In another embodiment, the chiral molecule is an (*S*)-enantiomer. In one embodiment of the invention, one particular enzyme can have R-specificity for one particular substrate and the same enzyme can have S-specificity for a different particular substrate.

In one aspect, nitrilases of the invention can be used for making a composition or an intermediate thereof, wherein the nitrilase of the invention hydrolyzes a cyanohydrin or a aminonitrile moiety. In one embodiment, the composition or intermediate thereof comprises (*S*)-2-amino-4-phenyl butanoic acid. In a further embodiment, the composition or intermediate thereof comprises an L-amino acid. In a further embodiment, the composition comprises a food additive or a pharmaceutical drug.

In another aspect, nitrilases of the invention can be used for making an (*R*)-ethyl 4-cyano-3-hydroxybutyric acid, wherein the nitrilase of the invention acts upon a hydroxyglutaryl nitrile and selectively produces an (*R*)-enantiomer, so as to make (*R*)-ethyl 4-cyano-3-hydroxybutyric acid. In one embodiment, the *ee* is at least 95% or at least 99%. In another embodiment, the hydroxyglutaryl nitrile comprises 1,3-di-cyano-2-hydroxy-propane or 3-hydroxyglutaronitrile.

In another aspect, nitrilases of the invention can be used for making an (*S*)-ethyl 4-cyano-3-hydroxybutyric acid, wherein the nitrilase of the invention acts upon a hydroxyglutaryl nitrile and selectively produces an (*S*)-enantiomer, so as to make (*S*)-ethyl 4-cyano-3-hydroxybutyric acid.

In another aspect, the nitrilases of the invention can be used for making a (*R*)-mandelic acid, wherein the nitrilase of the invention acts upon a mandelonitrile to produce a (*R*)-mandelic acid. In one embodiment, the (*R*)-mandelic acid comprises (*R*)-2-chloromandelic acid. In another embodiment, the (*R*)-mandelic acid comprises an aromatic ring substitution in the *ortho*-, *meta*-, or *para*- positions; a 1-naphthyl derivative of (*R*)-mandelic acid, a pyridyl derivative of (*R*)-mandelic acid or a thienyl derivative of (*R*)-mandelic acid or a combination thereof.

In another aspect, the nitrilases of the invention can be used for making a (*S*)-mandelic acid, wherein the nitrilase of the invention acts upon a mandelonitrile to produce a (*S*)-mandelic acid. In one embodiment, the (*S*)-mandelic acid comprises (*S*)-methyl benzyl cyanide and the mandelonitrile comprises (*S*)-methoxy-benzyl cyanide. In

one embodiment, the (*S*)-mandelic acid comprises an aromatic ring substitution in the *ortho*-, *meta*-, or *para*- positions; a 1-naphthyl derivative of (*S*)-mandelic acid, a pyridyl derivative of (*S*)-mandelic acid or a thienyl derivative of (*S*)-mandelic acid or a combination thereof.

In yet another aspect, the nitrilases of the invention can be used for making a (*S*)-phenyl lactic acid derivative or a (*R*)-phenyllactic acid derivative, wherein the nitrilase of the invention acts upon a phenyllactonitrile and selectively produces an (*S*)-enantiomer or an (*R*)-enantiomer, thereby producing an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyl lactic acid derivative.

P450 enzymes

In one aspect, the invention provides P450 enzymes, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a P450 enzymatic activity, including thermostable and thermotolerant P450 enzymatic activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

P450s are oxidative enzymes that are widespread in nature and polypeptides of the invention having P450 activity can be used in processes such as detoxifying xenobiotics, catabolism of unusual carbon sources and biosynthesis of secondary metabolites (e.g., detoxification of toxic composition, e.g., pesticides, poisons, chemical warfare agents and the like). These oxygenases activate molecular oxygen using an iron-heme center and utilize a redox electron shuttle to support the epoxidation reaction.

In one aspect, the P450 activity comprises a monooxygenation reaction. In one aspect, the P450 activity comprises catalysis of incorporation of oxygen into a substrate. In one aspect, the P450 activity can further comprise hydroxylation of aliphatic or aromatic carbons. In another aspect, the P450 activity can comprise epoxidation. Alternatively, the P450 activity can comprise N-, O-, or S-dealkylation. In one aspect, the P450 activity can comprise dehalogenation. In another aspect the P450 activity can comprise oxidative deamination. Alternatively, the P450 activity can comprise N-oxidation or N-hydroxylation. In one aspect, the P450 activity can comprise sulfoxide formation.

In one aspect, the epoxidase activity further comprises an alkene substrate. The epoxidase activity can further comprise production of a chiral product. In one aspect, the epoxidase activity can be enantioselective.

Pectate lyases

In one aspect, the invention provides pectate lyases, e.g. pectinases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a pectate lyase, e.g. a pectinase activity, including thermostable and thermotolerant pectate lyase, e.g. a pectinase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

The pectate lyases, e.g. pectinases, of the invention can be used to catalyze the beta-elimination or hydrolysis of pectin and/or polygalacturonic acid, such as 1,4-linked alpha-D-galacturonic acid. They can be used in variety of industrial applications, e.g., to treat plant cell walls, such as those in cotton or other natural fibers. In another exemplary industrial application, the polypeptides of the invention can be used in textile scouring.

In one aspect, pectate lyase activity comprises catalysis of beta-elimination (trans-elimination) or hydrolysis of pectin or polygalacturonic acid (pectate). The pectate lyase activity can comprise the breakup or dissolution of plant cell walls. The pectate lyase activity can comprise beta-elimination (trans-elimination) or hydrolysis of 1,4-linked alpha-D-galacturonic acid. The pectate lyase activity can comprise catalysis of beta-elimination (trans-elimination) or hydrolysis of methyl-esterified galacturonic acid. The pectate lyase activity can be exo-acting or endo-acting. In one aspect, the pectate lyase activity is endo-acting and acts at random sites within a polymer chain to give a mixture of oligomers. In one aspect, the pectate lyase activity is exo-acting and acts from one end of a polymer chain and produces monomers or dimers. The pectate lyase activity can catalyze the random cleavage of alpha-1,4-glycosidic linkages in pectic acid (polygalacturonic acid) by trans-elimination or hydrolysis. The pectate lyase activity can comprise activity the same or similar to pectate lyase (EC 4.2.2.2), poly(1,4-alpha-D-galacturonide) lyase, polygalacturonate lyase (EC 4.2.2.2), pectin lyase (EC 4.2.2.10), polygalacturonase (EC 3.2.1.15), exo-polygalacturonase (EC 3.2.1.67), exo-polygalacturonate lyase (EC 4.2.2.9) or exo-poly-alpha-galacturonosidase (EC 3.2.1.82). The pectate lyase activity can comprise beta-elimination (trans-elimination) or hydrolysis of galactan to galactose or galactooligomers. The pectate lyase activity can comprise beta-elimination (trans-elimination) or hydrolysis of a plant fiber. The plant fiber can comprise cotton fiber, hemp fiber or flax fiber.

The pectate lyases, e.g. pectinases, of the invention can be used for hydrolyzing, breaking up or disrupting a pectin- or pectate (polygalacturonic acid)-comprising

composition, for liquefying or removing a pectin or pectate (polygalacturonic acid) from a composition. Alternatively, the pectate lyases, e.g. pectinases, of the invention can be used in detergent compositions. In one aspect, the pectate lyase is a nonsurface-active pectate lyase or a surface-active pectate lyase. The pectate lyase can be formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel form, a paste or a slurry form.

In one aspect, the pectate lyases, e.g. pectinases, of the invention can be used for washing an object. In another aspect, textiles or fabrics comprise a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, wherein the polypeptide has pectate lyase, e.g. pectinase activity. Additionally, the pectate lyases, e.g. pectinases, of the invention can be used for fiber, thread, textile or fabric scouring. In one aspect, the pectate lyase is an alkaline active and thermostable pectate lyase. The desizing and scouring treatments can be combined in a single bath. The method can further comprise addition of an alkaline and thermostable amylase. The desizing or scouring treatments can comprise conditions of between about pH 8.5 to pH 10.0 and temperatures of at about 40°C. The method can further comprise addition of a bleaching step. The desizing, scouring and bleaching treatments can be done simultaneously or sequentially in a single-bath container. The bleaching treatment can comprise hydrogen peroxide or at least one peroxy compound that can generate hydrogen peroxide when dissolved in water, or combinations thereof, and at least one bleach activator. The fiber, thread, textile or fabric can comprise a cellulosic material. The cellulosic material can comprise a crude fiber, a yarn, a woven or knit textile, a cotton, a linen, a flax, a ramie, a rayon, a hemp, a jute or a blend of natural or synthetic fibers.

Alternatively, the pectate lyases, e.g. pectinases, of the invention can be used in feeds or foods. For example, the pectate lyases, e.g. pectinases, of the invention can be used to improve the extraction of oil from an oil-rich plant material. In one aspect, the oil-rich plant material comprises an oil-rich seed. The oil can be a soybean oil, an olive oil, a rapeseed (canola) oil or a sunflower oil.

In another aspect, the pectate lyases, e.g. pectinases, of the invention can be used for preparing a fruit or vegetable juice, syrup, puree or extract. In yet another aspect, the pectate lyases, e.g. pectinases, of the invention can be used for treating a paper or a paper or wood pulp. Alternatively, the invention provides papers or paper products or paper pulps comprising a pectate lyase of the invention, or a polypeptide encoded by a nucleic acid of the invention.

In yet another aspect, the invention provides pharmaceutical compositions comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, wherein the polypeptide has pectate lyase, e.g. pectinase activity. The pharmaceutical composition can act as a digestive aid.

Alternatively, the invention provides oral care products comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, wherein the polypeptide has pectate lyase, e.g. pectinase activity. The oral care product can comprise a toothpaste, a dental cream, a gel or a tooth powder, an odontic, a mouth wash, a pre- or post brushing rinse formulation, a chewing gum, a lozenge or a candy.

Phosphatases

In one aspect, the invention provides phosphatases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a phosphatase activity, including thermostable and thermotolerant phosphatase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Phosphatases are a group of enzymes that remove phosphate groups from organophosphate ester compounds. There are numerous phosphatases, including alkaline phosphatases, phosphodiesterases and phytases.

Alkaline phosphatases are widely distributed enzymes and are composed of a group of enzymes which hydrolyze organic phosphate ester bonds at alkaline pH.

Phosphodiesterases are capable of hydrolyzing nucleic acids by hydrolyzing the phosphodiester bridges of DNA and RNA. The classification of phosphodiesterases depends upon which side of the phosphodiester bridge is attacked. The 3' enzymes specifically hydrolyze the ester linkage between the 3' carbon and the phosphoric group whereas the 5' enzymes hydrolyze the ester linkage between the phosphoric group and the 5' carbon of the phosphodiester bridge. The best known of the class 3' enzymes is a phosphodiesterase from the venom of the rattlesnake or from a rustle's viper, which hydrolyses all the 3' bonds in either RNA or DNA liberating nearly all the nucleotide units as nucleotide 5' phosphates. This enzyme requires a free 3' hydroxyl group on the terminal nucleotide residue and proceeds stepwise from that end of the polynucleotide chain. This enzyme and all other nucleases which attack only at the ends of the polynucleotide chains are called exonucleases. The 5' enzymes are represented by a phosphodiesterase from bovine spleen, also an exonuclease, which hydrolyses all the

5' linkages of both DNA and RNA and thus liberates only nucleoside 3' phosphates. It begins its attack at the end of the chain having a free 3' hydroxyl group.

Phytase enzymes remove phosphate from phytic acid (inositol hexaphosphoric acid), a compound found in plants such as corn, wheat and rice. The enzyme has commercial use for the treatment of animal feed, making the inositol of the phytic acid available for animal nutrition. Phytases are used to improve the utilization of natural phosphorus in animal feed. Use of phytase as a feed additive enables the animal to metabolize a larger degree of its cereal feed's natural mineral content thereby reducing or altogether eliminating the need for synthetic phosphorus additives. More important than the reduced need for phosphorus additives is the corresponding reduction of phosphorus in pig and chicken waste. Many European countries severely limit the amount of manure that can be spread per acre due to concerns regarding phosphorus contamination of ground water.

Alkaline phosphatases hydrolyze monophosphate esters, releasing an organic phosphate and the cognate alcohol compound. It is non-specific with respect to the alcohol moiety and it is this feature which accounts for the many uses of this enzyme.

Phospholipases

In one aspect, the invention provides phospholipases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a phospholipase activity, including thermostable and thermotolerant phospholipase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Phospholipases are enzymes that hydrolyze the ester bonds of phospholipids. Corresponding to their importance in the metabolism of phospholipids, these enzymes are widespread among prokaryotes and eukaryotes. The phospholipases affect the metabolism, construction and reorganization of biological membranes and are involved in signal cascades. Several types of phospholipases are known which differ in their specificity according to the position of the bond attacked in the phospholipid molecule. Phospholipase A1 (PLA1) removes the 1-position fatty acid to produce free fatty acid and 1-lyso-2-acylphospholipid. Phospholipase A2 (PLA2) removes the 2-position fatty acid to produce free fatty acid and 1-acyl-2-lysophospholipid. PLA1 and PLA2 enzymes can be intra- or extra-cellular, membrane-bound or soluble. Intracellular PLA2 is found in almost every mammalian cell. Phospholipase C (PLC) removes the phosphate moiety to

produce 1,2 diacylglycerol and phospho base. Phospholipase D (PLD) produces 1,2-diacylglycerophosphate and base group. PLC and PLD are important in cell function and signaling. PLD had been the dominant phospholipase in biocatalysis. Patatins are another type of phospholipase, thought to work as a PLA.

The invention provides methods for cleaving a glycerolphosphate ester linkage comprising the following steps: (a) providing a polypeptide having a phospholipase activity, wherein the polypeptide comprises an amino acid sequence of the invention, or the polypeptide is encoded by a nucleic acid of the invention; (b) providing a composition comprising a glycerolphosphate ester linkage; and, (c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the polypeptide cleaves the glycerolphosphate ester linkage. In one aspect, the conditions comprise between about pH 5 to about 5.5, or, between about pH 4.5 to about 5.0. In one aspect, the conditions comprise a temperature of between about 40°C and about 70°C. In one aspect, the composition comprises a vegetable oil. In one aspect, the composition comprises an oilseed phospholipid. In one aspect, the cleavage reaction can generate a water extractable phosphorylated base and a diglyceride.

Phospholipases of the invention can be used in oil degumming, wherein the phospholipase is used under conditions wherein the phospholipase can cleave ester linkages in an oil, thereby degumming the oil. In one aspect, the oil is a vegetable oil. In another aspect, the vegetable oil comprises oilseed. The vegetable oil can comprise palm oil, rapeseed oil, corn oil, soybean oil, canola oil, sesame oil, peanut oil or sunflower oil. In one aspect, the method further comprises addition of a phospholipase of the invention, another phospholipase, another enzyme, or a combination thereof.

In another aspect of the invention, phospholipases of the invention can be used for converting a non-hydratable phospholipid to a hydratable form or for caustic refining of a phospholipid-containing composition. In the latter use, the polypeptide of the invention can be added before caustic refining and the composition comprising the phospholipid can comprise a plant and the polypeptide can be expressed transgenically in the plant, the polypeptide having a phospholipase activity can be added during crushing of a seed or other plant part, or, the polypeptide having a phospholipase activity is added following crushing or prior to refining. The polypeptide can be added during caustic refining and varying levels of acid and caustic can be added depending on levels of phosphorous and levels of free fatty acids. The polypeptide can be added after caustic refining: in an

intense mixer or retention mixer prior to separation; following a heating step; in a centrifuge; in a soapstock; in a washwater; or, during bleaching or deodorizing steps.

In yet another aspect, the phospholipases of the invention can be used for purification of a phytosterol or a triterpene. The phytosterol or a triterpene can comprise a plant sterol. The plant sterol can be derived from a vegetable oil. The vegetable oil can comprise a coconut oil, canola oil, cocoa butter oil, corn oil, cottonseed oil, linseed oil, olive oil, palm oil, peanut oil, oil derived from a rice bran, safflower oil, sesame oil, soybean oil or a sunflower oil. The method can comprise use of nonpolar solvents to quantitatively extract free phytosterols and phytosteryl fatty-acid esters. The phytosterol or a triterpene can comprise a β -sitosterol, a campesterol, a stigmasterol, a stigmastanol, a β -sitostanol, a sitostanol, a desmosterol, a chalinasterol, a poriferasterol, a clionasterol or a brassicasterol.

In one embodiment, the phospholipases of the invention can be used for refining a crude oil. The polypeptide can have a phospholipase activity is in a water solution that is added to the composition. The water level can be between about 0.5 to 5%. The process time can be less than about 2 hours, less than about 60 minutes, less than about 30 minutes, less than 15 minutes, or less than 5 minutes. The hydrolysis conditions can comprise a temperature of between about 25°C-70°C. The hydrolysis conditions can comprise use of caustics. The hydrolysis conditions can comprise a pH of between about pH 3 and pH 10, between about pH 4 and pH 9, or between about pH 5 and pH 8. The hydrolysis conditions can comprise addition of emulsifiers and/or mixing after the contacting of step (c). The methods can comprise addition of an emulsion-breaker and/or heat to promote separation of an aqueous phase. The methods can comprise degumming before the contacting step to collect lecithin by centrifugation and then adding a PLC, a PLC and/or a PLA to remove non-hydratable phospholipids. The methods can comprise water degumming of crude oil to less than 10 ppm for edible oils and subsequent physical refining to less than about 50 ppm for biodiesel oils. The methods can comprise addition of acid to promote hydration of non-hydratable phospholipids.

Phytases

In one aspect, the invention provides phytases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a phytase activity, including thermostable and thermotolerant phytase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Conversion of phytate to inositol and inorganic phosphorous can be catalyzed by phytase enzymes. Phytases such as phytase #EC 3.1.3.8 are capable of catalyzing the hydrolysis of myo-inositol hexaphosphate to D-myo-inositol 1,2,4,5,6-pentaphosphate and orthophosphate. Other phytases hydrolyze inositol pentaphosphate to tetra-, tri-, and lower phosphates. Acid phosphatases are enzymes that catalytically hydrolyze a wide variety of phosphate esters. For example, #EC 3.1.3.2 enzymes catalyze the hydrolysis of orthophosphoric monoesters to orthophosphate products.

Phytases of the invention can be used in producing phytase as a feed additive, e.g. for monogastric animals, fish, poultry, ruminants and other non-ruminants. Phytases of the invention can also be used for producing animal feed from certain industrial processes, e.g., wheat and corn waste products. In one aspect, the wet milling process of corn produces glutens sold as animal feeds. The addition of phytase improves the nutritional value of the feed product.

Phytases of the invention may also be used in dietary aids or in pharmaceutical compositions, for reducing pollution and increasing nutrient availability in an environment or environmental sample by degrading environmental phytic acid, for liberating minerals from phytates in plant materials either *in vitro*, i.e., in feed treatment processes, or *in vivo*, i.e., by administering the enzymes to animals.

Polymerases

In one aspect, the invention provides polymerases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a polymerase activity, including thermostable and thermotolerant polymerase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

The polymerase enzymes of the invention can have different polymerase activities at various high temperatures. In one aspect, the polymerase activity comprises addition of deoxynucleotides at the 3' hydroxyl end of a polynucleotide. The invention also provides kits, e.g., diagnostic kits, and methods for performing various amplification reactions, e.g., polymerase chain reactions, transcription amplifications, ligase chain reactions, self-sustained sequence replication or Q Beta replicase amplifications.

In one aspect, the polymerase activity comprises addition of nucleotides at the 3' hydroxyl end of a nucleic acid. The polymerase activity can comprise a 5'→3' polymerase activity, a 3'→5' exonuclease activity or a 5'→3' exonuclease activity or all

or a combination thereof. In one aspect, the polymerase activity comprises only a 5'→3' polymerase activity, but not a 3'→5' exonuclease activity or a 5'→3' exonuclease activity. In another aspect, the polymerase activity can comprise a 5'→3' polymerase activity and a 3'→5' exonuclease activity, but not a 5'→3' exonuclease activity. Alternatively, the polymerase activity can comprise a 5'→3' polymerase activity and a 5'→3' exonuclease activity, but not a 3'→5' exonuclease activity. The polymerase activity can comprise addition of dUTP or dITP. The polymerase activity can comprise addition of a modified or a non-natural nucleotide to a polynucleotide, such as an analog of guanine, cytosine, thymine, adenine or uracil, e.g., a 2-aminopurine, an inosine or a 5-methylcytosine.

In one aspect, the polymerase activity can comprise strand displacement properties. In one aspect, the polymerase activity comprises reverse transcriptase activity.

Proteases

In one aspect, the invention provides proteases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a protease activity, including thermostable and thermotolerant protease activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Proteases of the invention can be carbonyl hydrolases which act to cleave peptide bonds of proteins or peptides. Proteolytic enzymes are ubiquitous in occurrence, found in all living organisms, and are essential for cell growth and differentiation. The extracellular proteases are of commercial value and find multiple applications in various industrial sectors. Industrial applications of proteases include food processing, brewing, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in the photographic industry, medical treatment, silk degumming, biofilm degradation, biomass conversion to ethanol, biodefense, antimicrobial agents and disinfectants, personal care and cosmetics, biotech reagents and in increasing starch yield from corn wet milling. Additionally, proteases are important components of laundry detergents and other products. Within biological research, proteases are used in purification processes to degrade unwanted proteins. It is often desirable to employ proteases of low specificity or mixtures of more specific proteases to obtain the necessary degree of degradation.

Proteases are classified according to their catalytic mechanisms. The International Union of Biochemistry and Molecular Biology (IUBMB) recognizes four mechanistic

classes: (1) the serine proteases; (2) the cysteine proteases; (3) the aspartic proteases; and (4) the metalloproteases. In addition, the IUBMB recognizes a class of endopeptidases (oligopeptidases) of unknown catalytic mechanism. The serine proteases have alkaline pH optima, the metalloproteases are optimally active around neutrality, and the cysteine and aspartic enzymes have acidic pH optima. Serine proteases class comprises two distinct families: the chymotrypsin family, which includes the mammalian enzymes such as chymotrypsin, trypsin, elastase, or kallikrein, and the subtilisin family, which include the bacterial enzymes such as subtilisin. Serine proteases are used for a variety of industrial purposes, such as laundry detergents to aid in the removal of proteinaceous stains. In the food processing industry, serine proteases are used to produce protein-rich concentrates from fish and livestock, and in the preparation of dairy products.

The proteases of the invention can be used in a variety of diagnostic, therapeutic, and industrial contexts. The proteases of the invention can be used as, e.g., an additive for a detergent, for processing foods and for chemical synthesis utilizing a reverse reaction. Additionally, the proteases of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in the photographic industry, medical treatment, silk degumming, biofilm degradation, biomass conversion to ethanol, biodefense, antimicrobial agents and disinfectants, personal care and cosmetics, biotech reagents, in increasing starch yield from corn wet milling and pharmaceuticals such as digestive aids and anti-inflammatory (anti-phlogistic) agents.

Xylanases

In one aspect, the invention provides xylanases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a xylanase activity, including thermostable and thermotolerant xylanase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Xylanases (e.g., endo-1,4-beta-xylanase, EC 3.2.1.8) of the invention can hydrolyze internal β -1,4-xylosidic linkages in xylan to produce smaller molecular weight xylose and xylo-oligomers. Xylans are polysaccharides formed from 1,4- β -glycoside-linked D-xylopyranoses. Xylanases of the invention are of considerable commercial value, being used in the food industry, for baking and fruit and vegetable processing,

breakdown of agricultural waste, in the manufacture of animal feed and in pulp and paper production.

Arabinoxylanase are major non-starch polysaccharides of cereals representing 2.5 – 7.1% w/w depending on variety and growth conditions. The physicochemical properties of this polysaccharide are such that it gives rise to viscous solutions or even gels under oxidative conditions. In addition, arabinoxylans have high water-binding capacity and may have a role in protein foam stability. All of these characteristics present problems for several industries including brewing, baking, animal nutrition and paper manufacturing. In brewing applications, the presence of xylan results in wort filterability and haze formation issues. In baking applications (especially for cookies and crackers), these arabinoxylans create sticky doughs that are difficult to machine and reduce biscuit size. In addition, this carbohydrate is implicated in rapid rehydration of the baked product resulting in loss of crispiness and reduced shelf-life. For monogastric animal feed applications with cereal diets, arabinoxylan is a major contributing factor to viscosity of gut contents and thereby adversely affects the digestibility of the feed and animal growth rate. For ruminant animals, these polysaccharides represent substantial components of fiber intake and more complete digestion of arabinoxylans would facilitate higher feed conversion efficiencies.

Xylanases are currently used as additives (dough conditioners) in dough processing for the hydrolysis of water soluble arabinoxylan. In baking applications (especially for cookies and crackers), arabinoxylan creates sticky doughs that are difficult to machine and reduce biscuit size. In addition, this carbohydrate is implicated in rapid rehydration of the baked product resulting in loss of crispiness and reduced shelf-life.

The enhancement of xylan digestion in animal feed may improve the availability and digestibility of valuable carbohydrate and protein feed nutrients. For monogastric animal feed applications with cereal diets, arabinoxylan is a major contributing factor to viscosity of gut contents and thereby adversely affects the digestibility of the feed and animal growth rate. For ruminant animals, these polysaccharides represent substantial components of fiber intake and more complete digestion would facilitate higher feed conversion efficiencies. It is desirable for animal feed xylanases to be active in the animal stomach. This requires a feed enzyme to have high activity at 37 °C and at low pH for monogastrics (pH 2-4) and near neutral pH for ruminants (pH 6.5-7). The enzyme should also possess resistance to animal gut xylanases and stability at the higher temperatures involved in feed pelleting. As such, there is a need in the art for xylanase

feed additives for monogastric feed with high specific activity, activity at 35-40°C and pH 2-4, half life greater than 30 minutes in SGF and a half-life > 5 minutes at 85°C in formulated state. For ruminant feed, there is a need for xylanase feed additives that have a high specific activity, activity at 35-40°C and pH 6.5-7.0, half life greater than 30 minutes in SRF and stability as a concentrated dry powder.

In one aspect, the xylanases of the invention are also used in improving the quality and quantity of milk protein production in lactating cows, increasing the amount of soluble saccharides in the stomach and small intestine of pigs, improving late egg production efficiency and egg yields in hens. Additionally, xylanases of the inventions can be used in biobleaching and treatment of chemical pulps, biobleaching and treatment of wood or paper pulps, in reducing lignin in wood and modifying wood, as feed additives and/or supplements or in manufacturing cellulose solutions. Detergent compositions comprising xylanases of the invention are used for fruit, vegetables and/or mud and clay compounds.

In another aspect, xylanases of the invention can be used in compositions for the treatments and/or prophylaxis of coccidiosis. In yet another aspect, xylanases of the invention can be used in the production of water soluble dietary fiber, in improving the filterability, separation and production of starch, the beverage industry in improving filterability of wort or beer, in reducing viscosity of plant material, or in increasing viscosity or gel strength of food products such as jam, marmalade, jelly, juice, paste, soup, salsa, etc. Xylanases of the invention may also be used in hydrolysis of hemicellulose for which it is selective, particularly in the presence of cellulose. In addition, xylanases of the invention can also be used in the production of ethanol, in transformation of a microbe that produces ethanol, in production of oenological tannins and enzymatic composition, in stimulating the natural defenses of plants, in production of sugars from hemicellulose substrates, in the cleaning of fruit, vegetables, mud or clay containing soils, in cleaning beer filtration membranes, and in killing or inhibiting microbial cells.

Table 1, below, lists the various EC (Enzyme Commission) Numbers along with the corresponding mode of action for each enzyme class, subclass and sub-subclass. Enzyme nomenclature is based upon the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB). Table 2, below, lists the various EC Numbers along with the corresponding name given to each enzyme class, subclass and sub-subclass. Tables 1 and 2 list exemplary enzymatic

activities of polypeptides of the invention, as can be determined by sequence identity (e.g., homology); and in one embodiment a sequence of the invention comprises an enzyme having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity (homology) to an enzyme encoded by an exemplary sequence of the invention, including all odd numbered SEQ ID NO:1 to SEQ ID NO:26,897, or an exemplary polypeptide of the invention, including all even numbered SEQ ID NO:2 to SEQ ID NO:26,898, and with an exemplary function as listed in Table 1 or Table 2.

Table 3, below, contains the exemplary SEQ ID NO:s of the invention, and the closest hit (BLAST) information for the polynucleotides and polypeptides of the invention. This information includes the closest hit organism, accession number, definition of the closest hit, EC number, percentage amino acid identity and the percent nucleotide identity, along with the Evalue for the closest hits. The information contained in Table 3 identifies exemplary activities of polypeptides of the invention, based on sequence identity (homology). In one embodiment a sequence of the invention comprises an enzyme with at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity (homology) to an enzyme as listed in Table 3.

Table 1: EC (Enzyme Commission) Numbers with the corresponding mode of action for each enzyme class, subclass and sub-subclass

| | |
|---|--|
| 1. -.- Oxidoreductases. | 1. 6. 3.- With a oxygen as acceptor. |
| 1. 1. -.- Acting on the CH-OH group of donors. | 1. 6. 4.- With a disulfide as acceptor. |
| 1. 1. 1.- With NAD(+) or NADP(+) as acceptor. | 1. 6. 5.- With a quinone or similar compound as acceptor. |
| 1. 1. 2.- With a cytochrome as acceptor. | 1. 6. 6.- With a nitrogenous group as acceptor. |
| 1. 1. 3.- With oxygen as acceptor. | 1. 6. 8.- With a flavin as acceptor. |
| 1. 1. 4.- With a disulfide as acceptor. | 1. 6.99.- With other acceptors. |
| 1. 1. 5.- With a quinone or similar compound as acceptor. | 1. 7. -.- Acting on other nitrogenous compounds as donors. |
| 1. 1.99.- With other acceptors. | 1. 7. 1.- With NAD(+) or NADP(+) as acceptor. |
| 1. 2. -.- Acting on the aldehyde or oxo group of donors. | 1. 7. 2.- With a cytochrome as acceptor. |
| 1. 2. 1.- With NAD(+) or NADP(+) as acceptor. | 1. 7. 3.- With oxygen as acceptor. |
| 1. 2. 2.- With a cytochrome as acceptor. | 1. 7. 7.- With an iron-sulfur protein as acceptor. |
| 1. 2. 3.- With oxygen as acceptor. | 1. 7.99.- With other acceptors. |
| 1. 2. 4.- With a disulfide as acceptor. | 1. 8. -.- Acting on a sulfur group of donors. |

| | |
|---|---|
| 1. 2. 7.- With an iron-sulfur protein as acceptor. | 1. 8. 1.- With NAD(+) or NADP(+) as acceptor. |
| 1. 2.99.- With other acceptors. | 1. 8. 2.- With a cytochrome as acceptor. |
| 1. 3. -.- Acting on the CH-CH group of donors. | 1. 8. 3.- With oxygen as acceptor. |
| 1. 3. 1.- With NAD(+) or NADP(+) as acceptor. | 1. 8. 4.- With a disulfide as acceptor. |
| 1. 3. 2.- With a cytochrome as acceptor. | 1. 8. 5.- With a quinone or similar compound as acceptor. |
| 1. 3. 3.- With oxygen as acceptor. | 1. 8. 7.- With an iron-sulfur protein as acceptor. |
| 1. 3. 5.- With a quinone or related compound as acceptor. | 1. 8.98.- With other, known, acceptors. |
| 1. 3. 7.- With an iron-sulfur protein as acceptor. | 1. 8.99.- With other acceptors. |
| 1. 3.99.- With other acceptors. | 1. 9. -.- Acting on a heme group of donors. |
| 1. 4. -.- Acting on the CH-NH(2) group of donors. | 1. 9. 3.- With oxygen as acceptor. |
| 1. 4. 1.- With NAD(+) or NADP(+) as acceptor. | 1. 9. 6.- With a nitrogenous group as acceptor. |
| 1. 4. 2.- With a cytochrome as acceptor. | 1. 9.99.- With other acceptors. |
| 1. 4. 3.- With oxygen as acceptor. | 1.10. -.- Acting on diphenols and related substances as donors. |
| 1. 4. 4.- With a disulfide as acceptor. | 1.10. 1.- With NAD(+) or NADP(+) as acceptor. |
| 1. 4. 7.- With an iron-sulfur protein as acceptor. | 1.10. 2.- With a cytochrome as acceptor. |
| 1. 4.99.- With other acceptors. | 1.10. 3.- With oxygen as acceptor. |
| 1. 5. -.- Acting on the CH-NH group of donors. | 1.10.99.- With other acceptors. |
| 1. 5. 1.- With NAD(+) or NADP(+) as acceptor. | 1.11. -.- Acting on a peroxide as acceptor (peroxidases). |
| 1. 5. 3.- With oxygen as acceptor. | 1.12. -.- Acting on hydrogen as donor. |
| 1. 5. 4.- With a disulfide as acceptor. | 1.12. 1.- With NAD(+) or NADP(+) as acceptor. |
| 1. 5. 5.- With a quinone or similar compound as acceptor. | 1.12. 2.- With a cytochrome as acceptor. |
| 1. 5. 8.- With a flavin as acceptor. | 1.12. 5.- With a quinone or similar compound as acceptor. |
| 1. 5.99.- With other acceptors. | 1.12. 7.- With an iron-sulfur protein as acceptor. |
| 1. 6. -.- Acting on NADH or NADPH. | 1.12.98.- With other known acceptors. |
| 1. 6. 1.- With NAD(+) or NADP(+) as acceptor. | 1.12.99.- With other acceptors. |
| 1. 6. 2.- With a heme protein as acceptor. | 1.13. -.- Acting on single donors with incorporation of molecular oxygen. |

| | |
|---|--|
| 1.13.11.- With incorporation of two atoms of oxygen. | 1.19. 6.- With dinitrogen as acceptor. |
| 1.13.12.- With incorporation of one atom of oxygen. | 1.20. -.- Acting on phosphorus or arsenic in donors. |
| 1.14. -.- Acting on paired donors, with incorporation or reduction of molecular oxygen | 1.20. 1.- Acting on phosphorus or arsenic in donors, with NAD(P)(+) as acceptor |
| 1.14.11.- With 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors | 1.20. 4.- Acting on phosphorus or arsenic in donors, with disulfide as acceptor |
| 1.14.12.- With NADH or NADPH as one donor, and incorporation of two atoms of oxygen into one donor | 1.20.98.- Acting on phosphorus or arsenic in donors, with other, known acceptors |
| 1.14.13.- With NADH or NADPH as one donor, and incorporation of one atom of oxygen | 1.20.99.- Acting on phosphorus or arsenic in donors, with other acceptors |
| 1.14.14.- With reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen | 1.21. -.- Acting on x-H and y-H to form an x-y bond. |
| 1.14.15.- With a reduced iron-sulfur protein as one donor, and incorporation of one atom of oxygen | 1.21. 3.- With oxygen as acceptor. |
| 1.14.16.- With reduced pteridine as one donor, and incorporation of one atom of oxygen | 1.21. 4.- With a disulfide as acceptor. |

| | |
|---|---|
| 1.14.17.- With reduced ascorbate as one donor, and incorporation of one atom of oxygen | 1.21.99.- With other acceptors. |
| 1.14.18.- With another compound as one donor, and incorporation of one incorporation of one atom of oxygen | 1.97. -- Other oxidoreductases. |
| 1.14.19.- With oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water | 2. -- -- Transferases. |
| 1.14.20.- With 2-oxoglutarate as one donor, and the other dehydrogenated. | 2. 1. -- Transferring one-carbon groups. |
| 1.14.21.- With NADH or NADPH as one donor, and the other dehydrogenated. | 2. 1. 1.- Methyltransferases. |
| 1.15. -- Acting on superoxide as acceptor. | 2. 1. 2.- Hydroxymethyl-, formyl- and related transferases. |
| 1.16. -- Oxidizing metal ions. | 2. 1. 3.- Carboxyl- and carbamoyltransferases. |
| 1.16. 1.- With NAD(+) or NADP(+) as acceptor. | 2. 1. 4.- Amidinotransferases. |
| 1.16. 3.- With oxygen as acceptor. | 2. 2. -- Transferring aldehyde or ketone residues. |
| 1.16. 8.- With flavin as acceptor. | 2. 2. 1.- Transketolases and transaldolases. |
| 1.17. -- Acting on CH or CH(2) groups. | 2. 3. -- Acyltransferases. |
| 1.17. 1.- With NAD(+) or NADP(+) as acceptor. | 2. 3. 1.- Transferring groups other than amino-acyl groups. |
| 1.17. 3.- With oxygen as acceptor. | 2. 3. 2.- Aminoacyltransferases. |
| 1.17. 4.- With a disulfide as acceptor. | 2. 3. 3.- Acyl groups converted into alkyl on transfer. |
| 1.17. 5.- With a quinone or similar compound as acceptor | 2. 4. -- Glycosyltransferases. |
| 1.17.99.- With other acceptors. | 2. 4. 1.- Hexosyltransferases. |
| 1.18. -- Acting on iron-sulfur proteins as donors. | 2. 4. 2.- Pentosyltransferases. |
| 1.18. 1.- With NAD(+) or NADP(+) as acceptor. | 2. 4.99.- Transferring other glycosyl groups. |
| 1.18. 6.- With dinitrogen as acceptor. | 2. 5. -- Transferring alkyl or aryl groups, other than methyl groups. |
| 1.18.96.- With other, known, acceptors. | 2. 6. -- Transferring nitrogenous groups. |
| 1.18.99.- With H(+) as acceptor. | 2. 6. 1.- Transaminases (aminotransferases). |
| 1.19. -- Acting on reduced flavodoxin as donor. | 2. 6. 3.- Oximinotransferases. |

| | |
|---|---|
| 2. 6.99.- Transferring other nitrogenous groups. | 3. 1.22.- Endodeoxyribonucleases producing other than 5'-phosphomonoesters. |
| 2. 7. -- Transferring phosphorous-containing groups. | 3. 1.25.- Site-specific endodeoxyribonucleases specific for altered bases. |
| 2. 7. 1.- Phosphotransferases with an alcohol group as acceptor. | 3. 1.26.- Endoribonucleases producing 5'-phosphomonoesters. |
| 2. 7. 2.- Phosphotransferases with a carboxyl group as acceptor. | 3. 1.27.- Endoribonucleases producing other than 5'-phosphomonoesters. |
| 2. 7. 3.- Phosphotransferases with a nitrogenous group as acceptor. | 3. 1.30.- Endoribonucleases active with either ribo- or deoxyribonucleic and producing 5'-phosphomonoesters |
| 2. 7. 4.- Phosphotransferases with a phosphate group as acceptor. | 3. 1.31.- Endoribonucleases active with either ribo- or deoxyribonucleic and producing 3'-phosphomonoesters |
| 2. 7. 6.- Diphosphotransferases. | 3. 2. -- Glycosylases. |
| 2. 7. 7.- Nucleotidyltransferases. | 3. 2. 1.- Glycosidases, i.e. enzymes hydrolyzing O- and S-glycosyl compounds |
| 2. 7. 8.- Transferases for other substituted phosphate groups. | 3. 2. 2.- Hydrolyzing N-glycosyl compounds. |

| | |
|---|--|
| 2. 7. 9.- Phosphotransferases with paired acceptors. | 3. 3. -.- Acting on ether bonds. |
| 2. 8. -.- Transferring sulfur-containing groups. | 3. 3. 1.- Thioether and trialkylsulfonium hydrolases. |
| 2. 8. 1.- Sulfurtransferases. | 3. 3. 2.- Ether hydrolases. |
| 2. 8. 2.- Sulfotransferases. | 3. 4. -.- Acting on peptide bonds (peptide hydrolases). |
| 2. 8. 3.- CoA-transferases. | 3. 4.11.- Aminopeptidases. |
| 2. 8. 4.- Transferring alkylthio groups. | 3. 4.13.- Dipeptidases. |
| 2. 9. -.- Transferring selenium-containing groups. | 3. 4.14.- Dipeptidyl-peptidases and tripeptidyl-peptidases. |
| 2. 9. 1.- Selenotransferases. | 3. 4.15.- Peptidyl-dipeptidases. |
| 3. -.- Hydrolases. | 3. 4.16.- Serine-type carboxypeptidases. |
| 3. 1. -.- Acting on ester bonds. | 3. 4.17.- Metallocoarboxypeptidases. |
| 3. 1. 1.- Carboxylic ester hydrolases. | 3. 4.18.- Cysteine-type carboxypeptidases. |
| 3. 1. 2.- Thiolester hydrolases. | 3. 4.19.- Omega peptidases. |
| 3. 1. 3.- Phosphoric monoester hydrolases. | 3. 4.21.- Serine endopeptidases. |
| 3. 1. 4.- Phosphoric diester hydrolases. | 3. 4.22.- Cysteine endopeptidases. |
| 3. 1. 5.- Triphosphoric monoester hydrolases. | 3. 4.23.- Aspartic endopeptidases. |
| 3. 1. 6.- Sulfuric ester hydrolases. | 3. 4.24.- Metalloendopeptidases. |
| 3. 1. 7.- Diphosphoric monoester hydrolases. | 3. 4.25.- Threonine endopeptidases. |
| 3. 1. 8.- Phosphoric triester hydrolases. | 3. 4.99.- Endopeptidases of unknown catalytic mechanism. |
| 3. 1.11.- Exodeoxyribonucleases producing 5'-phosphomonoesters. | 3. 5. -.- Acting on carbon-nitrogen bonds, other than peptide bonds. |
| 3. 1.13.- Exoribonucleases producing 5'-phosphomonoesters. | 3. 5. 1.- In linear amides. |
| 3. 1.14.- Exoribonucleases producing 3'-phosphomonoesters. | 3. 5. 2.- In cyclic amides. |
| 3. 1.15.- Exonucleases active with either ribo- or deoxyribonucleic acid and producing 5'-phosphomonoesters | 3. 5. 3.- In linear amidines. |
| 3. 1.16.- Exonucleases active with either ribo- or deoxyribonucleic acid producing 3'-phosphomonoesters | 3. 5. 4.- In cyclic amidines. |
| 3. 1.21.- Endodeoxyribonucleases producing 5'-phosphomonoesters. | 3. 5. 5.- In nitriles. |

| | |
|--|---|
| 3. 5.99.- In other compounds. | 5. 3. -.- Intramolecular oxidoreductases. |
| 3. 6. -.- Acting on acid anhydrides. | 5. 3. 1.- Interconverting aldoses and ketoses. |
| 3. 6. 1.- In phosphorous-containing anhydrides. | 5. 3. 2.- Interconverting keto- and enol- groups. |
| 3. 6. 2.- In sulfonyl-containing anhydrides. | 5. 3. 3.- Transposing C=C bonds. |
| 3. 6. 3.- Acting on acid anhydrides; catalyzing transmembrane movement of substances | 5. 3. 4.- Transposing S-S bonds. |
| 3. 6. 4.- Acting on acid anhydrides; involved in cellular and subcellular movement | 5. 3.99.- Other intramolecular oxidoreductases. |
| 3. 6. 5.- Acting on GTP; involved in cellular and subcellular movement. | 5. 4. -.- Intramolecular transferases (mutases). |
| 3. 7. -.- Acting on carbon-carbon bonds. | 5. 4. 1.- Transferring acyl groups. |
| 3. 7. 1.- In ketonic substances. | 5. 4. 2.- Phosphotransferases (phosphomutases). |
| 3. 8. -.- Acting on halide bonds. | 5. 4. 3.- Transferring amino groups. |
| 3. 8. 1.- In C-halide compounds. | 5. 4. 4.- Transferring hydroxy groups. |
| 3. 9. -.- Acting on phosphorus-nitrogen bonds. | 5. 4.99.- Transferring other groups. |
| 3.10. -.- Acting on sulfur-nitrogen bonds. | 5. 5. -.- Intramolecular lyases. |
| 3.11. -.- Acting on carbon-phosphorus bonds. | 5.99. -.- Other isomerases. |
| 3.12. -.- Acting on sulfur-sulfur bonds. | 6. -.- Ligases. |

| | |
|--|---|
| 3.13. -- Acting on carbon-sulfur bonds. | 6. 1. -- Forming carbon-oxygen bonds. |
| 4. -- -- Lyases. | 6. 1. 1.- Ligases forming aminoacyl-tRNA and related compounds. |
| 4. 1. -- Carbon-carbon lyases. | 6. 2. -- Forming carbon-sulfur bonds. |
| 4. 1. 1.- Carboxy-lyases. | 6. 2. 1.- Acid--thiol ligases. |
| 4. 1. 2.- Aldehyde-lyases. | 6. 3. -- Forming carbon-nitrogen bonds. |
| 4. 1. 3.- Oxo-acid-lyases. | 6. 3. 1.- Acid--ammonia (or amide) ligases (amide synthases). |
| 4. 1.99.- Other carbon-carbon lyases. | 6. 3. 2.- Acid--D-amino-acid ligases (peptide synthases). |
| 4. 2. -- Carbon-oxygen lyases. | 6. 3. 3.- Cyclo-ligases. |
| 4. 2. 1.- Hydro-lyases. | 6. 3. 4.- Other carbon--nitrogen ligases. |
| 4. 2. 2.- Acting on polysaccharides. | 6. 3. 5.- Carbon--nitrogen ligases with glutamine as amido-N-donor. |
| 4. 2. 3.- Acting on phosphates. | 6. 4. -- Forming carbon-carbon bonds. |
| 4. 2.99.- Other carbon-oxygen lyases. | 6. 5. -- Forming phosphoric ester bonds. |
| 4. 3. -- Carbon-nitrogen lyases. | 6. 6. -- Forming nitrogen-metal bonds. |
| 4. 3. 1.- Ammonia-lyases. | 6. 6. 1.- Forming nitrogen-metal bonds. |
| 4. 3. 2.- Lyases acting on amides, amidines, etc. | |
| 4. 3. 3.- Amine-lyases. | |
| 4. 3.99.- Other carbon-nitrogen-lyases. | |
| 4. 4. -- Carbon-sulfur lyases. | |
| 4. 5. -- Carbon-halide lyases. | |
| 4. 6. -- Phosphorus-oxygen lyases. | |
| 4.99. -- Other lyases. | |
| 5. -- -- Isomerases. | |
| 5. 1. -- Racemases and epimerases. | |
| 5. 1. 1.- Acting on amino acids and derivatives. | |
| 5. 1. 2.- Acting on hydroxy acids and derivatives. | |
| 5. 1. 3.- Acting on carbohydrates and derivatives. | |
| 5. 1.99.- Acting on other compounds. | |
| 5. 2. -- Cis-trans-isomerases. | |

Table 2: EC Numbers with the corresponding name given to each enzyme class, subclass and sub-subclass.

| | |
|--|---|
| ENZYME: 1. -- -- | 1.1.1.41 Isocitrate dehydrogenase (NAD+). |
| 1.1.1.1 Alcohol dehydrogenase. | 1.1.1.42 Isocitrate dehydrogenase (NADP+). |
| 1.1.1.2 Alcohol dehydrogenase (NADP+). | 1.1.1.43 Phosphogluconate 2-dehydrogenase. |
| 1.1.1.3 Homoserine dehydrogenase. | 1.1.1.44 Phosphogluconate dehydrogenase (decarboxylating). |
| 1.1.1.4 (R,R)-butanediol dehydrogenase. | 1.1.1.45 L-gulonate 3-dehydrogenase. |
| 1.1.1.5 Acetoin dehydrogenase. | 1.1.1.46 L-arabinose 1-dehydrogenase. |
| 1.1.1.6 Glycerol dehydrogenase. | 1.1.1.47 Glucose 1-dehydrogenase. |
| 1.1.1.7 Propanediol-phosphate dehydrogenase. | 1.1.1.48 Galactose 1-dehydrogenase. |
| 1.1.1.8 Glycerol-3-phosphate dehydrogenase (NAD+). | 1.1.1.49 Glucose-6-phosphate 1-dehydrogenase. |
| 1.1.1.9 D-xylulose reductase. | 1.1.1.50 3-alpha-hydroxysteroid dehydrogenase (B-specific). |
| 1.1.1.10 L-xylulose reductase. | 1.1.1.51 3(or 17)beta-hydroxysteroid dehydrogenase. |
| 1.1.1.11 D-arabinitol 4-dehydrogenase. | 1.1.1.52 3-alpha-hydroxycholanate dehydrogenase. |
| 1.1.1.12 L-arabinitol 4-dehydrogenase. | 1.1.1.53 3-alpha(or 20-beta)-hydroxysteroid dehydrogenase. |
| 1.1.1.13 L-arabinitol 2-dehydrogenase. | 1.1.1.54 Allyl-alcohol dehydrogenase. |

| | | | |
|----------|--|----------|---|
| 1.1.1.14 | L-iditol 2-dehydrogenase. | 1.1.1.55 | L-acetaldehyde reductase (NADPH). |
| 1.1.1.15 | D-iditol 2-dehydrogenase. | 1.1.1.56 | Ribitol 2-dehydrogenase. |
| 1.1.1.16 | Galactitol 2-dehydrogenase. | 1.1.1.57 | Fructuronate reductase. |
| 1.1.1.17 | Mannitol-1-phosphate 5-dehydrogenase. | 1.1.1.58 | Tagaturonate reductase. |
| 1.1.1.18 | Inositol 2-dehydrogenase. | 1.1.1.59 | 3-hydroxypropionate dehydrogenase. |
| 1.1.1.19 | L-glucuronate reductase. | 1.1.1.60 | 2-hydroxy-3-oxopropionate reductase. |
| 1.1.1.20 | Glucuronolactone reductase. | 1.1.1.61 | 4-hydroxybutyrate dehydrogenase. |
| 1.1.1.21 | Aldehyde reductase. | 1.1.1.62 | Estradiol 17-beta-dehydrogenase. |
| 1.1.1.22 | UDP-glucose 6-dehydrogenase. | 1.1.1.63 | Testosterone 17-beta-dehydrogenase. |
| 1.1.1.23 | Histidinol dehydrogenase. | 1.1.1.64 | Testosterone 17-beta-dehydrogenase (NADP+). |
| 1.1.1.24 | Quinate dehydrogenase. | 1.1.1.65 | Pyridoxine 4-dehydrogenase. |
| 1.1.1.25 | Shikimate dehydrogenase. | 1.1.1.66 | Omega-hydroxydecanoate dehydrogenase. |
| 1.1.1.26 | Glyoxylate reductase. | 1.1.1.67 | Mannitol 2-dehydrogenase. |
| 1.1.1.27 | L-lactate dehydrogenase. | 1.1.1.69 | Gluconate 5-dehydrogenase. |
| 1.1.1.28 | D-lactate dehydrogenase. | 1.1.1.71 | Alcohol dehydrogenase (NAD(P)+). |
| 1.1.1.29 | Glycerate dehydrogenase. | 1.1.1.72 | Glycerol dehydrogenase (NADP+). |
| 1.1.1.30 | 3-hydroxybutyrate dehydrogenase. | 1.1.1.73 | Octanol dehydrogenase. |
| 1.1.1.31 | 3-hydroxyisobutyrate dehydrogenase. | 1.1.1.75 | (R)-aminopropanol dehydrogenase. |
| 1.1.1.32 | Mevaldate reductase. | 1.1.1.76 | (S,S)-butanediol dehydrogenase. |
| 1.1.1.33 | Mevaldate reductase (NADPH). | 1.1.1.77 | Lactaldehyde reductase. |
| 1.1.1.34 | Hydroxymethylglutaryl-CoA reductase (NADPH). | 1.1.1.78 | D-lactaldehyde dehydrogenase. |
| 1.1.1.35 | 3-hydroxyacyl-CoA dehydrogenase. | 1.1.1.79 | Glyoxylate reductase (NADP+). |
| 1.1.1.36 | Acetoacetyl-CoA reductase. | 1.1.1.80 | Isopropanol dehydrogenase (NADP+). |
| 1.1.1.37 | Malate dehydrogenase. | 1.1.1.81 | Hydroxypyruvate reductase. |
| 1.1.1.38 | Malate dehydrogenase (oxaloacetate-decarboxylating). | 1.1.1.82 | Malate dehydrogenase (NADP+). |
| 1.1.1.39 | Malate dehydrogenase (decarboxylating). | 1.1.1.83 | D-malate dehydrogenase (decarboxylating). |
| 1.1.1.40 | Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+). | 1.1.1.84 | Dimethylmalate dehydrogenase. |

| | | | |
|----------|---|-----------|--|
| 1.1.1.85 | 3-isopropylmalate dehydrogenase. | 1.1.1.127 | 2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase. |
| 1.1.1.86 | Ketol-acid reductoisomerase. | 1.1.1.128 | L-idonate 2-dehydrogenase. |
| 1.1.1.87 | Homoisocitrate dehydrogenase. | 1.1.1.129 | L-threonate 3-dehydrogenase. |
| 1.1.1.88 | Hydroxymethylglutaryl-CoA reductase. | 1.1.1.130 | 3-dehydro-L-gulonate 2-dehydrogenase. |
| 1.1.1.90 | Aryl-alcohol dehydrogenase. | 1.1.1.131 | Mannuronate reductase. |
| 1.1.1.91 | Aryl-alcohol dehydrogenase (NADP+). | 1.1.1.132 | GDP-mannose 6-dehydrogenase. |
| 1.1.1.92 | Oxalglycolate reductase (decarboxylating). | 1.1.1.133 | dTDP-4-dehydrorhamnose reductase. |
| 1.1.1.93 | Tartrate dehydrogenase. | 1.1.1.134 | dTDP-6-deoxy-L-talose 4-dehydrogenase. |
| 1.1.1.94 | Glycerol-3-phosphate dehydrogenase (NAD(P)+). | 1.1.1.135 | GDP-6-deoxy-D-talose 4-dehydrogenase. |
| 1.1.1.95 | Phosphoglycerate dehydrogenase. | 1.1.1.136 | UDP-N-acetylglucosamine 6-dehydrogenase. |
| 1.1.1.96 | Diiodophenylpyruvate reductase. | 1.1.1.137 | Ribitol-5-phosphate 2-dehydrogenase. |
| 1.1.1.97 | 3-hydroxybenzyl-alcohol dehydrogenase. | 1.1.1.138 | Mannitol 2-dehydrogenase (NADP+). |
| 1.1.1.98 | (R)-2-hydroxy-fatty-acid dehydrogenase. | 1.1.1.140 | Sorbitol-6-phosphate 2-dehydrogenase. |

| | |
|--|---|
| 1.1.1.99 (S)-2-hydroxy-fatty-acid dehydrogenase. | 1.1.1.141 15-hydroxyprostaglandin dehydrogenase (NAD+). |
| 1.1.1.100 3-oxoacyl-[acyl-carrier-protein] reductase. | 1.1.1.142 D-pinitol dehydrogenase. |
| 1.1.1.101 Acylglycerone-phosphate reductase. | 1.1.1.143 Sequoyitol dehydrogenase. |
| 1.1.1.102 3-dehydrosphinganine reductase. | 1.1.1.144 Perillyl-alcohol dehydrogenase. |
| 1.1.1.103 L-threonine 3-dehydrogenase. | 1.1.1.145 3-beta-hydroxy-delta(5)-steroid dehydrogenase. |
| 1.1.1.104 4-oxoproline reductase. | 1.1.1.146 11-beta-hydroxysteroid dehydrogenase. |
| 1.1.1.105 Retinol dehydrogenase. | 1.1.1.147 16-alpha-hydroxysteroid dehydrogenase. |
| 1.1.1.106 Pantoate 4-dehydrogenase. | 1.1.1.148 Estradiol 17-alpha-dehydrogenase. |
| 1.1.1.107 Pyridoxal 4-dehydrogenase. | 1.1.1.149 20-alpha-hydroxysteroid dehydrogenase. |
| 1.1.1.108 Carnitine 3-dehydrogenase. | 1.1.1.150 21-hydroxysteroid dehydrogenase (NAD+). |
| 1.1.1.110 Indolelactate dehydrogenase. | 1.1.1.152 3-alpha-hydroxy-5-beta-androstane-17-one 3-alpha-dehydrogenase. |
| 1.1.1.111 3-(imidazol-5-yl)lactate dehydrogenase. | 1.1.1.153 Sepiapterin reductase. |
| 1.1.1.112 Indanol dehydrogenase. | 1.1.1.154 Ureidoglycolate dehydrogenase. |
| 1.1.1.113 L-xylose 1-dehydrogenase. | 1.1.1.155 Homoisocitrate dehydrogenase. |
| 1.1.1.114 Apiose 1-reductase. | 1.1.1.156 Glycerol 2-dehydrogenase (NADP+). |
| 1.1.1.115 Ribose 1-dehydrogenase (NADP+). | 1.1.1.157 3-hydroxybutyryl-CoA dehydrogenase. |
| 1.1.1.116 D-arabinose 1-dehydrogenase. | 1.1.1.158 UDP-N-acetylmuramate dehydrogenase. |
| 1.1.1.117 D-arabinose 1-dehydrogenase (NAD(P)+). | 1.1.1.159 7-alpha-hydroxysteroid dehydrogenase. |
| 1.1.1.118 Glucose 1-dehydrogenase (NAD+). | 1.1.1.160 Dihydrobunolol dehydrogenase. |
| 1.1.1.119 Glucose 1-dehydrogenase (NADP+). | 1.1.1.161 Cholestanetetraol 26-dehydrogenase. |
| 1.1.1.120 Galactose 1-dehydrogenase (NADP+). | 1.1.1.162 Erythrulose reductase. |
| 1.1.1.121 Aldose 1-dehydrogenase. | 1.1.1.163 Cyclopentanol dehydrogenase. |
| 1.1.1.122 D-threo-aldose 1-dehydrogenase. | 1.1.1.164 Hexadecanol dehydrogenase. |
| 1.1.1.123 Sorbose 5-dehydrogenase (NADP+). | 1.1.1.165 2-alkyn-1-ol dehydrogenase. |
| 1.1.1.124 Fructose 5-dehydrogenase (NADP+). | 1.1.1.166 Hydroxycyclohexanecarboxylate dehydrogenase. |
| 1.1.1.125 2-deoxy-D-gluconate 3-dehydrogenase. | 1.1.1.167 Hydroxymalonate dehydrogenase. |
| 1.1.1.126 2-dehydro-3-deoxy-D-gluconate 6-dehydrogenase. | 1.1.1.168 2-dehydropantolactone reductase (A-specific). |

| | |
|---|--|
| 1.1.1.169 2-dehydropantoate 2-reductase. | 1.1.1.207 (-)-menthol dehydrogenase. |
| 1.1.1.170 Sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating). | 1.1.1.208 (+)-neomenthol dehydrogenase. |
| 1.1.1.172 2-oxoadipate reductase. | 1.1.1.209 3(or 17)-alpha-hydroxysteroid dehydrogenase. |
| 1.1.1.173 L-rhamnose 1-dehydrogenase. | 1.1.1.210 3-beta(or 20-alpha)-hydroxysteroid dehydrogenase. |
| 1.1.1.174 Cyclohexane-1,2-diol dehydrogenase. | 1.1.1.211 Long-chain-3-hydroxyacyl-CoA dehydrogenase. |
| 1.1.1.175 D-xylose 1-dehydrogenase. | 1.1.1.212 3-oxoacyl-[acyl-carrier-protein] reductase (NADH). |
| 1.1.1.176 12-alpha-hydroxysteroid dehydrogenase. | 1.1.1.213 3-alpha-hydroxysteroid dehydrogenase (A-specific). |
| 1.1.1.177 Glycerol-3-phosphate 1-dehydrogenase (NADP+). | 1.1.1.214 2-dehydropantolactone reductase (B-specific). |
| 1.1.1.178 3-hydroxy-2-methylbutyryl-CoA dehydrogenase. | 1.1.1.215 Gluconate 2-dehydrogenase. |
| 1.1.1.179 D-xylose 1-dehydrogenase (NADP+). | 1.1.1.216 Farnesol dehydrogenase. |

| | |
|---|--|
| 1.1.1.181 Cholest-5-ene-3-beta,7-alpha-diol 3-beta-dehydrogenase. | 1.1.1.217 Benzyl-2-methyl-hydroxybutyrate dehydrogenase. |
| 1.1.1.183 Geraniol dehydrogenase. | 1.1.1.218 Morphine 6-dehydrogenase. |
| 1.1.1.184 Carbonyl reductase (NADPH). | 1.1.1.219 Dihydrokaempferol 4-reductase. |
| 1.1.1.185 L-glycol dehydrogenase. | 1.1.1.220 6-pyruvoyltetrahydropterin 2'-reductase. |
| 1.1.1.186 dTDP-galactose 6-dehydrogenase. | 1.1.1.221 Vomifoliol 4'-dehydrogenase. |
| 1.1.1.187 GDP-4-dehydro-D-rhamnose reductase. | 1.1.1.222 (R)-4-hydroxyphenyllactate dehydrogenase. |
| 1.1.1.188 Prostaglandin-F synthase. | 1.1.1.223 Isopiperitenol dehydrogenase. |
| 1.1.1.189 Prostaglandin-E(2) 9-reductase. | 1.1.1.224 Mannose-6-phosphate 6-reductase. |
| 1.1.1.190 Indole-3-acetaldehyde reductase (NADH). | 1.1.1.225 Chlordecone reductase. |
| 1.1.1.191 Indole-3-acetaldehyde reductase (NADPH). | 1.1.1.226 4-hydroxycyclohexanecarboxylate dehydrogenase. |
| 1.1.1.192 Long-chain-alcohol dehydrogenase. | 1.1.1.227 (-)-borneol dehydrogenase. |
| 1.1.1.193 5-amino-6-(5-phosphoribosylamino)uracil reductase. | 1.1.1.228 (+)-sabinol dehydrogenase. |
| 1.1.1.194 Coniferyl-alcohol dehydrogenase. | 1.1.1.229 Diethyl 2-methyl-3-oxosuccinate reductase. |
| 1.1.1.195 Cinnamyl-alcohol dehydrogenase. | 1.1.1.230 3-alpha-hydroxyglycyrrhetinate dehydrogenase. |
| 1.1.1.196 15-hydroxyprostaglandin-D dehydrogenase (NADP+). | 1.1.1.231 15-hydroxyprostaglandin-I dehydrogenase (NADP+). |
| 1.1.1.197 15-hydroxyprostaglandin dehydrogenase (NADP+). | 1.1.1.232 15-hydroxyicosatetraenoate dehydrogenase. |
| 1.1.1.198 (+)-borneol dehydrogenase. | 1.1.1.233 N-acylmannosamine 1-dehydrogenase. |
| 1.1.1.199 (S)-usnate reductase. | 1.1.1.234 Flavanone 4-reductase. |
| 1.1.1.200 Aldose-6-phosphate reductase (NADPH). | 1.1.1.235 8-oxocofomycin reductase. |
| 1.1.1.201 7-beta-hydroxysteroid dehydrogenase (NADP+). | 1.1.1.236 Tropinone reductase. |
| 1.1.1.202 1,3-propanediol dehydrogenase. | 1.1.1.237 Hydroxyphenylpyruvate reductase. |
| 1.1.1.203 Uronate dehydrogenase. | 1.1.1.238 12-beta-hydroxysteroid dehydrogenase. |
| 1.1.1.205 IMP dehydrogenase. | 1.1.1.239 3-alpha-(17-beta)-hydroxysteroid dehydrogenase (NAD+). |
| 1.1.1.206 Tropine dehydrogenase. | 1.1.1.240 N-acetylhexosamine 1-dehydrogenase. |

| | |
|---|--|
| 1.1.1.241 6-endo-hydroxycineole dehydrogenase. | 1.1.1.281 GDP-4-dehydro-6-deoxy-D-mannose reductase. |
| 1.1.1.243 Carveol dehydrogenase. | 1.1.1.282 Quinate/shikimate dehydrogenase. |
| 1.1.1.244 Methanol dehydrogenase. | 1.1.2.2 Mannitol dehydrogenase (cytochrome). |
| 1.1.1.245 Cyclohexanol dehydrogenase. | 1.1.2.3 L-lactate dehydrogenase (cytochrome). |
| 1.1.1.246 Pterocarpin synthase. | 1.1.2.4 D-lactate dehydrogenase (cytochrome). |
| 1.1.1.247 Codeinone reductase (NADPH). | 1.1.2.5 D-lactate dehydrogenase (cytochrome c-553). |
| 1.1.1.248 Salutaridine reductase (NADPH). | 1.1.3.3 Malate oxidase. |
| 1.1.1.250 D-arabinitol 2-dehydrogenase. | 1.1.3.4 Glucose oxidase. |
| 1.1.1.251 Galactitol-1-phosphate 5-dehydrogenase. | 1.1.3.5 Hexose oxidase. |
| 1.1.1.252 Tetrahydroxynaphthalene reductase. | 1.1.3.6 Cholesterol oxidase. |
| 1.1.1.254 (S)-carnitine 3-dehydrogenase. | 1.1.3.7 Aryl-alcohol oxidase. |
| 1.1.1.255 Mannitol dehydrogenase. | 1.1.3.8 L-gulonolactone oxidase. |
| 1.1.1.256 Fluoren-9-ol dehydrogenase. | 1.1.3.9 Galactose oxidase. |

| | |
|--|--|
| 1.1.1.257 4-(hydroxymethyl)benzenesulfonate dehydrogenase. | 1.1.3.10 Pyranose oxidase. |
| 1.1.1.258 6-hydroxyhexanoate dehydrogenase. | 1.1.3.11 L-sorbose oxidase. |
| 1.1.1.259 3-hydroxypimeloyl-CoA dehydrogenase. | 1.1.3.12 Pyridoxine 4-oxidase. |
| 1.1.1.260 Sulcatone reductase. | 1.1.3.13 Alcohol oxidase. |
| 1.1.1.261 Glycerol-1-phosphate dehydrogenase (NAD(P) ⁺). | 1.1.3.14 Catechol oxidase (dimerizing). |
| 1.1.1.262 4-hydroxythreonine-4-phosphate dehydrogenase. | 1.1.3.15 (S)-2-hydroxy-acid oxidase. |
| 1.1.1.263 1,5-anhydro-D-fructose reductase. | 1.1.3.16 Ecdysone oxidase. |
| 1.1.1.264 L-idonate 5-dehydrogenase. | 1.1.3.17 Choline oxidase. |
| 1.1.1.265 3-methylbutanal reductase. | 1.1.3.18 Secondary-alcohol oxidase. |
| 1.1.1.266 dTDP-4-dehydro-6-deoxyglucose reductase. | 1.1.3.19 4-hydroxymandelate oxidase. |
| 1.1.1.267 1-deoxy-D-xylulose-5-phosphate reductoisomerase. | 1.1.3.20 Long-chain-alcohol oxidase. |
| 1.1.1.268 2-(R)-hydroxypropyl-CoM dehydrogenase. | 1.1.3.21 Glycerol-3-phosphate oxidase. |
| 1.1.1.269 2-(S)-hydroxypropyl-CoM dehydrogenase. | 1.1.3.23 Thiamine oxidase. |
| 1.1.1.270 3-keto-steroid reductase. | 1.1.3.24 L-galactonolactone oxidase. |
| 1.1.1.271 GDP-L-fucose synthase. | 1.1.3.25 Cellobiose oxidase. |
| 1.1.1.272 (R)-2-hydroxyacid dehydrogenase. | 1.1.3.27 Hydroxyphytanate oxidase. |
| 1.1.1.273 Vellosimine dehydrogenase. | 1.1.3.28 Nucleoside oxidase. |
| 1.1.1.274 2,5-didehydrogluconate reductase. | 1.1.3.29 N-acylhexosamine oxidase. |
| 1.1.1.275 (+)-trans-carveol dehydrogenase. | 1.1.3.30 Polyvinyl-alcohol oxidase. |
| 1.1.1.276 Serine 3-dehydrogenase. | 1.1.3.37 D-arabinono-1,4-lactone oxidase. |
| 1.1.1.277 3-beta-hydroxy-5-beta-steroid dehydrogenase. | 1.1.3.38 Vanillyl-alcohol oxidase. |
| 1.1.1.278 3-beta-hydroxy-5-alpha-steroid dehydrogenase. | 1.1.3.39 Nucleoside oxidase (H ₂ O(2)-forming). |
| 1.1.1.279 (R)-3-hydroxyacid-ester dehydrogenase. | 1.1.3.40 D-mannitol oxidase. |
| 1.1.1.280 (S)-3-hydroxyacid-ester dehydrogenase. | 1.1.3.41 Xylitol oxidase. |

| | |
|---|---|
| 1.1.4.1 Vitamin-K-epoxide reductase (warfarin-sensitive). | 1.2.1.8 Betaine-aldehyde dehydrogenase. |
| 1.1.4.2 Vitamin-K-epoxide reductase (warfarin-insensitive). | 1.2.1.9 Glyceraldehyde-3-phosphate dehydrogenase (NADP ⁺). |
| 1.1.5.2 Quinoprotein glucose dehydrogenase. | 1.2.1.10 Acetaldehyde dehydrogenase (acetylating). |
| 1.1.99.1 Choline dehydrogenase. | 1.2.1.11 Aspartate-semialdehyde dehydrogenase. |
| 1.1.99.2 2-hydroxyglutarate dehydrogenase. | 1.2.1.12 Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating). |
| 1.1.99.3 Gluconate 2-dehydrogenase (acceptor). | 1.2.1.13 Glyceraldehyde-3-phosphate dehydrogenase (NADP ⁺) (phosphorylating). |
| 1.1.99.4 Dehydrogluconate dehydrogenase. | 1.2.1.15 Malonate-semialdehyde dehydrogenase. |
| 1.1.99.5 Glycerol-3-phosphate dehydrogenase. | 1.2.1.16 Succinate-semialdehyde dehydrogenase (NAD(P) ⁺). |
| 1.1.99.6 D-2-hydroxy-acid dehydrogenase. | 1.2.1.17 Glyoxylate dehydrogenase (acylating). |
| 1.1.99.7 Lactate--malate transhydrogenase. | 1.2.1.18 Malonate-semialdehyde dehydrogenase (acetylating). |
| 1.1.99.8 Alcohol dehydrogenase (acceptor). | 1.2.1.19 Aminobutyraldehyde dehydrogenase. |
| 1.1.99.9 Pyridoxine 5-dehydrogenase. | 1.2.1.20 Glutarate-semialdehyde dehydrogenase. |
| 1.1.99.10 Glucose dehydrogenase (acceptor). | 1.2.1.21 Glycolaldehyde dehydrogenase. |

| | |
|--|---|
| 1.1.99.11 Fructose 5-dehydrogenase. | 1.2.1.22 Lactaldehyde dehydrogenase. |
| 1.1.99.12 Sorbose dehydrogenase. | 1.2.1.23 2-oxoaldehyde dehydrogenase (NAD+). |
| 1.1.99.13 Glucoside 3-dehydrogenase. | 1.2.1.24 Succinate-semialdehyde dehydrogenase. |
| 1.1.99.14 Glycolate dehydrogenase. | 1.2.1.25 2-oxoisovalerate dehydrogenase (acylating). |
| 1.1.99.16 Malate dehydrogenase (acceptor). | 1.2.1.26 2,5-dioxovalerate dehydrogenase. |
| 1.1.99.18 Cellobiose dehydrogenase (acceptor). | 1.2.1.27 Methylmalonate-semialdehyde dehydrogenase (acylating). |
| 1.1.99.19 Uracil dehydrogenase. | 1.2.1.28 Benzaldehyde dehydrogenase (NAD+). |
| 1.1.99.20 Alkan-1-ol dehydrogenase (acceptor). | 1.2.1.29 Aryl-aldehyde dehydrogenase. |
| 1.1.99.21 D-sorbitol dehydrogenase (acceptor). | 1.2.1.30 Aryl-aldehyde dehydrogenase (NADP+). |
| 1.1.99.22 Glycerol dehydrogenase (acceptor). | 1.2.1.31 L-aminoadipate-semialdehyde dehydrogenase. |
| 1.1.99.23 Polyvinyl-alcohol dehydrogenase (acceptor). | 1.2.1.32 Aminomuconate-semialdehyde dehydrogenase. |
| 1.1.99.24 Hydroxyacid-oxoacid transhydrogenase. | 1.2.1.33 (R)-dehydropantoate dehydrogenase. |
| 1.1.99.25 Quinate dehydrogenase (pyrroloquinoline-quinone). | 1.2.1.36 Retinal dehydrogenase. |
| 1.1.99.26 3-hydroxycyclohexanone dehydrogenase. | 1.2.1.38 N-acetyl-gamma-glutamyl-phosphate reductase. |
| 1.1.99.27 (R)-pantolactone dehydrogenase (flavin). | 1.2.1.39 Phenylacetaldehyde dehydrogenase. |
| 1.1.99.28 Glucose--fructose oxidoreductase. | 1.2.1.40 3-alpha,7-alpha,12-alpha-trihydroxycholestan-26-al 26-oxidoreductase. |
| 1.1.99.29 Pyranose dehydrogenase (acceptor). | 1.2.1.41 Glutamate-5-semialdehyde dehydrogenase. |
| 1.1.99.30 2-oxo-acid reductase. | 1.2.1.42 Hexadecanal dehydrogenase (acylating). |
| 1.2.1.1 Formaldehyde dehydrogenase (glutathione). | 1.2.1.43 Formate dehydrogenase (NADP+). |
| 1.2.1.2 Formate dehydrogenase. | 1.2.1.44 Cinnamoyl-CoA reductase. |
| 1.2.1.3 Aldehyde dehydrogenase (NAD+). | 1.2.1.45 4-carboxy-2-hydroxymuconate-6-semialdehyde dehydrogenase. |
| 1.2.1.4 Aldehyde dehydrogenase (NADP+). | 1.2.1.46 Formaldehyde dehydrogenase. |
| 1.2.1.5 Aldehyde dehydrogenase (NAD(P)+). | 1.2.1.47 4-trimethylammoniumbutyraldehyde dehydrogenase. |
| 1.2.1.7 Benzaldehyde dehydrogenase (NADP+). | 1.2.1.48 Long-chain-aldehyde dehydrogenase. |
| 1.2.1.49 2-oxoaldehyde dehydrogenase (NADP+). | 1.2.4.4 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring). |
| 1.2.1.50 Long-chain-fatty-acyl-CoA reductase. | 1.2.7.1 Pyruvate synthase. |
| 1.2.1.51 Pyruvate dehydrogenase (NADP+). | 1.2.7.2 2-oxobutyrate synthase. |
| 1.2.1.52 Oxoglutarate dehydrogenase (NADP+). | 1.2.7.3 2-oxoglutarate synthase. |
| 1.2.1.53 4-hydroxyphenylacetaldehyde dehydrogenase. | 1.2.7.4 Carbon-monoxide dehydrogenase (ferredoxin). |
| 1.2.1.54 Gamma-guanidinobutyraldehyde dehydrogenase. | 1.2.7.5 Aldehyde ferredoxin oxidoreductase. |
| 1.2.1.57 Butanal dehydrogenase. | 1.2.7.6 Glyceraldehyde-3-phosphate dehydrogenase (ferredoxin). |
| 1.2.1.58 Phenylglyoxylate dehydrogenase (acylating). | 1.2.7.7 3-methyl-2-oxobutanoate dehydrogenase (ferredoxin). |
| 1.2.1.59 Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)(+)) (phosphorylating). | 1.2.7.8 Indolepyruvate ferredoxin oxidoreductase. |
| 1.2.1.60 5-carboxymethyl-2-hydroxymuconic-semialdehyde dehydrogenase. | 1.2.7.9 2-oxoglutarate ferredoxin oxidoreductase. |
| 1.2.1.61 4-hydroxymuconic-semialdehyde dehydrogenase. | 1.2.99.2 Carbon-monoxide dehydrogenase (acceptor). |

| | |
|---|--|
| 1.2.1.62 4-formylbenzenesulfonate dehydrogenase. | 1.2.99.3 Aldehyde dehydrogenase (pyrroloquinoline-quinone). |
| 1.2.1.63 6-oxohexanoate dehydrogenase. | 1.2.99.4 Formaldehyde dismutase. |
| 1.2.1.64 4-hydroxybenzaldehyde dehydrogenase. | 1.2.99.5 Formylmethanofuran dehydrogenase. |
| 1.2.1.65 Salicylaldehyde dehydrogenase. | 1.2.99.6 Carboxylate reductase. |
| 1.2.1.66 Mycothiol-dependent formaldehyde dehydrogenase. | 1.2.99.7 Aldehyde dehydrogenase (FAD-independent). |
| 1.2.1.67 Vanillin dehydrogenase. | 1.3.1.1 Dihydrouracil dehydrogenase (NAD ⁺). |
| 1.2.1.68 Coniferyl-aldehyde dehydrogenase. | 1.3.1.2 Dihydropyrimidine dehydrogenase (NADP ⁺). |
| 1.2.1.69 Fluoroacetaldehyde dehydrogenase. | 1.3.1.3 Cortisone beta-reductase. |
| 1.2.2.1 Formate dehydrogenase (cytochrome). | 1.3.1.4 Cortisone alpha-reductase. |
| 1.2.2.2 Pyruvate dehydrogenase (cytochrome). | 1.3.1.5 Cucurbitacin delta(23)-reductase. |
| 1.2.2.3 Formate dehydrogenase (cytochrome c-553). | 1.3.1.6 Fumarate reductase (NADH). |
| 1.2.2.4 Carbon-monoxide dehydrogenase (cytochrome b-561). | 1.3.1.7 Meso-tartrate dehydrogenase. |
| 1.2.3.1 Aldehyde oxidase. | 1.3.1.8 Acyl-CoA dehydrogenase (NADP ⁺). |
| 1.2.3.3 Pyruvate oxidase. | 1.3.1.9 Enoyl-[acyl-carrier-protein] reductase (NADH). |
| 1.2.3.4 Oxalate oxidase. | 1.3.1.10 Enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific). |
| 1.2.3.5 Glyoxylate oxidase. | 1.3.1.11 2-coumarate reductase. |
| 1.2.3.6 Pyruvate oxidase (CoA-acetylating). | 1.3.1.12 Prephenate dehydrogenase. |
| 1.2.3.7 Indole-3-acetaldehyde oxidase. | 1.3.1.13 Prephenate dehydrogenase (NADP ⁺). |
| 1.2.3.8 Pyridoxal oxidase. | 1.3.1.14 Orotate reductase (NADH). |
| 1.2.3.9 Aryl-aldehyde oxidase. | 1.3.1.15 Orotate reductase (NADPH). |
| 1.2.3.11 Retinal oxidase. | 1.3.1.16 Beta-nitroacrylate reductase. |
| 1.2.3.13 4-hydroxyphenylpyruvate oxidase. | 1.3.1.17 3-methyleneoxindole reductase. |
| 1.2.4.1 Pyruvate dehydrogenase (acetyl-transferring). | 1.3.1.18 Kynurenate-7,8-dihydrodiol dehydrogenase. |
| 1.2.4.2 Oxoglutarate dehydrogenase (succinyl-transferring). | 1.3.1.19 Cis-1,2-dihydrobenzene-1,2-diol dehydrogenase. |

| | |
|--|---|
| 1.3.1.20 Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase. | 1.3.1.59 1,6-dihydroxy-5-methylcyclohexa-2,4-dienecarboxylate dehydrogenase. |
| 1.3.1.21 7-dehydrocholesterol reductase. | 1.3.1.60 Dibenzothiophene dihydrodiol dehydrogenase. |
| 1.3.1.22 Cholestenone 5-alpha-reductase. | 1.3.1.61 Terephthalate 1,2-cis-dihydrodiol dehydrogenase. |
| 1.3.1.23 Cholestenone 5-beta-reductase. | 1.3.1.62 Pimeloyl-CoA dehydrogenase. |
| 1.3.1.24 Biliverdin reductase. | 1.3.1.63 2,4-dichlorobenzoyl-CoA reductase. |
| 1.3.1.25 1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase. | 1.3.1.64 Phthalate 4,5-cis-dihydrodiol dehydrogenase. |
| 1.3.1.26 Dihydrodipicolinate reductase. | 1.3.1.65 5,6-dihydroxy-3-methyl-2-oxo-1,2,5,6-tetrahydroquinoline dehydrogenase. |
| 1.3.1.27 2-hexadecenal reductase. | 1.3.1.66 Cis-dihydroethylcatechol dehydrogenase. |
| 1.3.1.28 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase. | 1.3.1.67 Cis-1,2-dihydroxy-4-methylcyclohexa-3,5-diene-1-carboxylate dehydrogenase. |
| 1.3.1.29 Cis-1,2-dihydro-1,2-dihydroxynaphthalene dehydrogenase. | 1.3.1.68 1,2-dihydroxy-6-methylcyclohexa-3,5-dienecarboxylate dehydrogenase. |
| 1.3.1.30 Progesterone 5-alpha-reductase. | 1.3.1.69 Zeatin reductase. |

| | | | |
|----------|---|----------|--|
| 1.3.1.31 | 2-enoate reductase. | 1.3.1.70 | Delta(14)-sterol reductase. |
| 1.3.1.32 | Maleylacetate reductase. | 1.3.1.71 | Delta(24(24(1))) -sterol reductase. |
| 1.3.1.33 | Protochlorophyllide reductase. | 1.3.1.72 | Delta(24)-sterol reductase. |
| 1.3.1.34 | 2,4-dienoyl-CoA reductase (NADPH). | 1.3.1.73 | 1,2-dihydrovomilenine reductase. |
| 1.3.1.35 | Phosphatidylcholine desaturase. | 1.3.1.74 | 2-alkenal reductase. |
| 1.3.1.36 | Geissoschizine dehydrogenase. | 1.3.1.75 | Divinyl chlorophyllide a 8-vinyl-reductase. |
| 1.3.1.37 | Cis-2-enoyl-CoA reductase (NADPH). | 1.3.1.76 | Precorrin-2 dehydrogenase. |
| 1.3.1.38 | Trans-2-enoyl-CoA reductase (NADPH). | 1.3.2.3 | Galactonolactone dehydrogenase. |
| 1.3.1.39 | Enoyl-[acyl-carrier-protein] reductase (NADPH, A-specific). | 1.3.3.1 | Dihydroorotate oxidase. |
| 1.3.1.40 | 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate reductase. | 1.3.3.2 | Lathosterol oxidase. |
| 1.3.1.41 | Xanthommatin reductase. | 1.3.3.3 | Coproporphyrinogen oxidase. |
| 1.3.1.42 | 12-oxophytodienoate reductase. | 1.3.3.4 | Protoporphyrinogen oxidase. |
| 1.3.1.43 | Cyclohexadienyl dehydrogenase. | 1.3.3.5 | Bilirubin oxidase. |
| 1.3.1.44 | Trans-2-enoyl-CoA reductase (NAD+). | 1.3.3.6 | Acyl-CoA oxidase. |
| 1.3.1.45 | 2'-hydroxyisoflavone reductase. | 1.3.3.7 | Dihydrouracil oxidase. |
| 1.3.1.46 | Biochanin-A reductase. | 1.3.3.8 | Tetrahydroberberine oxidase. |
| 1.3.1.47 | Alpha-santonin 1,2-reductase. | 1.3.3.9 | Secologanin synthase. |
| 1.3.1.48 | 15-oxoprostaglandin 13-oxidase. | 1.3.3.10 | Tryptophan alpha,beta-oxidase. |
| 1.3.1.49 | Cis-3,4-dihydrophenanthrene-3,4-diol dehydrogenase. | 1.3.5.1 | Succinate dehydrogenase (ubiquinone). |
| 1.3.1.51 | 2'-hydroxydaidzein reductase. | 1.3.7.1 | 6-hydroxynicotinate reductase. |
| 1.3.1.52 | 2-methyl-branched-chain-enoyl-CoA reductase. | 1.3.7.2 | 15,16-dihydrobiliverdin:ferredoxin oxidoreductase. |
| 1.3.1.53 | (3S,4R)-3,4-dihydroxycyclohexa-1,5-diene-1,4-dicarboxylate dehydrogenase. | 1.3.7.3 | Phytoerythrobilin:ferredoxin oxidoreductase. |
| 1.3.1.54 | Precorrin-6A reductase. | 1.3.7.4 | Phytochromobilin:ferredoxin oxidoreductase. |
| 1.3.1.56 | Cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase. | 1.3.7.5 | Phycocyanobilin:ferredoxin oxidoreductase. |
| 1.3.1.57 | Phloroglucinol reductase. | 1.3.99.1 | Succinate dehydrogenase. |
| 1.3.1.58 | 2,3-dihydroxy-2,3-dihydro-p-cumate dehydrogenase. | 1.3.99.2 | Butyryl-CoA dehydrogenase. |

| | | | |
|-----------|---|----------|--|
| 1.3.99.3 | Acyl-CoA dehydrogenase. | 1.4.3.5 | Pyridoxamine-phosphate oxidase. |
| 1.3.99.4 | 3-oxosteroid 1-dehydrogenase. | 1.4.3.6 | Amine oxidase (copper-containing). |
| 1.3.99.5 | 3-oxo-5-alpha-steroid 4-dehydrogenase. | 1.4.3.7 | D-glutamate oxidase. |
| 1.3.99.6 | 3-oxo-5-beta-steroid 4-dehydrogenase. | 1.4.3.8 | Ethanolamine oxidase. |
| 1.3.99.7 | Glutaryl-CoA dehydrogenase. | 1.4.3.10 | Putrescine oxidase. |
| 1.3.99.8 | 2-furoyl-CoA dehydrogenase. | 1.4.3.11 | L-glutamate oxidase. |
| 1.3.99.10 | Isovaleryl-CoA dehydrogenase. | 1.4.3.12 | Cyclohexylamine oxidase. |
| 1.3.99.11 | Dihydroorotate dehydrogenase. | 1.4.3.13 | Protein-lysine 6-oxidase. |
| 1.3.99.12 | 2-methylacyl-CoA dehydrogenase. | 1.4.3.14 | L-lysine oxidase. |
| 1.3.99.13 | Long-chain-acyl-CoA dehydrogenase. | 1.4.3.15 | D-glutamate(D-aspartate) oxidase. |
| 1.3.99.14 | Cyclohexanone dehydrogenase. | 1.4.3.16 | L-aspartate oxidase. |
| 1.3.99.15 | Benzoyl-CoA reductase. | 1.4.3.19 | Glycine oxidase. |
| 1.3.99.16 | Isoquinoline 1-oxidoreductase. | 1.4.4.2 | Glycine dehydrogenase (decarboxylating). |
| 1.3.99.17 | Quinoline 2-oxidoreductase. | 1.4.7.1 | Glutamate synthase (ferredoxin). |
| 1.3.99.18 | Quinaldate 4-oxidoreductase. | 1.4.99.1 | D-amino-acid dehydrogenase. |
| 1.3.99.19 | Quinoline-4-carboxylate 2-oxidoreductase. | 1.4.99.2 | Taurine dehydrogenase. |
| 1.3.99.20 | 4-hydroxybenzoyl-CoA reductase. | 1.4.99.3 | Amine dehydrogenase. |

| | |
|--|---|
| 1.3.99.21 (R)-benzylsuccinyl-CoA dehydrogenase. | 1.4.99.4 Aalkylamine dehydrogenase. |
| 1.4.1.1 Alanine dehydrogenase. | 1.4.99.5 Glycine dehydrogenase (cyanide-forming). |
| 1.4.1.2 Glutamate dehydrogenase. | 1.5.1.1 Pyrroline-2-carboxylate reductase. |
| 1.4.1.3 Glutamate dehydrogenase (NAD(P)+). | 1.5.1.2 Pyrroline-5-carboxylate reductase. |
| 1.4.1.4 Glutamate dehydrogenase (NADP+). | 1.5.1.3 Dihydrofolate reductase. |
| 1.4.1.5 L-amino-acid dehydrogenase. | 1.5.1.5 Methylene-tetrahydrofolate dehydrogenase (NADP+). |
| 1.4.1.7 Serine 2-dehydrogenase. | 1.5.1.6 Formyltetrahydrofolate dehydrogenase. |
| 1.4.1.8 Valine dehydrogenase (NADP+). | 1.5.1.7 Saccharopine dehydrogenase (NAD+, L-lysine-forming). |
| 1.4.1.9 Leucine dehydrogenase. | 1.5.1.8 Saccharopine dehydrogenase (NADP+, L-lysine-forming). |
| 1.4.1.10 Glycine dehydrogenase. | 1.5.1.9 Saccharopine dehydrogenase (NAD+, L-glutamate-forming). |
| 1.4.1.11 L-erythro-3,5-diaminohexanoate dehydrogenase. | 1.5.1.10 Saccharopine dehydrogenase (NADP+, L-glutamate-forming). |
| 1.4.1.12 2,4-diaminopentanoate dehydrogenase. | 1.5.1.11 D-octopine dehydrogenase. |
| 1.4.1.13 Glutamate synthase (NADPH). | 1.5.1.12 1-pyrroline-5-carboxylate dehydrogenase. |
| 1.4.1.14 Glutamate synthase (NADH). | 1.5.1.15 Methylene-tetrahydrofolate dehydrogenase (NAD+). |
| 1.4.1.15 Lysine dehydrogenase. | 1.5.1.16 D-lysopine dehydrogenase. |
| 1.4.1.16 Diaminopimelate dehydrogenase. | 1.5.1.17 Alanopine dehydrogenase. |
| 1.4.1.17 N-methylalanine dehydrogenase. | 1.5.1.18 Ephedrine dehydrogenase. |
| 1.4.1.18 Lysine 6-dehydrogenase. | 1.5.1.19 D-nopaline dehydrogenase. |
| 1.4.1.19 Tryptophan dehydrogenase. | 1.5.1.20 Methylene-tetrahydrofolate reductase (NADPH). |
| 1.4.1.20 Phenylalanine dehydrogenase. | 1.5.1.21 Delta(1)-piperidine-2-carboxylate reductase. |
| 1.4.2.1 Glycine dehydrogenase (cytochrome). | 1.5.1.22 Strombine dehydrogenase. |
| 1.4.3.1 D-aspartate oxidase. | 1.5.1.23 Tauropine dehydrogenase. |
| 1.4.3.2 L-amino-acid oxidase. | 1.5.1.24 N(5)-(carboxyethyl)ornithine synthase. |
| 1.4.3.3 D-amino-acid oxidase. | 1.5.1.25 Thiomorpholine-carboxylate dehydrogenase. |
| 1.4.3.4 Amine oxidase (flavin-containing). | 1.5.1.26 Beta-alanopine dehydrogenase. |

| | |
|---|---|
| 1.5.1.27 1,2-dehydroreticulium reductase (NADPH). | 1.6.5.7 2-hydroxy-1,4-benzoquinone reductase. |
| 1.5.1.28 Opine dehydrogenase. | 1.6.6.9 Trimethylamine-N-oxide reductase. |
| 1.5.1.29 FMN reductase. | 1.6.99.1 NADPH dehydrogenase. |
| 1.5.1.30 Flavin reductase. | 1.6.99.2 NAD(P)H dehydrogenase (quinone). |
| 1.5.1.31 Berberine reductase. | 1.6.99.3 NADH dehydrogenase. |
| 1.5.1.32 Vomilenine reductase. | 1.6.99.5 NADH dehydrogenase (quinone). |
| 1.5.1.33 Pteridine reductase. | 1.6.99.6 NADPH dehydrogenase (quinone). |
| 1.5.1.34 6,7-dihydropteridine reductase. | 1.7.1.1 Nitrate reductase (NADH). |
| 1.5.3.1 Sarcosine oxidase. | 1.7.1.2 Nitrate reductase (NAD(P)H). |
| 1.5.3.2 N-methyl-L-amino-acid oxidase. | 1.7.1.3 Nitrate reductase (NADPH). |
| 1.5.3.4 N(6)-methyl-lysine oxidase. | 1.7.1.4 Nitrite reductase (NAD(P)H). |
| 1.5.3.5 (S)-6-hydroxynicotine oxidase. | 1.7.1.5 Hyponitrite reductase. |
| 1.5.3.6 (R)-6-hydroxynicotine oxidase. | 1.7.1.6 Azobenzene reductase. |
| 1.5.3.7 L-pipecolate oxidase. | 1.7.1.7 GMP reductase. |
| 1.5.3.10 Dimethylglycine oxidase. | 1.7.1.9 Nitroquinoline-N-oxide reductase. |
| 1.5.3.11 Polyamine oxidase. | 1.7.1.10 Hydroxylamine reductase (NADH). |

| | |
|--|--|
| 1.5.3.12 Dihydrobenzophenanthridine oxidase. | 1.7.1.11 4-(dimethylamino)phenylazoxybenzene reductase. |
| 1.5.4.1 Pyrimidodiazepine synthase. | 1.7.1.12 N-hydroxy-2-acetamidofluorene reductase. |
| 1.5.5.1 Electron-transferring-flavoprotein dehydrogenase. | 1.7.2.1 Nitrite reductase (NO-forming). |
| 1.5.8.1 Dimethylamine dehydrogenase. | 1.7.2.2 Nitrite reductase (cytochrome; ammonia-forming). |
| 1.5.8.2 Trimethylamine dehydrogenase. | 1.7.2.3 Trimethylamine-N-oxide reductase (cytochrome c). |
| 1.5.99.1 Sarcosine dehydrogenase. | 1.7.3.1 Nitroethane oxidase. |
| 1.5.99.2 Dimethylglycine dehydrogenase. | 1.7.3.2 Acetylindoxyl oxidase. |
| 1.5.99.3 L-pipecolate dehydrogenase. | 1.7.3.3 Urate oxidase. |
| 1.5.99.4 Nicotine dehydrogenase. | 1.7.3.4 Hydroxylamine oxidase. |
| 1.5.99.5 Methylglutamate dehydrogenase. | 1.7.3.5 3-aci-nitropropanoate oxidase. |
| 1.5.99.6 Spermidine dehydrogenase. | 1.7.7.1 Ferredoxin-nitrite reductase. |
| 1.5.99.8 Proline dehydrogenase. | 1.7.7.2 Ferredoxin-nitrate reductase. |
| 1.5.99.9 Methylenetetrahydromethanopterin dehydrogenase. | 1.7.99.1 Hydroxylamine reductase. |
| 1.5.99.11 5,10-methylenetetrahydromethanopterin reductase. | 1.7.99.4 Nitrate reductase. |
| 1.5.99.12 Cytokinin dehydrogenase. | 1.7.99.5 5,10-methylenetetrahydrofolate reductase (FADH(2)). |
| 1.6.1.1 NAD(P)(+) transhydrogenase (B-specific). | 1.7.99.6 Nitrous-oxide reductase. |
| 1.6.1.2 NAD(P)(+) transhydrogenase (AB-specific). | 1.7.99.7 Nitric-oxide reductase. |
| 1.6.2.2 Cytochrome-b5 reductase. | 1.7.99.8 Hydroxylamine oxidoreductase. |
| 1.6.2.4 NADPH--hemoprotein reductase. | 1.8.1.2 Sulfite reductase (NADPH). |
| 1.6.2.5 NADPH--cytochrome-c2 reductase. | 1.8.1.3 Hypotaurine dehydrogenase. |
| 1.6.2.6 Leghemoglobin reductase. | 1.8.1.4 Dihydrolipoyl dehydrogenase. |
| 1.6.3.1 NAD(P)H oxidase. | 1.8.1.5 2-oxopropyl-CoM reductase (carboxylating). |
| 1.6.5.3 NADH dehydrogenase (ubiquinone). | 1.8.1.6 Cystine reductase. |
| 1.6.5.4 Monodehydroascorbate reductase (NADH). | 1.8.1.7 Glutathione-disulfide reductase. |
| 1.6.5.5 NADPH:quinone reductase. | 1.8.1.8 Protein-disulfide reductase. |
| 1.6.5.6 p-benzoquinone reductase (NADPH). | 1.8.1.9 Thioredoxin-disulfide reductase. |

| | |
|---|--|
| 1.8.1.10 CoA-glutathione reductase. | 1.11.1.3 Fatty-acid peroxidase. |
| 1.8.1.11 Asparaguate reductase. | 1.11.1.5 Cytochrome-c peroxidase. |
| 1.8.1.12 Trypanothione-disulfide reductase. | 1.11.1.6 Catalase. |
| 1.8.1.13 Bis-gamma-glutamylcystine reductase. | 1.11.1.7 Peroxidase. |
| 1.8.1.14 CoA-disulfide reductase. | 1.11.1.8 Iodide peroxidase. |
| 1.8.1.15 Mycothione reductase. | 1.11.1.9 Glutathione peroxidase. |
| 1.8.2.1 Sulfite dehydrogenase. | 1.11.1.10 Chloride peroxidase. |
| 1.8.2.2 Thiosulfate dehydrogenase. | 1.11.1.11 L-ascorbate peroxidase. |
| 1.8.3.1 Sulfite oxidase. | 1.11.1.12 Phospholipid-hydroperoxide glutathione peroxidase. |
| 1.8.3.2 Thiol oxidase. | 1.11.1.13 Manganese peroxidase. |
| 1.8.3.3 Glutathione oxidase. | 1.11.1.14 Diarylpropane peroxidase. |
| 1.8.3.4 Methanethiol oxidase. | 1.12.1.2 Hydrogen dehydrogenase. |
| 1.8.3.5 Prenylcysteine oxidase. | 1.12.1.3 Hydrogen dehydrogenase (NADP+). |
| 1.8.4.1 Glutathione-homocystine transhydrogenase. | 1.12.2.1 Cytochrome-c3 hydrogenase. |
| 1.8.4.2 Protein-disulfide reductase | 1.12.5.1 Hydrogen:quinone oxidoreductase. |

| | |
|--|---|
| (glutathione). | |
| 1.8.4.3 Glutathione-CoA-glutathione transhydrogenase. | 1.12.7.2 Ferredoxin hydrogenase. |
| 1.8.4.4 Glutathione-cystine transhydrogenase. | 1.12.98.1 Coenzyme F420 hydrogenase. |
| 1.8.4.5 Methionine-S-oxide reductase. | 1.12.98.2 5,10-methenyltetrahydromethanopterin hydrogenase. |
| 1.8.4.6 Protein-methionine-S-oxide reductase. | 1.12.98.3 Methanosarcina-phenazine hydrogenase. |
| 1.8.4.7 Enzyme-thiol transhydrogenase (glutathione-disulfide). | 1.12.99.6 Hydrogenase (acceptor). |
| 1.8.4.8 Phosphoadenylyl-sulfate reductase (thioredoxin). | 1.13.11.1 Catechol 1,2-dioxygenase. |
| 1.8.4.9 Adenylyl-sulfate reductase (glutathione). | 1.13.11.2 Catechol 2,3-dioxygenase. |
| 1.8.4.10 Adenylyl-sulfate reductase (thioredoxin). | 1.13.11.3 Protocatechuate 3,4-dioxygenase. |
| 1.8.5.1 Glutathione dehydrogenase (ascorbate). | 1.13.11.4 Gentisate 1,2-dioxygenase. |
| 1.8.7.1 Sulfite reductase (ferredoxin). | 1.13.11.5 Homogentisate 1,2-dioxygenase. |
| 1.8.98.1 CoB-CoM heterodisulfide reductase. | 1.13.11.6 3-hydroxyanthranilate 3,4-dioxygenase. |
| 1.8.99.1 Sulfite reductase. | 1.13.11.8 Protocatechuate 4,5-dioxygenase. |
| 1.8.99.2 Adenylyl-sulfate reductase. | 1.13.11.9 2,5-dihydropyridine 5,6-dioxygenase. |
| 1.8.99.3 Hydrogensulfite reductase. | 1.13.11.10 7,8-dihydroxykynurenate 8,8a-dioxygenase. |
| 1.9.3.1 Cytochrome-c oxidase. | 1.13.11.11 Tryptophan 2,3-dioxygenase. |
| 1.9.6.1 Nitrate reductase (cytochrome). | 1.13.11.12 Lipoygenase. |
| 1.9.99.1 Iron-cytochrome-c reductase. | 1.13.11.13 Ascorbate 2,3-dioxygenase. |
| 1.10.1.1 Trans-acenaphthene-1,2-diol dehydrogenase. | 1.13.11.14 2,3-dihydroxybenzoate 3,4-dioxygenase. |
| 1.10.2.1 L-ascorbate-cytochrome-b5 reductase. | 1.13.11.15 3,4-dihydroxyphenylacetate 2,3-dioxygenase. |
| 1.10.2.2 Ubiquinol-cytochrome-c reductase. | 1.13.11.16 3-carboxyethylcatechol 2,3-dioxygenase. |
| 1.10.3.1 Catechol oxidase. | 1.13.11.17 Indole 2,3-dioxygenase. |
| 1.10.3.2 Laccase. | 1.13.11.18 Sulfur dioxygenase. |
| 1.10.3.3 L-ascorbate oxidase. | 1.13.11.19 Cysteamine dioxygenase. |
| 1.10.3.4 O-aminophenol oxidase. | 1.13.11.20 Cysteine dioxygenase. |
| 1.10.3.5 3-hydroxyanthranilate oxidase. | 1.13.11.22 Caffeate 3,4-dioxygenase. |
| 1.10.3.6 Rifamycin-B oxidase. | 1.13.11.23 2,3-dihydroxyindole 2,3-dioxygenase. |
| 1.10.99.1 Plastoquinol-plastocyanin reductase. | 1.13.11.24 Quercetin 2,3-dioxygenase. |
| 1.11.1.1 NADH peroxidase. | 1.13.11.25 3,4-dihydroxy-9,10-secoandrosta-1,3,5(10)-triene-9,17-dione 4,5-dioxygenase. |
| 1.11.1.2 NADPH peroxidase. | 1.13.11.26 Peptide-tryptophan 2,3-dioxygenase. |

| | |
|---|---|
| 1.13.11.27 4-hydroxyphenylpyruvate dioxygenase. | 1.14.11.4 Procollagen-lysine 5-dioxygenase. |
| 1.13.11.28 2,3-dihydroxybenzoate 2,3-dioxygenase. | 1.14.11.6 Thymine dioxygenase. |
| 1.13.11.29 Stizolobate synthase. | 1.14.11.7 Procollagen-proline 3-dioxygenase. |
| 1.13.11.30 Stizolobinate synthase. | 1.14.11.8 Trimethyllysine dioxygenase. |
| 1.13.11.31 Arachidonate 12-lipoxygenase. | 1.14.11.9 Naringenin 3-dioxygenase. |
| 1.13.11.32 2-nitropropane dioxygenase. | 1.14.11.10 Pyrimidine-deoxynucleoside 1'-dioxygenase. |
| 1.13.11.33 Arachidonate 15-lipoxygenase. | 1.14.11.11 Hyoscyamine (6S)-dioxygenase. |
| 1.13.11.34 Arachidonate 5-lipoxygenase. | 1.14.11.12 Gibberellin-44 dioxygenase. |
| 1.13.11.35 Pyrogallol 1,2-oxygenase. | 1.14.11.13 Gibberellin 2-beta-dioxygenase. |
| 1.13.11.36 Chloridazon-catechol dioxygenase. | 1.14.11.14 6-beta-hydroxyhyoscyamine epoxidase. |
| 1.13.11.37 Hydroxyquinol 1,2-dioxygenase. | 1.14.11.15 Gibberellin 3-beta-dioxygenase. |

| | |
|---|--|
| 1.13.11.38 1-hydroxy-2-naphthoate 1,2-dioxygenase. | 1.14.11.16 Peptide-aspartate beta-dioxygenase. |
| 1.13.11.39 Biphenyl-2,3-diol 1,2-dioxygenase. | 1.14.11.17 Taurine dioxygenase. |
| 1.13.11.40 Arachidonate 8-lipoxygenase. | 1.14.11.18 Phytanoyl-CoA dioxygenase. |
| 1.13.11.41 2,4'-dihydroxyacetophenone dioxygenase. | 1.14.11.19 Leucocyanidin oxygenase. |
| 1.13.11.42 Indoleamine-pyrrole 2,3-dioxygenase. | 1.14.11.20 Desacetoxyvindoline 4-hydroxylase. |
| 1.13.11.43 Lignostilbene alpha-beta-dioxygenase. | 1.14.11.21 Clavamate synthase. |
| 1.13.11.44 Linoleate diol synthase. | 1.14.12.1 Anthranilate 1,2-dioxygenase (deaminating, decarboxylating). |
| 1.13.11.45 Linoleate 11-lipoxygenase. | 1.14.12.3 Benzene 1,2-dioxygenase. |
| 1.13.11.46 4-hydroxymandelate synthase. | 1.14.12.4 3-hydroxy-2-methylpyridinecarboxylate dioxygenase. |
| 1.13.11.47 3-hydroxy-4-oxoquinoline 2,4-dioxygenase. | 1.14.12.5 5-pyridoxate dioxygenase. |
| 1.13.11.48 3-hydroxy-2-methylquinolin-4-one 2,4-dioxygenase. | 1.14.12.7 Phthalate 4,5-dioxygenase. |
| 1.13.11.49 Chlorite O(2)-lyase. | 1.14.12.8 4-sulfobenzoate 3,4-dioxygenase. |
| 1.13.11.50 Acetylacetone-cleaving enzyme. | 1.14.12.9 4-chlorophenylacetate 3,4-dioxygenase. |
| 1.13.12.1 Arginine 2-monooxygenase. | 1.14.12.10 Benzoate 1,2-dioxygenase. |
| 1.13.12.2 Lysine 2-monooxygenase. | 1.14.12.11 Toluene dioxygenase. |
| 1.13.12.3 Tryptophan 2-monooxygenase. | 1.14.12.12 Naphthalene 1,2-dioxygenase. |
| 1.13.12.4 Lactate 2-monooxygenase. | 1.14.12.13 2-chlorobenzoate 1,2-dioxygenase. |
| 1.13.12.5 Renilla-luciferin 2-monooxygenase. | 1.14.12.14 2-aminobenzenesulfonate 2,3-dioxygenase. |
| 1.13.12.6 Cypridina-luciferin 2-monooxygenase. | 1.14.12.15 Terephthalate 1,2-dioxygenase. |
| 1.13.12.7 Photinus-luciferin 4-monooxygenase (ATP-hydrolyzing). | 1.14.12.16 2-hydroxyquinoline 5,6-dioxygenase. |
| 1.13.12.8 Watasenia-luciferin 2-monooxygenase. | 1.14.12.17 Nitric oxide dioxygenase. |
| 1.13.12.9 Phenylalanine 2-monooxygenase. | 1.14.12.18 Biphenyl 2,3-dioxygenase. |
| 1.13.12.11 Methylphenyltetrahydropyridine N-monooxygenase. | 1.14.13.1 Salicylate 1-monooxygenase. |
| 1.13.12.12 Apo-beta-carotenoid-14',13'-dioxygenase. | 1.14.13.2 4-hydroxybenzoate 3-monooxygenase. |
| 1.13.12.13 Oplophorus-luciferin 2-monooxygenase. | 1.14.13.3 4-hydroxyphenylacetate 3-monooxygenase. |
| 1.13.99.1 Inositol oxygenase. | 1.14.13.4 Melilotate 3-monooxygenase. |
| 1.13.99.3 Tryptophan 2'-dioxygenase. | 1.14.13.5 Imidazoleacetate 4-monooxygenase. |
| 1.14.11.1 Gamma-butyrobetaine dioxygenase. | 1.14.13.6 Orcinol 2-monooxygenase. |
| 1.14.11.2 Procollagen-proline dioxygenase. | 1.14.13.7 Phenol 2-monooxygenase. |
| 1.14.11.3 Pyrimidine-deoxynucleoside 2'-dioxygenase. | 1.14.13.8 Dimethylaniline monooxygenase (N-oxide-forming). |

| | |
|---|--|
| 1.14.16.4 Tryptophan 5-monooxygenase. | 1.14.99.33 Delta(12)-fatty acid dehydrogenase. |
| 1.14.16.5 Glyceryl-ether monooxygenase. | 1.14.99.34 Monoprenyl isoflavone epoxidase. |
| 1.14.16.6 Mandelate 4-monooxygenase. | 1.14.99.35 Thiophene-2-carbonyl-CoA monooxygenase. |
| 1.14.17.1 Dopamine beta-monooxygenase. | 1.14.99.36 Beta-carotene 15,15'-monooxygenase. |
| 1.14.17.3 Peptidylglycine monooxygenase. | 1.14.99.37 Taxadiene 5-alpha-hydroxylase. |
| 1.14.17.4 Aminocyclopropanecarboxylate oxidase. | 1.15.1.1 Superoxide dismutase. |
| 1.14.18.1 Monophenol monooxygenase. | 1.15.1.2 Superoxide reductase. |

| | | | |
|------------|--|-----------|---|
| 1.14.18.2 | CMP-N-acetylneuraminate monooxygenase. | 1.16.1.1 | Mercury(II) reductase. |
| 1.14.19.1 | Stearoyl-CoA 9-desaturase. | 1.16.1.2 | Diferriic-transferrin reductase. |
| 1.14.19.2 | Acyl-[acyl-carrier-protein] desaturase. | 1.16.1.3 | Aquacobalamin reductase. |
| 1.14.19.3 | Linoleoyl-CoA desaturase. | 1.16.1.4 | Cob(II)alamin reductase. |
| 1.14.20.1 | Deacetoxycephalosporin-C synthase. | 1.16.1.5 | Aquacobalamin reductase (NADPH). |
| 1.14.21.1 | (S)-stylopine synthase. | 1.16.1.6 | Cyanocobalamin reductase (cyanide-eliminating). |
| 1.14.21.2 | (S)-cheilanthifoline synthase. | 1.16.1.7 | Ferric-chelate reductase. |
| 1.14.21.3 | Berbamunine synthase. | 1.16.1.8 | [Methionine synthase] reductase. |
| 1.14.21.4 | Salutaridine synthase. | 1.16.3.1 | Ferroxidase. |
| 1.14.21.5 | (S)-canadine synthase. | 1.16.8.1 | Cob(II)yrinic acid a,c-diamide reductase. |
| 1.14.99.1 | Prostaglandin-endoperoxide synthase. | 1.17.1.1 | CDP-4-dehydro-6-deoxyglucose reductase. |
| 1.14.99.2 | Kynurenine 7,8-hydroxylase. | 1.17.1.2 | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase. |
| 1.14.99.3 | Heme oxygenase (decyclizing). | 1.17.1.3 | Leucoanthocyanidin reductase. |
| 1.14.99.4 | Progesterone monooxygenase. | 1.17.1.4 | Xanthine dehydrogenase. |
| 1.14.99.7 | Squalene monooxygenase. | 1.17.1.5 | Nicotinate dehydrogenase. |
| 1.14.99.9 | Steroid 17-alpha-monooxygenase. | 1.17.3.1 | Pteridine oxidase. |
| 1.14.99.10 | Steroid 21-monooxygenase. | 1.17.3.2 | Xanthine oxidase. |
| 1.14.99.11 | Estradiol 6-beta-monooxygenase. | 1.17.3.3 | 6-hydroxynicotinate dehydrogenase. |
| 1.14.99.12 | Androst-4-ene-3,17-dione monooxygenase. | 1.17.4.1 | Ribonucleoside-diphosphate reductase. |
| 1.14.99.14 | Progesterone 11-alpha-monooxygenase. | 1.17.4.2 | Ribonucleoside-triphosphate reductase. |
| 1.14.99.15 | 4-methoxybenzoate monooxygenase (O-demethylating). | 1.17.4.3 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase. |
| 1.14.99.19 | Plasmanyethanolamine desaturase. | 1.17.5.1 | Phenylacetyl-CoA dehydrogenase. |
| 1.14.99.20 | Phylloquinone monooxygenase (2,3-epoxidizing). | 1.17.99.1 | 4-cresol dehydrogenase (hydroxylating). |
| 1.14.99.21 | Latia-luciferin monooxygenase (demethylating). | 1.17.99.2 | Ethylbenzene hydroxylase. |
| 1.14.99.22 | Ecdysone 20-monooxygenase. | 1.18.1.1 | Rubredoxin--NAD(+) reductase. |
| 1.14.99.23 | 3-hydroxybenzoate 2-monooxygenase. | 1.18.1.2 | Ferredoxin--NADP(+) reductase. |
| 1.14.99.24 | Steroid 9-alpha-monooxygenase. | 1.18.1.3 | Ferredoxin--NAD(+) reductase. |
| 1.14.99.26 | 2-hydroxypyridine 5-monooxygenase. | 1.18.1.4 | Rubredoxin--NAD(P)(+) reductase. |
| 1.14.99.27 | Juglone 3-monooxygenase. | 1.18.6.1 | Nitrogenase. |
| 1.14.99.28 | Linalool 8-monooxygenase. | 1.19.6.1 | Nitrogenase (flavodoxin). |
| 1.14.99.29 | Deoxyhypusine monooxygenase. | 1.20.1.1 | Phosphonate dehydrogenase. |
| 1.14.99.30 | Carotene 7,8-desaturase. | 1.20.4.1 | Arsenate reductase (glutaredoxin). |
| 1.14.99.31 | Myristoyl-CoA 11-(E) desaturase. | 1.20.4.2 | Methylarsenate reductase. |
| 1.14.99.32 | Myristoyl-CoA 11-(Z) desaturase. | 1.20.98.1 | Arsenate reductase (azurin). |

| | | | |
|-----------|-----------------------------|----------|---|
| 1.20.99.1 | Arsenate reductase (donor). | 2.1.1.15 | Fatty-acid O-methyltransferase. |
| 1.21.3.1 | Isopenicillin-N synthase. | 2.1.1.16 | Methylene-fatty-acyl-phospholipid synthase. |
| 1.21.3.2 | Columbamine oxidase. | 2.1.1.17 | Phosphatidylethanolamine N-methyltransferase. |
| 1.21.3.3 | Reticuline oxidase. | 2.1.1.18 | Polysaccharide O-methyltransferase. |

| | | | |
|---------------|--|----------|---|
| 1.21.3.4 | Sulochrin oxidase ((+)-bisdechlorogeodin-forming). | 2.1.1.19 | Trimethylsulfonium--tetrahydrofolate N-methyltransferase. |
| 1.21.3.5 | Sulochrin oxidase ((-)-bisdechlorogeodin-forming). | 2.1.1.20 | Glycine N-methyltransferase. |
| 1.21.3.6 | Aureusidin synthase. | 2.1.1.21 | Methylamine--glutamate N-methyltransferase. |
| 1.21.4.1 | D-proline reductase (dithiol). | 2.1.1.22 | Carnosine N-methyltransferase. |
| 1.21.4.2 | Glycine reductase. | 2.1.1.25 | Phenol O-methyltransferase. |
| 1.21.4.3 | Sarcosine reductase. | 2.1.1.26 | Iodophenol O-methyltransferase. |
| 1.21.4.4 | Betaine reductase. | 2.1.1.27 | Tyramine N-methyltransferase. |
| 1.21.99.1 | Beta-cyclopiazonate dehydrogenase. | 2.1.1.28 | Phenylethanolamine N-methyltransferase. |
| 1.97.1.1 | Chlorate reductase. | 2.1.1.29 | tRNA (cytosine-5-)-methyltransferase. |
| 1.97.1.2 | Pyrogallol hydroxytransferase. | 2.1.1.31 | tRNA (guanine-N(1)-)-methyltransferase. |
| 1.97.1.3 | Sulfur reductase. | 2.1.1.32 | tRNA (guanine-N(2)-)-methyltransferase. |
| 1.97.1.4 | [Formate acetyltransferase] activating enzyme. | 2.1.1.33 | tRNA (guanine-N(7)-)-methyltransferase. |
| 1.97.1.8 | Tetrachloroethene reductive dehalogenase. | 2.1.1.34 | tRNA (guanosine-2'-O-)-methyltransferase. |
| 1.97.1.9 | Selenate reductase. | 2.1.1.35 | tRNA (uracil-5-)-methyltransferase. |
| 1.97.1.10 | Thyroxine 5'-deiodinase. | 2.1.1.36 | tRNA (adenine-N(1)-)-methyltransferase. |
| 1.97.1.11 | Thyroxine 5-deiodinase. | 2.1.1.37 | DNA (cytosine-5-)-methyltransferase. |
| | | 2.1.1.38 | O-demethylpuromycin O-methyltransferase. |
| ENZYME: 2.-.- | | 2.1.1.39 | Inositol 3-methyltransferase. |
| 2.1.1.1 | Nicotinamide N-methyltransferase. | 2.1.1.40 | Inositol 1-methyltransferase. |
| 2.1.1.2 | Guanidinoacetate N-methyltransferase. | 2.1.1.41 | Sterol 24-C-methyltransferase. |
| 2.1.1.3 | Thetin--homocysteine S-methyltransferase. | 2.1.1.42 | Luteolin O-methyltransferase. |
| 2.1.1.4 | Acetylserotonin O-methyltransferase. | 2.1.1.43 | Histone-lysine N-methyltransferase. |
| 2.1.1.5 | Betaine--homocysteine S-methyltransferase. | 2.1.1.44 | Dimethylhistidine N-methyltransferase. |
| 2.1.1.6 | Catechol O-methyltransferase. | 2.1.1.45 | Thymidylate synthase. |
| 2.1.1.7 | Nicotinate N-methyltransferase. | 2.1.1.46 | Isoflavone 4'-O-methyltransferase. |
| 2.1.1.8 | Histamine N-methyltransferase. | 2.1.1.47 | Indolepyruvate C-methyltransferase. |
| 2.1.1.9 | Thiol S-methyltransferase. | 2.1.1.48 | rRNA (adenine-N(6)-)-methyltransferase. |
| 2.1.1.10 | Homocysteine S-methyltransferase. | 2.1.1.49 | Amine N-methyltransferase. |
| 2.1.1.11 | Magnesium protoporphyrin IX methyltransferase. | 2.1.1.50 | Loganate O-methyltransferase. |
| 2.1.1.12 | Methionine S-methyltransferase. | 2.1.1.51 | rRNA (guanine-N(1)-)-methyltransferase. |
| 2.1.1.13 | Methionine synthase. | 2.1.1.52 | rRNA (guanine-N(2)-)-methyltransferase. |
| 2.1.1.14 | 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase. | 2.1.1.53 | Putrescine N-methyltransferase. |
| 2.1.1.54 | Deoxycytidylate C-methyltransferase. | 2.1.1.86 | Tetrahydromethanopterin S-methyltransferase. |

| | |
|--|---|
| 2.1.1.55 tRNA (adenine-N(6)-)-methyltransferase. | 2.1.1.87 Pyridine N-methyltransferase. |
| 2.1.1.56 mRNA (guanine-N(7)-)-methyltransferase. | 2.1.1.88 8-hydroxyquercetin 8-O-methyltransferase. |
| 2.1.1.57 mRNA (nucleoside-2'-O)-methyltransferase. | 2.1.1.89 Tetrahydrocolumbamine 2-O-methyltransferase. |
| 2.1.1.59 [Cytochrome c]-lysine N-methyltransferase. | 2.1.1.90 Methanol--5-hydroxybenzimidazolylcobamide Co-methyltransferase. |
| 2.1.1.60 Calmodulin-lysine N-methyltransferase. | 2.1.1.91 Isobutyraldoxime O-methyltransferase. |
| 2.1.1.61 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase. | 2.1.1.92 Bergaptol O-methyltransferase. |
| 2.1.1.62 mRNA (2'-O-methyladenosine-N(6)-)-methyltransferase. | 2.1.1.93 Xanthoxol O-methyltransferase. |
| 2.1.1.63 Methylated-DNA--[protein]-cysteine S-methyltransferase. | 2.1.1.94 11-O-demethyl-17-O-deacetylvindoline O-methyltransferase. |
| 2.1.1.64 3-demethylubiquinone-9 3-O-methyltransferase. | 2.1.1.95 Tocopherol O-methyltransferase. |
| 2.1.1.65 Licodione 2'-O-methyltransferase. | 2.1.1.96 Thioether S-methyltransferase. |
| 2.1.1.66 rRNA (adenosine-2'-O)-methyltransferase. | 2.1.1.97 3-hydroxyanthranilate 4-C-methyltransferase. |
| 2.1.1.67 Thiopurine S-methyltransferase. | 2.1.1.98 Diphtine synthase. |
| 2.1.1.68 Caffeate O-methyltransferase. | 2.1.1.99 16-methoxy-2,3-dihydro-3-hydroxytabersonine N-methyltransferase. |
| 2.1.1.69 5-hydroxyfuranocoumarin 5-O-methyltransferase. | 2.1.1.100 Protein-S-isoprenylcysteine O-methyltransferase. |
| 2.1.1.70 8-hydroxyfuranocoumarin 8-O-methyltransferase. | 2.1.1.101 Macrocin O-methyltransferase. |
| 2.1.1.71 Phosphatidyl-N-methylethanolamine N-methyltransferase. | 2.1.1.102 Demethylmacrocin O-methyltransferase. |
| 2.1.1.72 Site-specific DNA-methyltransferase (adenine-specific). | 2.1.1.103 Phosphoethanolamine N-methyltransferase. |
| 2.1.1.74 Methylenetetrahydrofolate-tRNA-(uracil-5-)-methyltransferase (FADH(2)-oxidizing). | 2.1.1.104 Caffeoyl-CoA O-methyltransferase. |
| 2.1.1.75 Apigenin 4'-O-methyltransferase. | 2.1.1.105 N-benzoyl-4-hydroxyanthranilate 4-O-methyltransferase. |
| 2.1.1.76 Quercetin 3-O-methyltransferase. | 2.1.1.106 Tryptophan 2-C-methyltransferase. |
| 2.1.1.77 Protein-L-isoaspartate(D-aspartate) O-methyltransferase. | 2.1.1.107 Uroporphyrin-III C-methyltransferase. |
| 2.1.1.78 Isoorientin 3'-O-methyltransferase. | 2.1.1.108 6-hydroxymellein O-methyltransferase. |
| 2.1.1.79 Cyclopropane-fatty-acyl-phospholipid synthase. | 2.1.1.109 Demethylsterigmatocystin 6-O-methyltransferase. |
| 2.1.1.80 Protein-glutamate O-methyltransferase. | 2.1.1.110 Sterigmatocystin 7-O-methyltransferase. |
| 2.1.1.82 3-methylquercetin 7-O-methyltransferase. | 2.1.1.111 Anthranilate N-methyltransferase. |
| 2.1.1.83 3,7-dimethylquercetin 4'-O-methyltransferase. | 2.1.1.112 Glucuronoxylan 4-O-methyltransferase. |
| 2.1.1.84 Methylquercetagenin 6-O-methyltransferase. | 2.1.1.113 Site-specific DNA-methyltransferase (cytosine-N(4)-specific). |
| 2.1.1.85 Protein-histidine N-methyltransferase. | 2.1.1.114 Hexaprenyldihydroxybenzoate methyltransferase. |
| 2.1.1.115 (RS)-1-benzyl-1,2,3,4-tetrahydroisoquinoline N-methyltransferase. | 2.1.2.1 Glycine hydroxymethyltransferase. |

| | |
|---|--|
| 2.1.1.116 3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase. | 2.1.2.2 Phosphoribosylglycinamide formyltransferase. |
| 2.1.1.117 (S)-scoulerine 9-O-methyltransferase. | 2.1.2.3 Phosphoribosylaminoimidazolecarboxamide formyltransferase. |
| 2.1.1.118 Columbamine O-methyltransferase. | 2.1.2.4 Glycine formimidoyltransferase. |
| 2.1.1.119 10-hydroxydihydrosanguinarine 10-O-methyltransferase. | 2.1.2.5 Glutamate formimidoyltransferase. |
| 2.1.1.120 12-hydroxydihydrochelirubine 12-O-methyltransferase. | 2.1.2.7 D-alanine 2-hydroxymethyltransferase. |
| 2.1.1.121 6-O-methylnorlaudanoline 5'-O-methyltransferase. | 2.1.2.8 Deoxycytidylate 5-hydroxymethyltransferase. |
| 2.1.1.122 (S)-tetrahydroprotoberberine N-methyltransferase. | 2.1.2.9 Methionyl-tRNA formyltransferase. |
| 2.1.1.123 [Cytochrome-c]-methionine S-methyltransferase. | 2.1.2.10 Aminomethyltransferase. |
| 2.1.1.124 [Cytochrome-c]-arginine N-methyltransferase. | 2.1.2.11 3-methyl-2-oxobutanoate hydroxymethyltransferase. |
| 2.1.1.125 Histone-arginine N-methyltransferase. | 2.1.3.1 Methylmalonyl-CoA carboxytransferase. |
| 2.1.1.126 [Myelin basic protein]-arginine N-methyltransferase. | 2.1.3.2 Aspartate carbamoyltransferase. |
| 2.1.1.127 [Ribulose-bisphosphate carboxylase]-lysine N-methyltransferase. | 2.1.3.3 Ornithine carbamoyltransferase. |
| 2.1.1.128 (RS)-norcoclaurine 6-O-methyltransferase. | 2.1.3.5 Oxamate carbamoyltransferase. |
| 2.1.1.129 Inositol 4-methyltransferase. | 2.1.3.6 Putrescine carbamoyltransferase. |
| 2.1.1.130 Precorrin-2 C(20)-methyltransferase. | 2.1.3.7 3-hydroxymethylcephem carbamoyltransferase. |
| 2.1.1.131 Precorrin-3B C(17)-methyltransferase. | 2.1.3.8 Lysine carbamoyltransferase. |
| 2.1.1.132 Precorrin-6Y C(5,15)-methyltransferase (decarboxylating). | 2.1.4.1 Glycine amidinotransferase. |
| 2.1.1.133 Precorrin-4 C(11)-methyltransferase. | 2.1.4.2 Scyllo-inosamine-4-phosphate amidinotransferase. |
| 2.1.1.136 Chlorophenol O-methyltransferase. | 2.2.1.1 Transketolase. |
| 2.1.1.137 Arsenite methyltransferase. | 2.2.1.2 Transaldolase. |
| 2.1.1.139 3'-demethylstaurosporine O-methyltransferase. | 2.2.1.3 Formaldehyde transketolase. |
| 2.1.1.140 (S)-coclaurine-N-methyltransferase. | 2.2.1.4 Acetoin-ribose-5-phosphate transaldolase. |
| 2.1.1.141 Jasmonate O-methyltransferase. | 2.2.1.5 2-hydroxy-3-oxoadipate synthase. |
| 2.1.1.142 Cycloartenol 24-C-methyltransferase. | 2.2.1.6 Acetolactate synthase. |
| 2.1.1.143 24-methylenesterol C-methyltransferase. | 2.2.1.7 1-deoxy-D-xylulose-5-phosphate synthase. |
| 2.1.1.144 Trans-aconitate 2-methyltransferase. | 2.2.1.8 Fluorothreonine transaldolase. |
| 2.1.1.145 Trans-aconitate 3-methyltransferase. | 2.3.1.1 Amino-acid N-acetyltransferase. |
| 2.1.1.146 (Iso)eugenol O-methyltransferase. | 2.3.1.2 Imidazole N-acetyltransferase. |
| 2.1.1.147 Corydaline synthase. | 2.3.1.3 Glucosamine N-acetyltransferase. |
| 2.1.1.148 Thymidylate synthase (FAD). | 2.3.1.4 Glucosamine 6-phosphate N-acetyltransferase. |
| 2.1.1.149 Myricetin O-methyltransferase. | 2.3.1.5 Arylamine N-acetyltransferase. |
| 2.1.1.150 Isoflavone 7-O-methyltransferase. | 2.3.1.6 Choline O-acetyltransferase. |
| 2.1.1.151 Cobalt-factor II C(20)-methyltransferase. | 2.3.1.7 Carnitine O-acetyltransferase. |
| 2.1.1.152 Precorrin-6A synthase (deacetylating). | 2.3.1.8 Phosphate acetyltransferase. |
| 2.3.1.9 Acetyl-CoA C-acetyltransferase. | 2.3.1.48 Histone acetyltransferase. |

| | |
|--|---|
| 2.3.1.10 Hydrogen-sulfide S-acetyltransferase. | 2.3.1.49 Deacetyl-[citrate-(pro-3S)-lyase] S-acetyltransferase. |
| 2.3.1.11 Thioethanolamine S-acetyltransferase. | 2.3.1.50 Serine C-palmitoyltransferase. |
| 2.3.1.12 Dihydrolipoyllysine-residue acetyltransferase. | 2.3.1.51 1-acylglycerol-3-phosphate O-acyltransferase. |
| 2.3.1.13 Glycine N-acyltransferase. | 2.3.1.52 2-acylglycerol-3-phosphate O-acyltransferase. |
| 2.3.1.14 Glutamine N-phenylacetyltransferase. | 2.3.1.53 Phenylalanine N-acetyltransferase. |
| 2.3.1.15 Glycerol-3-phosphate O-acyltransferase. | 2.3.1.54 Formate C-acetyltransferase. |
| 2.3.1.16 Acetyl-CoA C-acyltransferase. | 2.3.1.56 Aromatic-hydroxylamine O-acetyltransferase. |
| 2.3.1.17 Aspartate N-acetyltransferase. | 2.3.1.57 Diamine N-acetyltransferase. |
| 2.3.1.18 Galactoside O-acetyltransferase. | 2.3.1.58 2,3-diaminopropionate N-oxalyltransferase. |
| 2.3.1.19 Phosphate butyryltransferase. | 2.3.1.59 Gentamicin 2'-N-acetyltransferase. |
| 2.3.1.20 Diacylglycerol O-acyltransferase. | 2.3.1.60 Gentamicin 3'-N-acetyltransferase. |
| 2.3.1.21 Carnitine O-palmitoyltransferase. | 2.3.1.61 Dihydrolipoyllysine-residue succinyltransferase. |
| 2.3.1.22 2-acylglycerol O-acyltransferase. | 2.3.1.62 2-acylglycerophosphocholine O-acyltransferase. |
| 2.3.1.23 1-acylglycerophosphocholine O-acyltransferase. | 2.3.1.63 1-alkylglycerophosphocholine O-acyltransferase. |
| 2.3.1.24 Sphingosine N-acyltransferase. | 2.3.1.64 Agmatine N(4)-coumaroyltransferase. |
| 2.3.1.25 Plasmalogen synthase. | 2.3.1.65 Glycine N-choloyltransferase. |
| 2.3.1.26 Sterol O-acyltransferase. | 2.3.1.66 Leucine N-acetyltransferase. |
| 2.3.1.27 Cortisol O-acetyltransferase. | 2.3.1.67 1-alkylglycerophosphocholine O-acetyltransferase. |
| 2.3.1.28 Chloramphenicol O-acetyltransferase. | 2.3.1.68 Glutamine N-acyltransferase. |
| 2.3.1.29 Glycine C-acetyltransferase. | 2.3.1.69 Monoterpenol O-acetyltransferase. |
| 2.3.1.30 Serine O-acetyltransferase. | 2.3.1.70 CDP-acylglycerol O-arachidonoyltransferase. |
| 2.3.1.31 Homoserine O-acetyltransferase. | 2.3.1.71 Glycine N-benzoyltransferase. |
| 2.3.1.32 Lysine N-acetyltransferase. | 2.3.1.72 Indoleacetylglucose-inositol O-acyltransferase. |
| 2.3.1.33 Histidine N-acetyltransferase. | 2.3.1.73 Diacylglycerol-sterol O-acyltransferase. |
| 2.3.1.34 D-tryptophan N-acetyltransferase. | 2.3.1.74 Naringenin-chalcone synthase. |
| 2.3.1.35 Glutamate N-acetyltransferase. | 2.3.1.75 Long-chain-alcohol O-fatty-acyltransferase. |
| 2.3.1.36 D-amino-acid N-acetyltransferase. | 2.3.1.76 Retinol O-fatty-acyltransferase. |
| 2.3.1.37 5-aminolevulinate synthase. | 2.3.1.77 Triacylglycerol-sterol O-acyltransferase. |
| 2.3.1.38 [Acyl-carrier-protein] S-acetyltransferase. | 2.3.1.78 Heparan-alpha-glucosaminide N-acetyltransferase. |
| 2.3.1.39 [Acyl-carrier-protein] S-malonyltransferase. | 2.3.1.79 Maltose O-acetyltransferase. |
| 2.3.1.40 Acyl-[acyl-carrier-protein]-phospholipid O-acyltransferase. | 2.3.1.80 Cysteine-S-conjugate N-acetyltransferase. |
| 2.3.1.41 3-oxoacyl-[acyl-carrier-protein] synthase. | 2.3.1.81 Aminoglycoside N(3')-acetyltransferase. |
| 2.3.1.42 Glycerone-phosphate O-acyltransferase. | 2.3.1.82 Aminoglycoside N(6')-acetyltransferase. |
| 2.3.1.43 Phosphatidylcholine-sterol O-acyltransferase. | 2.3.1.83 Phosphatidylcholine-dolichol O-acyltransferase. |
| 2.3.1.44 N-acetylneuramate 4-O-acetyltransferase. | 2.3.1.84 Alcohol O-acetyltransferase. |
| 2.3.1.45 N-acetylneuramate 7-O(or 9-O)- | 2.3.1.85 Fatty-acid synthase. |

| | |
|---|---|
| acetyltransferase. | |
| 2.3.1.46 Homoserine O-succinyltransferase. | 2.3.1.86 Fatty-acyl-CoA synthase. |
| 2.3.1.47 8-amino-7-oxononanoate synthase. | 2.3.1.87 Aralkylamine N-acetyltransferase. |
| 2.3.1.88 Peptide alpha-N-acetyltransferase. | 2.3.1.122 Trehalose O-mycosyltransferase. |
| 2.3.1.89 Tetrahydrodipicolinate N-acetyltransferase. | 2.3.1.123 Dolichol O-acyltransferase. |
| 2.3.1.90 Beta-glucogallin O-galloyltransferase. | 2.3.1.125 1-alkyl-2-acetylgllycerol O-acyltransferase. |
| 2.3.1.91 Sinapoylglucose--choline O-sinapoyltransferase. | 2.3.1.126 Isocitrate O-dihydroxycinnamoyltransferase. |
| 2.3.1.92 Sinapoylglucose--malate O-sinapoyltransferase. | 2.3.1.127 Ornithine N-benzoyltransferase. |
| 2.3.1.93 13-hydroxylupinine O-tigloyltransferase. | 2.3.1.128 Ribosomal-protein-alanine N-acetyltransferase. |
| 2.3.1.94 Erythronolide synthase. | 2.3.1.129 Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase. |
| 2.3.1.95 Trihydroxystilbene synthase. | 2.3.1.130 Galactarate O-hydroxycinnamoyltransferase. |
| 2.3.1.96 Glycoprotein N-palmitoyltransferase. | 2.3.1.131 Glucarate O-hydroxycinnamoyltransferase. |
| 2.3.1.97 Glycylpeptide N-tetradecanoyltransferase. | 2.3.1.132 Glucarolactone O-hydroxycinnamoyltransferase. |
| 2.3.1.98 Chlorogenate--glucarate O-hydroxycinnamoyltransferase. | 2.3.1.133 Shikimate O-hydroxycinnamoyltransferase. |
| 2.3.1.99 Quinate O-hydroxycinnamoyltransferase. | 2.3.1.134 Galactolipid O-acyltransferase. |
| 2.3.1.100 Myelin-proteolipid O-palmitoyltransferase. | 2.3.1.135 Phosphatidylcholine--retinol O-acyltransferase. |
| 2.3.1.101 Formylmethanofuran--tetrahydromethanopterin N-formyltransferase. | 2.3.1.136 Polysialic-acid O-acetyltransferase. |
| 2.3.1.102 N(6)-hydroxylysine O-acetyltransferase. | 2.3.1.137 Carnitine O-octanoyltransferase. |
| 2.3.1.103 Sinapoylglucose--sinapoylglucose O-sinapoyltransferase. | 2.3.1.138 Putrescine N-hydroxycinnamoyltransferase. |
| 2.3.1.104 1-alkenylglycerophosphocholine O-acyltransferase. | 2.3.1.139 Ecdysone O-acyltransferase. |
| 2.3.1.105 Alkylglycerophosphate 2-O-acetyltransferase. | 2.3.1.140 Rosmarinate synthase. |
| 2.3.1.106 Tartronate O-hydroxycinnamoyltransferase. | 2.3.1.141 Galactosylacylglycerol O-acyltransferase. |
| 2.3.1.107 17-O-deacetylindoline O-acetyltransferase. | 2.3.1.142 Glycoprotein O-fatty-acyltransferase. |
| 2.3.1.108 Tubulin N-acetyltransferase. | 2.3.1.143 Beta-glucogallin--tetrakisgalloylglucose O-galloyltransferase. |
| 2.3.1.109 Arginine N-succinyltransferase. | 2.3.1.144 Anthranilate N-benzoyltransferase. |
| 2.3.1.110 Tyramine N-feruloyltransferase. | 2.3.1.145 Piperidine N-piperoyltransferase. |
| 2.3.1.111 Mycocerosate synthase. | 2.3.1.146 Pinosylvin synthase. |
| 2.3.1.112 D-tryptophan N-malonyltransferase. | 2.3.1.147 Glycerophospholipid arachidonoyltransferase (CoA-independent). |
| 2.3.1.113 Anthranilate N-malonyltransferase. | 2.3.1.148 Glycerophospholipid acyltransferase (CoA-dependent). |
| 2.3.1.114 3,4-dichloroaniline N-malonyltransferase. | 2.3.1.149 Platelet-activating factor acetyltransferase. |
| 2.3.1.115 Isoflavone-7-O-beta-glucoside 6"-O-malonyltransferase. | 2.3.1.150 Salutaridinol 7-O-acetyltransferase. |
| 2.3.1.116 Flavonol-3-O-beta-glucoside O-malonyltransferase. | 2.3.1.151 Benzophenone synthase. |
| 2.3.1.117 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase. | 2.3.1.152 Alcohol O-cinnamoyltransferase. |
| 2.3.1.118 N-hydroxyarylamine O-acetyltransferase. | 2.3.1.153 Anthocyanin 5-aromatic |

| | |
|--|---|
| | acyltransferase. |
| 2.3.1.119 Icosanoyl-CoA synthase. | 2.3.1.154 Propionyl-CoA C(2)-trimethyltridecanoyltransferase. |
| 2.3.1.121 1-alkenylglycerophosphoethanolamine O-acyltransferase. | 2.3.1.155 Acetyl-CoA C-myristoyltransferase. |

| | |
|--|--|
| 2.3.1.156 Phloroisovalerophenone synthase. | 2.3.3.12 3-propylmalate synthase. |
| 2.3.1.157 Glucosamine-1-phosphate N-acetyltransferase. | 2.3.3.13 2-isopropylmalate synthase. |
| 2.3.1.158 Phospholipid:diacylglycerol acyltransferase. | 2.3.3.14 Homocitrate synthase. |
| 2.3.1.159 Acridone synthase. | 2.3.3.15 Sulfoacetaldehyde acetyltransferase. |
| 2.3.1.160 Vinorine synthase. | 2.4.1.1 Phosphorylase. |
| 2.3.1.161 Lovastatin nonaketide synthase. | 2.4.1.2 Dextrin dextranase. |
| 2.3.1.162 Taxadien-5-alpha-ol O-acetyltransferase. | 2.4.1.4 Amylosucrase. |
| 2.3.1.163 10-hydroxytaxane O-acetyltransferase. | 2.4.1.5 Dextransucrase. |
| 2.3.1.164 Isopenicillin-N N-acyltransferase. | 2.4.1.7 Sucrose phosphorylase. |
| 2.3.1.165 6-methylsalicylic acid synthase. | 2.4.1.8 Maltose phosphorylase. |
| 2.3.1.166 2-alpha-hydroxytaxane 2-O-benzoyltransferase. | 2.4.1.9 Inulosucrase. |
| 2.3.1.167 10-deacetylbaicatin III 10-O-acetyltransferase. | 2.4.1.10 Levansucrase. |
| 2.3.1.168 Dihydrolypoyllysine-residue (2-methylpropanoyl)transferase. | 2.4.1.11 Glycogen (starch) synthase. |
| 2.3.1.169 CO-methylating acetyl-CoA synthase. | 2.4.1.12 Cellulose synthase (UDP-forming). |
| 2.3.2.1 D-glutamyltransferase. | 2.4.1.13 Sucrose synthase. |
| 2.3.2.2 Gamma-glutamyltransferase. | 2.4.1.14 Sucrose-phosphate synthase. |
| 2.3.2.3 Lysyltransferase. | 2.4.1.15 Alpha,alpha-trehalose-phosphate synthase (UDP-forming). |
| 2.3.2.4 Gamma-glutamylcyclotransferase. | 2.4.1.16 Chitin synthase. |
| 2.3.2.5 Glutaminy-peptide cyclotransferase. | 2.4.1.17 Glucuronosyltransferase. |
| 2.3.2.6 Leucyltransferase. | 2.4.1.18 1,4-alpha-glucan branching enzyme. |
| 2.3.2.7 Aspartyltransferase. | 2.4.1.19 Cyclomaltodextrin glucanotransferase. |
| 2.3.2.8 Arginyltransferase. | 2.4.1.20 Cellobiose phosphorylase. |
| 2.3.2.9 Agaritine gamma-glutamyltransferase. | 2.4.1.21 Starch synthase. |
| 2.3.2.10 UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase. | 2.4.1.22 Lactose synthase. |
| 2.3.2.11 Alanylphosphatidylglycerol synthase. | 2.4.1.23 Sphingosine beta-galactosyltransferase. |
| 2.3.2.12 Peptidyltransferase. | 2.4.1.24 1,4-alpha-glucan 6-alpha-glucosyltransferase. |
| 2.3.2.13 Protein-glutamine gamma-glutamyltransferase. | 2.4.1.25 4-alpha-glucanotransferase. |
| 2.3.2.14 D-alanine gamma-glutamyltransferase. | 2.4.1.26 DNA alpha-glucosyltransferase. |
| 2.3.2.15 Glutathione gamma-glutamylcysteinyltransferase. | 2.4.1.27 DNA beta-glucosyltransferase. |
| 2.3.3.1 Citrate (Si)-synthase. | 2.4.1.28 Glucosyl-DNA beta-glucosyltransferase. |
| 2.3.3.2 Decylcitrate synthase. | 2.4.1.29 Cellulose synthase (GDP-forming). |
| 2.3.3.3 Citrate (Re)-synthase. | 2.4.1.30 1,3-beta-oligoglucan phosphorylase. |
| 2.3.3.4 Decylhomocitrate synthase. | 2.4.1.31 Laminaribiose phosphorylase. |

| | | | |
|----------|-------------------------------------|----------|---|
| 2.3.3.5 | 2-methylcitrate synthase. | 2.4.1.32 | Glucomannan 4-beta-mannosyltransferase. |
| 2.3.3.6 | 2-ethylmalate synthase. | 2.4.1.33 | Alginate synthase. |
| 2.3.3.7 | 3-ethylmalate synthase. | 2.4.1.34 | 1,3-beta-glucan synthase. |
| 2.3.3.8 | ATP citrate synthase. | 2.4.1.35 | Phenol beta-glucosyltransferase. |
| 2.3.3.9 | Malate synthase. | 2.4.1.36 | Alpha, alpha-trehalose-phosphate synthase (GDP-forming). |
| 2.3.3.10 | Hydroxymethylglutaryl-CoA synthase. | 2.4.1.37 | Fucosylgalactoside 3-alpha-galactosyltransferase. |
| 2.3.3.11 | 2-hydroxyglutarate synthase. | 2.4.1.38 | Beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase. |

| | | | |
|----------|---|----------|--|
| 2.4.1.39 | Steroid N-acetylglucosaminyltransferase. | 2.4.1.71 | Arylamine glucosyltransferase. |
| 2.4.1.40 | Glycoprotein-fucosylgalactoside alpha-N-acetylglactosaminyltransferase. | 2.4.1.73 | Lipopolysaccharide glucosyltransferase II. |
| 2.4.1.41 | Polypeptide N-acetylglactosaminyltransferase. | 2.4.1.74 | Glycosaminoglycan galactosyltransferase. |
| 2.4.1.43 | Polygalacturonate 4-alpha-galacturonosyltransferase. | 2.4.1.75 | UDP-galacturonosyltransferase. |
| 2.4.1.44 | Lipopolysaccharide 3-alpha-galactosyltransferase. | 2.4.1.78 | Phosphopolyprenol glucosyltransferase. |
| 2.4.1.45 | 2-hydroxyacylsphingosine 1-beta-galactosyltransferase. | 2.4.1.79 | Galactosylgalactosylglucosylceramide beta-D- acetylglactosaminyltransferase. |
| 2.4.1.46 | 1,2-diacylglycerol 3-beta-galactosyltransferase. | 2.4.1.80 | Ceramide glucosyltransferase. |
| 2.4.1.47 | N-acylsphingosine galactosyltransferase. | 2.4.1.81 | Flavone 7-O-beta-glucosyltransferase. |
| 2.4.1.48 | Heteroglycan alpha-mannosyltransferase. | 2.4.1.82 | Galactinol-sucrose galactosyltransferase. |
| 2.4.1.49 | Cellodextrin phosphorylase. | 2.4.1.83 | Dolichyl-phosphate beta-D-mannosyltransferase. |
| 2.4.1.50 | Procollagen galactosyltransferase. | 2.4.1.85 | Cyanohydrin beta-glucosyltransferase. |
| 2.4.1.52 | Poly(glycerol-phosphate) alpha-glucosyltransferase. | 2.4.1.86 | Glucosaminylgalactosylglucosylceramide beta-galactosyltransferase. |
| 2.4.1.53 | Poly(ribitol-phosphate) beta-glucosyltransferase. | 2.4.1.87 | N-acetylactosaminide 3-alpha-galactosyltransferase. |
| 2.4.1.54 | Undecaprenyl-phosphate mannosyltransferase. | 2.4.1.88 | Globoside alpha-N-acetylglactosaminyltransferase. |
| 2.4.1.56 | Lipopolysaccharide N-acetylglucosaminyltransferase. | 2.4.1.90 | N-acetylactosamine synthase. |
| 2.4.1.57 | Phosphatidylinositol alpha-mannosyltransferase. | 2.4.1.91 | Flavonol 3-O-glucosyltransferase. |
| 2.4.1.58 | Lipopolysaccharide glucosyltransferase I. | 2.4.1.92 | (N-acetylneuraminy)-galactosylglucosylceramide N-acetylglactosaminyltransferase. |
| 2.4.1.60 | Abequosyltransferase. | 2.4.1.94 | Protein N-acetylglucosaminyltransferase. |
| 2.4.1.62 | Ganglioside galactosyltransferase. | 2.4.1.95 | Bilirubin-glucuronoside glucuronosyltransferase. |
| 2.4.1.63 | Linamarin synthase. | 2.4.1.96 | Sn-glycerol-3-phosphate 1-galactosyltransferase. |
| 2.4.1.64 | Alpha, alpha-trehalose phosphorylase. | 2.4.1.97 | 1,3-beta-D-glucan phosphorylase. |
| 2.4.1.65 | 3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase. | 2.4.1.99 | Sucrose:sucrose fructosyltransferase. |

| | |
|---|---|
| 2.4.1.66 Procollagen glucosyltransferase. | 2.4.1.100 2,1-fructan:2,1-fructan 1-fructosyltransferase. |
| 2.4.1.67 Galactinol--raffinose galactosyltransferase. | 2.4.1.101 Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase. |
| 2.4.1.68 Glycoprotein 6-alpha-L-fucosyltransferase. | 2.4.1.102 Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase. |
| 2.4.1.69 Galactoside 2-alpha-L-fucosyltransferase. | 2.4.1.103 Alizarin 2-beta-glucosyltransferase. |
| 2.4.1.70 Poly(ribitol-phosphate) N-acetylglucosaminyltransferase. | 2.4.1.104 O-dihydroxycoumarin 7-O-glucosyltransferase. |

| | |
|---|--|
| 2.4.1.105 Vitexin beta-glucosyltransferase. | 2.4.1.135 Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase. |
| 2.4.1.106 Isovitexin beta-glucosyltransferase. | 2.4.1.136 Gallate 1-beta-glucosyltransferase. |
| 2.4.1.109 Dolichyl-phosphate-mannose--protein mannosyltransferase. | 2.4.1.137 Sn-glycerol-3-phosphate 2-alpha-galactosyltransferase. |
| 2.4.1.110 tRNA-queuosine beta-mannosyltransferase. | 2.4.1.138 Mannotetraose 2-alpha-N-acetylglucosaminyltransferase. |
| 2.4.1.111 Coniferyl-alcohol glucosyltransferase. | 2.4.1.139 Maltose synthase. |
| 2.4.1.112 Alpha-1,4-glucan-protein synthase (UDP-forming). | 2.4.1.140 Alternansucrase. |
| 2.4.1.113 Alpha-1,4-glucan-protein synthase (ADP-forming). | 2.4.1.141 N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase. |
| 2.4.1.114 2-coumarate O-beta-glucosyltransferase. | 2.4.1.142 Chitobiosyldiphosphodolichol beta-mannosyltransferase. |
| 2.4.1.115 Anthocyanidin 3-O-glucosyltransferase. | 2.4.1.143 Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase. |
| 2.4.1.116 Cyanidin-3-rhamnosylglucoside 5-O-glucosyltransferase. | 2.4.1.144 Beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase. |
| 2.4.1.117 Dolichyl-phosphate beta-glucosyltransferase. | 2.4.1.145 Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase. |
| 2.4.1.118 Cytokinin 7-beta-glucosyltransferase. | 2.4.1.146 Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,3-N-acetylglucosaminyltransferase. |
| 2.4.1.119 Dolichyl-diphosphooligosaccharide-protein glycotransferase. | 2.4.1.147 Acetylgalactosaminyl-O-glycosyl-glycoprotein beta-1,3-N-acetylglucosaminyltransferase. |
| 2.4.1.120 Sinapate 1-glucosyltransferase. | 2.4.1.148 Acetylgalactosaminyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase. |
| 2.4.1.121 Indole-3-acetate beta-glucosyltransferase. | 2.4.1.149 N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase. |
| 2.4.1.122 Glycoprotein-N-acetylglactosamine 3-beta-galactosyltransferase. | 2.4.1.150 N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase. |
| 2.4.1.123 Inositol 3-alpha-galactosyltransferase. | 2.4.1.152 4-galactosyl-N-acetylglucosaminide 3-alpha-L-fucosyltransferase. |
| 2.4.1.125 Sucrose-1,6-alpha-glucan 3(6)-alpha-glucosyltransferase. | 2.4.1.153 Dolichyl-phosphate alpha-N-acetylglucosaminyltransferase. |
| 2.4.1.126 Hydroxycinnamate 4-beta-glucosyltransferase. | 2.4.1.154 Globotriosylceramide beta-1,6-N-acetylglactosaminyl-transferase. |
| 2.4.1.127 Monoterpenol beta-glucosyltransferase. | 2.4.1.155 Alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglucosaminyltransferase. |
| 2.4.1.128 Scopoletin glucosyltransferase. | 2.4.1.156 Indolylacetyl-myo-inositol galactosyltransferase. |

| | |
|---|--|
| 2.4.1.129 Peptidoglycan glycosyltransferase. | 2.4.1.157 1,2-diacylglycerol 3-glucosyltransferase. |
| 2.4.1.130 Dolichyl-phosphate-mannose--glycolipid alpha-mannosyltransferase. | 2.4.1.158 13-hydroxydocosanoate 13-beta-glucosyltransferase. |
| 2.4.1.131 Glycolipid 2-alpha-mannosyltransferase. | 2.4.1.159 Flavonol-3-O-glucoside L-rhamnosyltransferase. |
| 2.4.1.132 Glycolipid 3-alpha-mannosyltransferase. | 2.4.1.160 Pyridoxine 5'-O-beta-D-glucosyltransferase. |
| 2.4.1.133 Xylosylprotein 4-beta-galactosyltransferase. | 2.4.1.161 Oligosaccharide 4-alpha-D-glucosyltransferase. |
| 2.4.1.134 Galactosylxylosylprotein 3-beta-galactosyltransferase. | 2.4.1.162 Aldose beta-D-fructosyltransferase. |

| | |
|---|--|
| 2.4.1.163 Beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,3-acetylglucosaminyltransferase. | 2.4.1.191 Luteolin-7-O-diglucuronide 4'-O-glucuronosyltransferase. |
| 2.4.1.164 Galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,6-N-acetylglucosaminyltransferase. | 2.4.1.192 Nuatigenin 3-beta-glucosyltransferase. |
| 2.4.1.165 N-acetylneuraminylgalactosylglucosylceramide beta-1,4-N-acetylglactosaminyltransferase. | 2.4.1.193 Sarsapogenin 3-beta-glucosyltransferase. |
| 2.4.1.166 Raffinose--raffinose alpha-galactosyltransferase. | 2.4.1.194 4-hydroxybenzoate 4-O-beta-D-glucosyltransferase. |
| 2.4.1.167 Sucrose 6(F)-alpha-galactosyltransferase. | 2.4.1.195 Thiohydroximate beta-D-glucosyltransferase. |
| 2.4.1.168 Xyloglucan 4-glucosyltransferase. | 2.4.1.196 Nicotinate glucosyltransferase. |
| 2.4.1.170 Isoflavone 7-O-glucosyltransferase. | 2.4.1.197 High-mannose-oligosaccharide beta-1,4-N-acetylglucosaminyltransferase. |
| 2.4.1.171 Methyl-ONN-azoxymethanol beta-D-glucosyltransferase. | 2.4.1.198 Phosphatidylinositol N-acetylglucosaminyltransferase. |
| 2.4.1.172 Salicyl-alcohol beta-D-glucosyltransferase. | 2.4.1.199 Beta-mannosylphosphodecaprenol--mannooligosaccharide 6-mannosyltransferase. |
| 2.4.1.173 Sterol 3-beta-glucosyltransferase. | 2.4.1.201 Alpha-1,6-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase. |
| 2.4.1.174 Glucuronylgalactosylproteoglycan 4-beta-N-acetylglactosaminyltransferase. | 2.4.1.202 2,4-dihydroxy-7-methoxy-2H-1,4-benzoxazin-3(4H)-one 2-D-glucosyltransferase. |
| 2.4.1.175 Glucuronosyl-N-acetylglactosaminyl-proteoglycan 4-beta-N-acetylglactosaminyltransferase. | 2.4.1.203 Trans-zeatin O-beta-D-glucosyltransferase. |
| 2.4.1.176 Gibberellin beta-D-glucosyltransferase. | 2.4.1.205 Galactogen 6-beta-galactosyltransferase. |
| 2.4.1.177 Cinnamate beta-D-glucosyltransferase. | 2.4.1.206 Lactosylceramide 1,3-N-acetyl-beta-D-glucosaminyltransferase. |
| 2.4.1.178 Hydroxymandelonitrile glucosyltransferase. | 2.4.1.207 Xyloglucan:xyloglucosyl transferase. |
| 2.4.1.179 Lactosylceramide beta-1,3-galactosyltransferase. | 2.4.1.208 Diglucosyl diacylglycerol synthase. |
| 2.4.1.180 Lipopolysaccharide N-acetylmannosaminouronosyltransferase. | 2.4.1.209 Cis-p-coumarate glucosyltransferase. |
| 2.4.1.181 Hydroxyanthraquinone glucosyltransferase. | 2.4.1.210 Limonoid glucosyltransferase. |
| 2.4.1.182 Lipid-A-disaccharide synthase. | 2.4.1.211 1,3-beta-galactosyl-N-acetylhexosamine phosphorylase. |
| 2.4.1.183 Alpha-1,3-glucan synthase. | 2.4.1.212 Hyaluronan synthase. |

| | |
|---|--|
| 2.4.1.184 Galactolipid galactosyltransferase. | 2.4.1.213 Glucosylglycerol-phosphate synthase. |
| 2.4.1.185 Flavanone 7-O-beta-glucosyltransferase. | 2.4.1.214 Glycoprotein 3-alpha-L-fucosyltransferase. |
| 2.4.1.186 Glycogenin glucosyltransferase. | 2.4.1.215 Cis-zeatin O-beta-D-glucosyltransferase. |
| 2.4.1.187 N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-beta-D-mannosaminytransferase. | 2.4.1.216 Trehalose 6-phosphate phosphorylase. |
| 2.4.1.188 N-acetylglucosaminyldiphosphoundecaprenol glucosyltransferase. | 2.4.1.217 Mannosyl-3-phosphoglycerate synthase. |
| 2.4.1.189 Luteolin 7-O-glucuronosyltransferase. | 2.4.1.218 Hydroquinone glucosyltransferase. |
| 2.4.1.190 Luteolin-7-O-glucuronide 7-O-glucuronosyltransferase. | 2.4.1.219 Vomilenine glucosyltransferase. |

| | |
|---|---|
| 2.4.1.220 Indoxyl-UDPG glucosyltransferase. | 2.4.2.19 Nicotinate-nucleotide diphosphorylase (carboxylating). |
| 2.4.1.221 Peptide-O-fucosyltransferase. | 2.4.2.20 Dioxotetrahydropyrimidine phosphoribosyltransferase. |
| 2.4.1.222 O-fucosylpeptide 3-beta-N-acetylglucosaminytransferase. | 2.4.2.21 Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase. |
| 2.4.1.223 Glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminytransferase. | 2.4.2.22 Xanthine phosphoribosyltransferase. |
| 2.4.1.224 Glucuronosyl-N-acetylglucosaminy-proteoglycan 4-alpha-N-acetylglucosaminytransferase. | 2.4.2.23 Deoxyuridine phosphorylase. |
| 2.4.1.225 N-acetylglucosaminy-proteoglycan 4-beta-glucuronosyltransferase. | 2.4.2.24 1,4-beta-D-xylan synthase. |
| 2.4.1.226 N-acetylglactosaminy-proteoglycan 3-beta-glucuronosyltransferase. | 2.4.2.25 Flavone apiosyltransferase. |
| 2.4.1.227 Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminytransferase. | 2.4.2.26 Protein xylosyltransferase. |
| 2.4.1.228 Lactosylceramide 4-alpha-galactosyltransferase. | 2.4.2.27 dTDP-dihydrostreptose--streptidine-6-phosphate dihydrostreptosyltransferase. |
| 2.4.1.229 [Skp1-protein]-hydroxyproline N-acetylglucosaminytransferase. | 2.4.2.28 S-methyl-5-thioadenosine phosphorylase. |
| 2.4.1.230 Kojibiose phosphorylase. | 2.4.2.29 Queuine tRNA-ribosyltransferase. |
| 2.4.1.231 Alpha, alpha-trehalose phosphorylase (configuration-retaining). | 2.4.2.30 NAD(+) ADP-ribosyltransferase. |
| 2.4.1.232 Initiation-specific alpha-1,6-mannosyltransferase. | 2.4.2.31 NAD(P)(+)-arginine ADP-ribosyltransferase. |
| 2.4.2.1 Purine-nucleoside phosphorylase. | 2.4.2.32 Dolichyl-phosphate D-xylosyltransferase. |
| 2.4.2.2 Pyrimidine-nucleoside phosphorylase. | 2.4.2.33 Dolichyl-xylosyl-phosphate-protein xylosyltransferase. |
| 2.4.2.3 Uridine phosphorylase. | 2.4.2.34 Indolylacetylinoitol arabinosyltransferase. |
| 2.4.2.4 Thymidine phosphorylase. | 2.4.2.35 Flavonol-3-O-glycoside xylosyltransferase. |
| 2.4.2.5 Nucleoside ribosyltransferase. | 2.4.2.36 NAD(+)-diphthamide ADP-ribosyltransferase. |
| 2.4.2.6 Nucleoside deoxyribosyltransferase. | 2.4.2.37 NAD(+)-dinitrogen-reductase ADP-D-ribosyltransferase. |
| 2.4.2.7 Adenine phosphoribosyltransferase. | 2.4.2.38 Glycoprotein 2-beta-D-xylosyltransferase. |
| 2.4.2.8 Hypoxanthine phosphoribosyltransferase. | 2.4.2.39 Xyloglucan 6-xylosyltransferase. |
| 2.4.2.9 Uracil phosphoribosyltransferase. | 2.4.2.40 Zeatin O-beta-D-xylosyltransferase. |

| | | | |
|----------|---|----------|---|
| 2.4.2.10 | Orotate phosphoribosyltransferase. | 2.4.99.1 | Beta-galactoside alpha-2,6-sialyltransferase. |
| 2.4.2.11 | Nicotinate phosphoribosyltransferase. | 2.4.99.2 | Monosialoganglioside sialyltransferase. |
| 2.4.2.12 | Nicotinamide phosphoribosyltransferase. | 2.4.99.3 | Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase. |
| 2.4.2.14 | Amidophosphoribosyltransferase. | 2.4.99.4 | Beta-galactoside alpha-2,3-sialyltransferase. |
| 2.4.2.15 | Guanosine phosphorylase. | 2.4.99.5 | Galactosyldiacylglycerol alpha-2,3-sialyltransferase. |
| 2.4.2.16 | Urate-ribonucleotide phosphorylase. | 2.4.99.6 | N-acetyllactosaminide alpha-2,3-sialyltransferase. |
| 2.4.2.17 | ATP phosphoribosyltransferase. | 2.4.99.7 | (Alpha-N-acetylneuraminy-2,3-beta-galactosyl-1,3)-N-acetyl-galactosaminide 6-alpha-sialyltransferase. |
| 2.4.2.18 | Anthranelate phosphoribosyltransferase. | 2.4.99.8 | Alpha-N-acetylneuraminate alpha-2,8-sialyltransferase. |

| | | | |
|-----------|--|----------|---|
| 2.4.99.9 | Lactosylceramide alpha-2,3-sialyltransferase. | 2.5.1.42 | Geranylgeranyl-glycerol-phosphate geranylgeranyltransferase. |
| 2.4.99.10 | Neolactotetraosylceramide alpha-2,3-sialyltransferase. | 2.5.1.43 | Nicotianamine synthase. |
| 2.4.99.11 | Lactosylceramide alpha-2,6-N-sialyltransferase. | 2.5.1.44 | Homospermidine synthase. |
| 2.5.1.1 | Dimethylallyltranstransferase. | 2.5.1.45 | Homospermidine synthase (spermidine-specific). |
| 2.5.1.2 | Thiamine pyridinylase. | 2.5.1.46 | Deoxyhypusine synthase. |
| 2.5.1.3 | Thiamine-phosphate diphosphorylase. | 2.5.1.47 | Cysteine synthase. |
| 2.5.1.4 | Adenosylmethionine cyclotransferase. | 2.5.1.48 | Cystathionine gamma-synthase. |
| 2.5.1.5 | Galactose-6-sulfurylase. | 2.5.1.49 | O-acetylhomoserine aminocarboxypropyltransferase. |
| 2.5.1.6 | Methionine adenosyltransferase. | 2.5.1.50 | Zeatin 9-aminocarboxyethyltransferase. |
| 2.5.1.7 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase. | 2.5.1.51 | Beta-pyrazolylalanine synthase. |
| 2.5.1.8 | tRNA isopentenyltransferase. | 2.5.1.52 | L-mimosine synthase. |
| 2.5.1.9 | Riboflavin synthase. | 2.5.1.53 | Uracilylalanine synthase. |
| 2.5.1.10 | Geranyltranstransferase. | 2.5.1.54 | 3-deoxy-7-phosphoheptulonate synthase. |
| 2.5.1.11 | Trans-octaprenyltranstransferase. | 2.5.1.55 | 3-deoxy-8-phosphooctulonate synthase. |
| 2.5.1.15 | Dihydropteroate synthase. | 2.5.1.56 | N-acetylneuraminate synthase. |
| 2.5.1.16 | Spermidine synthase. | 2.5.1.57 | N-acetylneuraminate-9-phosphate synthase. |
| 2.5.1.17 | Cob(I)yrinic acid a,c-diamide adenosyltransferase. | 2.5.1.58 | Protein farnesyltransferase. |
| 2.5.1.18 | Glutathione transferase. | 2.5.1.59 | Protein geranylgeranyltransferase type I. |
| 2.5.1.19 | 3-phosphoshikimate 1-carboxyvinyltransferase. | 2.5.1.60 | Protein geranylgeranyltransferase type II. |
| 2.5.1.20 | Rubber cis-polyprenylcistransferase. | 2.5.1.61 | Hydroxymethylbilane synthase. |
| 2.5.1.21 | Farnesyl-diphosphate farnesyltransferase. | 2.5.1.62 | Chlorophyll synthase. |
| 2.5.1.22 | Spermine synthase. | 2.5.1.63 | Adenosyl-fluoride synthase. |
| 2.5.1.23 | Sym-norspermidine synthase. | 2.5.1.64 | 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase. |
| 2.5.1.24 | Discadenine synthase. | 2.6.1.1 | Aspartate transaminase. |
| 2.5.1.25 | tRNA-uridine aminocarboxypropyltransferase. | 2.6.1.2 | Alanine transaminase. |
| 2.5.1.26 | Alkylglycerone-phosphate synthase. | 2.6.1.3 | Cysteine transaminase. |
| 2.5.1.27 | Adenylate dimethylallyltransferase. | 2.6.1.4 | Glycine transaminase. |

| | | | |
|----------|---|----------|---|
| 2.5.1.28 | Dimethylallylcistransferase. | 2.6.1.5 | Tyrosine transaminase. |
| 2.5.1.29 | Farnesyltranstransferase. | 2.6.1.6 | Leucine transaminase. |
| 2.5.1.30 | Trans-hexaprenyltranstransferase. | 2.6.1.7 | Kynurenine--oxoglutarate transaminase. |
| 2.5.1.31 | Di-trans,poly-cis-decaprenylcistransferase. | 2.6.1.8 | 2,5-diaminovalerate transaminase. |
| 2.5.1.32 | Geranylgeranyl-diphosphate geranylgeranyltransferase. | 2.6.1.9 | Histidinol-phosphate transaminase. |
| 2.5.1.33 | Trans-pentaprenyltranstransferase. | 2.6.1.11 | Acetylornithine transaminase. |
| 2.5.1.34 | Tryptophan dimethylallyltransferase. | 2.6.1.12 | Alanine--oxo-acid transaminase. |
| 2.5.1.35 | Aspulinone dimethylallyltransferase. | 2.6.1.13 | Ornithine--oxo-acid transaminase. |
| 2.5.1.36 | Trihydroxypterocarpan dimethylallyltransferase. | 2.6.1.14 | Asparagine--oxo-acid transaminase. |
| 2.5.1.38 | Isonocardicin synthase. | 2.6.1.15 | Glutamine--pyruvate transaminase. |
| 2.5.1.39 | 4-hydroxybenzoate nonaprenyltransferase. | 2.6.1.16 | Glutamine--fructose-6-phosphate transaminase (isomerizing). |
| 2.5.1.41 | Phosphoglycerol geranylgeranyltransferase. | 2.6.1.17 | Succinyldiaminopimelate transaminase. |

| | | | |
|----------|---|----------|--|
| 2.6.1.18 | Beta-alanine--pyruvate transaminase. | 2.6.1.62 | Adenosylmethionine--8-amino-7-oxononanoate transaminase. |
| 2.6.1.19 | 4-aminobutyrate transaminase. | 2.6.1.63 | Kynurenine--glyoxylate transaminase. |
| 2.6.1.21 | D-alanine transaminase. | 2.6.1.64 | Glutamine--phenylpyruvate transaminase. |
| 2.6.1.22 | (S)-3-amino-2-methylpropionate transaminase. | 2.6.1.65 | N(6)-acetyl-beta-lysine transaminase. |
| 2.6.1.23 | 4-hydroxyglutamate transaminase. | 2.6.1.66 | Valine--pyruvate transaminase. |
| 2.6.1.24 | Diiodotyrosine transaminase. | 2.6.1.67 | 2-aminohexanoate transaminase. |
| 2.6.1.26 | Thyroid-hormone transaminase. | 2.6.1.68 | Ornithine(lysine) transaminase. |
| 2.6.1.27 | Tryptophan transaminase. | 2.6.1.70 | Aspartate--phenylpyruvate transaminase. |
| 2.6.1.28 | Tryptophan--phenylpyruvate transaminase. | 2.6.1.71 | Lysine--pyruvate 6-transaminase. |
| 2.6.1.29 | Diamine transaminase. | 2.6.1.72 | D-4-hydroxyphenylglycine transaminase. |
| 2.6.1.30 | Pyridoxamine--pyruvate transaminase. | 2.6.1.73 | Methionine--glyoxylate transaminase. |
| 2.6.1.31 | Pyridoxamine--oxaloacetate transaminase. | 2.6.1.74 | Cephalosporin-C transaminase. |
| 2.6.1.32 | Valine--3-methyl-2-oxovalerate transaminase. | 2.6.1.75 | Cysteine-conjugate transaminase. |
| 2.6.1.33 | dTDP-4-amino-4,6-dideoxy-D-glucose transaminase. | 2.6.1.76 | Diaminobutyrate--2-oxoglutarate transaminase. |
| 2.6.1.34 | UDP-2-acetamido-4-amino-2,4,6-trideoxyglucose transaminase. | 2.6.1.77 | Taurine--pyruvate aminotransferase. |
| 2.6.1.35 | Glycine--oxaloacetate transaminase. | 2.6.3.1 | Oximinotransferase. |
| 2.6.1.36 | L-lysine 6-transaminase. | 2.6.99.1 | dATP(dGTP)--DNA purinetransferase. |
| 2.6.1.37 | 2-aminoethylphosphonate--pyruvate transaminase. | 2.7.1.1 | Hexokinase. |
| 2.6.1.38 | Histidine transaminase. | 2.7.1.2 | Glucokinase. |
| 2.6.1.39 | 2-aminoadipate transaminase. | 2.7.1.3 | Ketohexokinase. |
| 2.6.1.40 | (R)-3-amino-2-methylpropionate--pyruvate transaminase. | 2.7.1.4 | Fructokinase. |
| 2.6.1.41 | D-methionine--pyruvate transaminase. | 2.7.1.5 | Rhamnulokinase. |
| 2.6.1.42 | Branched-chain-amino-acid transaminase. | 2.7.1.6 | Galactokinase. |
| 2.6.1.43 | Aminolevulinate transaminase. | 2.7.1.7 | Mannokinase. |
| 2.6.1.44 | Alanine--glyoxylate transaminase. | 2.7.1.8 | Glucosamine kinase. |
| 2.6.1.45 | Serine--glyoxylate transaminase. | 2.7.1.10 | Phosphoglucokinase. |

| | |
|--|--------------------------------------|
| 2.6.1.46 Diaminobutyrate-pyruvate transaminase. | 2.7.1.11 6-phosphofructokinase. |
| 2.6.1.47 Alanine-oxomalonate transaminase. | 2.7.1.12 Gluconokinase. |
| 2.6.1.48 5-aminovalerate transaminase. | 2.7.1.13 Dehydrogluconokinase. |
| 2.6.1.49 Dihydroxyphenylalanine transaminase. | 2.7.1.14 Sedoheptulokinase. |
| 2.6.1.50 Glutamine-scylo-inositol transaminase. | 2.7.1.15 Ribokinase. |
| 2.6.1.51 Serine-pyruvate transaminase. | 2.7.1.16 Ribulokinase. |
| 2.6.1.52 Phosphoserine transaminase. | 2.7.1.17 Xylulokinase. |
| 2.6.1.54 Pyridoxamine-phosphate transaminase. | 2.7.1.18 Phosphoribokinase. |
| 2.6.1.55 Taurine-2-oxoglutarate transaminase. | 2.7.1.19 Phosphoribulokinase. |
| 2.6.1.56 1D-1-guanidino-3-amino-1,3-dideoxy-scylo-inositol transaminase. | 2.7.1.20 Adenosine kinase. |
| 2.6.1.57 Aromatic-amino-acid transaminase. | 2.7.1.21 Thymidine kinase. |
| 2.6.1.58 Phenylalanine(histidine) transaminase. | 2.7.1.22 Ribosylnicotinamide kinase. |
| 2.6.1.59 dTDP-4-amino-4,6-dideoxygalactose transaminase. | 2.7.1.23 NAD(+) kinase. |
| 2.6.1.60 Aromatic-amino-acid-glyoxylate transaminase. | 2.7.1.24 Dephospho-CoA kinase. |

| | |
|--|---|
| 2.7.1.25 Adenylyl-sulfate kinase. | 2.7.1.69 Protein-N(pi)-phosphohistidine-sugar phosphotransferase. |
| 2.7.1.26 Riboflavin kinase. | 2.7.1.71 Shikimate kinase. |
| 2.7.1.27 Erythritol kinase. | 2.7.1.72 Streptomycin 6-kinase. |
| 2.7.1.28 Triokinase. | 2.7.1.73 Inosine kinase. |
| 2.7.1.29 Glycerone kinase. | 2.7.1.74 Deoxycytidine kinase. |
| 2.7.1.30 Glycerol kinase. | 2.7.1.76 Deoxyadenosine kinase. |
| 2.7.1.31 Glycerate kinase. | 2.7.1.77 Nucleoside phosphotransferase. |
| 2.7.1.32 Choline kinase. | 2.7.1.78 Polynucleotide 5'-hydroxy-kinase. |
| 2.7.1.33 Pantothenate kinase. | 2.7.1.79 Diphosphate-glycerol phosphotransferase. |
| 2.7.1.34 Pantetheine kinase. | 2.7.1.80 Diphosphate-serine phosphotransferase. |
| 2.7.1.35 Pyridoxal kinase. | 2.7.1.81 Hydroxyllysine kinase. |
| 2.7.1.36 Mevalonate kinase. | 2.7.1.82 Ethanolamine kinase. |
| 2.7.1.37 Protein kinase. | 2.7.1.83 Pseudouridine kinase. |
| 2.7.1.38 Phosphorylase kinase. | 2.7.1.84 Alkylglycerone kinase. |
| 2.7.1.39 Homoserine kinase. | 2.7.1.85 Beta-glucoside kinase. |
| 2.7.1.40 Pyruvate kinase. | 2.7.1.86 NADH kinase. |
| 2.7.1.41 Glucose-1-phosphate phosphodismutase. | 2.7.1.87 Streptomycin 3"-kinase. |
| 2.7.1.42 Riboflavin phosphotransferase. | 2.7.1.88 Dihydrostreptomycin-6-phosphate 3'-alpha-kinase. |
| 2.7.1.43 Glucuronokinase. | 2.7.1.89 Thiamine kinase. |
| 2.7.1.44 Galacturonokinase. | 2.7.1.90 Diphosphate-fructose-6-phosphate 1-phosphotransferase. |
| 2.7.1.45 2-dehydro-3-deoxygluconokinase. | 2.7.1.91 Sphinganine kinase. |
| 2.7.1.46 L-arabinokinase. | 2.7.1.92 5-dehydro-2-deoxygluconokinase. |
| 2.7.1.47 D-ribulokinase. | 2.7.1.93 Alkylglycerol kinase. |
| 2.7.1.48 Uridine kinase. | 2.7.1.94 Acylglycerol kinase. |
| 2.7.1.49 Hydroxymethylpyrimidine kinase. | 2.7.1.95 Kanamycin kinase. |
| 2.7.1.50 Hydroxyethylthiazole kinase. | 2.7.1.99 [Pyruvate dehydrogenase (lipoamide)] kinase. |
| 2.7.1.51 L-fuculokinase. | 2.7.1.100 S-methyl-5-thioribose kinase. |
| 2.7.1.52 Fucokinase. | 2.7.1.101 Tagatose kinase. |
| 2.7.1.53 L-xylulokinase. | 2.7.1.102 Hamamelose kinase. |
| 2.7.1.54 D-arabinokinase. | 2.7.1.103 Viomycin kinase. |

| | | | |
|----------|--|-----------|---|
| 2.7.1.55 | Allose kinase. | 2.7.1.104 | Diphosphate-protein phosphotransferase. |
| 2.7.1.56 | 1-phosphofructokinase. | 2.7.1.105 | 6-phosphofructo-2-kinase. |
| 2.7.1.58 | 2-dehydro-3-deoxygalactonokinase. | 2.7.1.106 | Glucose-1,6-bisphosphate synthase. |
| 2.7.1.59 | N-acetylglucosamine kinase. | 2.7.1.107 | Diacylglycerol kinase. |
| 2.7.1.60 | N-acylmannosamine kinase. | 2.7.1.108 | Dolichol kinase. |
| 2.7.1.61 | Acyl-phosphate-hexose phosphotransferase. | 2.7.1.109 | [Hydroxymethylglutaryl-CoA reductase (NADPH)] kinase. |
| 2.7.1.62 | Phosphoramidate-hexose phosphotransferase. | 2.7.1.110 | Dephospho-[reductase kinase] kinase. |
| 2.7.1.63 | Polyphosphate-glucose phosphotransferase. | 2.7.1.112 | Protein-tyrosine kinase. |
| 2.7.1.64 | Inositol 3-kinase. | 2.7.1.113 | Deoxyguanosine kinase. |
| 2.7.1.65 | Scyllo-inosamine 4-kinase. | 2.7.1.114 | AMP-thymidine kinase. |
| 2.7.1.66 | Undecaprenol kinase. | 2.7.1.115 | [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)] kinase. |
| 2.7.1.67 | 1-phosphatidylinositol 4-kinase. | 2.7.1.116 | [Isocitrate dehydrogenase (NADP+)] kinase. |
| 2.7.1.68 | 1-phosphatidylinositol-4-phosphate 5-kinase. | 2.7.1.117 | [Myosin light-chain] kinase. |

| | | | |
|-----------|---|----------|---|
| 2.7.1.118 | ADP-thymidine kinase. | 2.7.2.6 | Formate kinase. |
| 2.7.1.119 | Hygromycin-B kinase. | 2.7.2.7 | Butyrate kinase. |
| 2.7.1.120 | Caldesmon kinase. | 2.7.2.8 | Acetylglutamate kinase. |
| 2.7.1.121 | Phosphoenolpyruvate-glycerone phosphotransferase. | 2.7.2.10 | Phosphoglycerate kinase (GTP). |
| 2.7.1.122 | Xylitol kinase. | 2.7.2.11 | Glutamate 5-kinase. |
| 2.7.1.123 | Calcium/calmodulin-dependent protein kinase. | 2.7.2.12 | Acetate kinase (diphosphate). |
| 2.7.1.124 | [Tyrosine 3-monooxygenase] kinase. | 2.7.2.13 | Glutamate 1-kinase. |
| 2.7.1.125 | Rhodopsin kinase. | 2.7.2.14 | Branched-chain-fatty-acid kinase. |
| 2.7.1.126 | [Beta-adrenergic-receptor] kinase. | 2.7.3.1 | Guanidinoacetate kinase. |
| 2.7.1.127 | Inositol-trisphosphate 3-kinase. | 2.7.3.2 | Creatine kinase. |
| 2.7.1.128 | [Acetyl-CoA carboxylase] kinase. | 2.7.3.3 | Arginine kinase. |
| 2.7.1.129 | [Myosin heavy-chain] kinase. | 2.7.3.4 | Taurocyamine kinase. |
| 2.7.1.130 | Tetraacyldisaccharide 4'-kinase. | 2.7.3.5 | Lombricine kinase. |
| 2.7.1.131 | [Low-density lipoprotein receptor] kinase. | 2.7.3.6 | Hypotaurocyamine kinase. |
| 2.7.1.132 | Tropomyosin kinase. | 2.7.3.7 | Opheline kinase. |
| 2.7.1.134 | Inositol-tetrakisphosphate 1-kinase. | 2.7.3.8 | Ammonia kinase. |
| 2.7.1.135 | [Tau protein] kinase. | 2.7.3.9 | Phosphoenolpyruvate-protein phosphotransferase. |
| 2.7.1.136 | Macrolide 2'-kinase. | 2.7.3.10 | Agmatine kinase. |
| 2.7.1.137 | Phosphatidylinositol 3-kinase. | 2.7.3.11 | Protein-histidine pros-kinase. |
| 2.7.1.138 | Ceramide kinase. | 2.7.3.12 | Protein-histidine tele-kinase. |
| 2.7.1.140 | Inositol-tetrakisphosphate 5-kinase. | 2.7.4.1 | Polyphosphate kinase. |
| 2.7.1.141 | [RNA-polymerase]-subunit kinase. | 2.7.4.2 | Phosphomevalonate kinase. |
| 2.7.1.142 | Glycerol-3-phosphate-glucose phosphotransferase. | 2.7.4.3 | Adenylate kinase. |
| 2.7.1.143 | Diphosphate-purine nucleoside kinase. | 2.7.4.4 | Nucleoside-phosphate kinase. |
| 2.7.1.144 | Tagatose-6-phosphate kinase. | 2.7.4.6 | Nucleoside-diphosphate kinase. |
| 2.7.1.145 | Deoxynucleoside kinase. | 2.7.4.7 | Phosphomethylpyrimidine kinase. |
| 2.7.1.146 | ADP-specific phosphofructokinase. | 2.7.4.8 | Guanylate kinase. |
| 2.7.1.147 | ADP-specific glucokinase. | 2.7.4.9 | dTMP kinase. |

| | |
|---|--|
| 2.7.1.148 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase. | 2.7.4.10 Nucleoside-triphosphate--adenylate kinase. |
| 2.7.1.149 1-phosphatidylinositol-5-phosphate 4-kinase. | 2.7.4.11 (Deoxy)adenylate kinase. |
| 2.7.1.150 1-phosphatidylinositol-3-phosphate 5-kinase. | 2.7.4.12 T(2)-induced deoxynucleotide kinase. |
| 2.7.1.151 Inositol-polyphosphate multikinase. | 2.7.4.13 (Deoxy)nucleoside-phosphate kinase. |
| 2.7.1.153 Phosphatidylinositol-4,5-bisphosphate 3-kinase. | 2.7.4.14 Cytidylate kinase. |
| 2.7.1.154 Phosphatidylinositol-4-phosphate 3-kinase. | 2.7.4.15 Thiamine-diphosphate kinase. |
| 2.7.1.155 Diphosphoinositol-pentakisphosphate kinase. | 2.7.4.16 Thiamine-phosphate kinase. |
| 2.7.1.156 Adenosylcobinamide kinase. | 2.7.4.17 3-phosphoglyceroyl-phosphate--polyphosphate phosphotransferase. |
| 2.7.2.1 Acetate kinase. | 2.7.4.18 Farnesyl-diphosphate kinase. |
| 2.7.2.2 Carbamate kinase. | 2.7.4.19 5-methyldeoxycytidine-5'-phosphate kinase. |
| 2.7.2.3 Phosphoglycerate kinase. | 2.7.4.20 Dolichyl-diphosphate--polyphosphate phosphotransferase. |
| 2.7.2.4 Aspartate kinase. | 2.7.4.21 Inositol-hexakisphosphate kinase. |

| | |
|--|---|
| 2.7.6.1 Ribose-phosphate diphosphokinase. | 2.7.7.34 Glucose-1-phosphate guanylyltransferase. |
| 2.7.6.2 Thiamine diphosphokinase. | 2.7.7.35 Ribose-5-phosphate adenylyltransferase. |
| 2.7.6.3 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase. | 2.7.7.36 Aldose-1-phosphate adenylyltransferase. |
| 2.7.6.4 Nucleotide diphosphokinase. | 2.7.7.37 Aldose-1-phosphate nucleotidyltransferase. |
| 2.7.6.5 GTP diphosphokinase. | 2.7.7.38 3-deoxy-manno-octulosonate cytidyltransferase. |
| 2.7.7.1 Nicotinamide-nucleotide adenylyltransferase. | 2.7.7.39 Glycerol-3-phosphate cytidyltransferase. |
| 2.7.7.2 FMN adenylyltransferase. | 2.7.7.40 D-ribitol-5-phosphate cytidyltransferase. |
| 2.7.7.3 Pantetheine-phosphate adenylyltransferase. | 2.7.7.41 Phosphatidate cytidyltransferase. |
| 2.7.7.4 Sulfate adenylyltransferase. | 2.7.7.42 [Glutamate--ammonia-ligase] adenylyltransferase. |
| 2.7.7.5 Sulfate adenylyltransferase (ADP). | 2.7.7.43 N-acylneuraminate cytidyltransferase. |
| 2.7.7.6 DNA-directed RNA polymerase. | 2.7.7.44 Glucuronate-1-phosphate uridylyltransferase. |
| 2.7.7.7 DNA-directed DNA polymerase. | 2.7.7.45 Guanosine-triphosphate guanylyltransferase. |
| 2.7.7.8 Polyribonucleotide nucleotidyltransferase. | 2.7.7.46 Gentamicin 2"-nucleotidyltransferase. |
| 2.7.7.9 UTP--glucose-1-phosphate uridylyltransferase. | 2.7.7.47 Streptomycin 3"-adenylyltransferase. |
| 2.7.7.10 UTP--hexose-1-phosphate uridylyltransferase. | 2.7.7.48 RNA-directed RNA polymerase. |
| 2.7.7.11 UTP--xylose-1-phosphate uridylyltransferase. | 2.7.7.49 RNA-directed DNA polymerase. |
| 2.7.7.12 UDP-glucose--hexose-1-phosphate uridylyltransferase. | 2.7.7.50 mRNA guanylyltransferase. |
| 2.7.7.13 Mannose-1-phosphate guanylyltransferase. | 2.7.7.51 Adenylylsulfate--ammonia adenylyltransferase. |

| | |
|---|--|
| 2.7.7.14 Ethanolamine-phosphate cytidylyltransferase. | 2.7.7.52 RNA uridylyltransferase. |
| 2.7.7.15 Choline-phosphate cytidylyltransferase. | 2.7.7.53 ATP adenylyltransferase. |
| 2.7.7.18 Nicotinate-nucleotide adenylyltransferase. | 2.7.7.54 Phenylalanine adenylyltransferase. |
| 2.7.7.19 Polynucleotide adenylyltransferase. | 2.7.7.55 Anthranilate adenylyltransferase. |
| 2.7.7.21 tRNA cytidylyltransferase. | 2.7.7.56 tRNA nucleotidyltransferase. |
| 2.7.7.22 Mannose-1-phosphate guanylyltransferase (GDP). | 2.7.7.57 N-methylphosphoethanolamine cytidylyltransferase. |
| 2.7.7.23 UDP-N-acetylglucosamine diphosphorylase. | 2.7.7.58 (2,3-dihydroxybenzoyl)adenylate synthase. |
| 2.7.7.24 Glucose-1-phosphate thymidylyltransferase. | 2.7.7.59 [Protein-P _{II}] uridylyltransferase. |
| 2.7.7.25 tRNA adenylyltransferase. | 2.7.7.60 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase. |
| 2.7.7.27 Glucose-1-phosphate adenylyltransferase. | 2.7.7.61 Holo-ACP synthase. |
| 2.7.7.28 Nucleoside-triphosphate-aldose 1-phosphate nucleotidyltransferase. | 2.7.7.62 Adenosylcobinamide-phosphate guanylyltransferase. |
| 2.7.7.30 Fucose-1-phosphate guanylyltransferase. | 2.7.8.1 Ethanolaminephosphotransferase. |
| 2.7.7.31 DNA nucleotidylexotransferase. | 2.7.8.2 Diacylglycerol cholinephosphotransferase. |
| 2.7.7.32 Galactose-1-phosphate thymidylyltransferase. | 2.7.8.3 Ceramide cholinephosphotransferase. |
| 2.7.7.33 Glucose-1-phosphate cytidylyltransferase. | 2.7.8.4 Serine-phosphoethanolamine synthase. |

| | |
|---|---|
| 2.7.8.5 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase. | 2.8.2.1 Aryl sulfotransferase. |
| 2.7.8.6 Undecaprenyl-phosphate galactose phosphotransferase. | 2.8.2.2 Alcohol sulfotransferase. |
| 2.7.8.7 Holo-[acyl-carrier-protein] synthase. | 2.8.2.3 Amine sulfotransferase. |
| 2.7.8.8 CDP-diacylglycerol-serine O-phosphatidyltransferase. | 2.8.2.4 Estrone sulfotransferase. |
| 2.7.8.9 Phosphomannan mannosephosphotransferase. | 2.8.2.5 Chondroitin 4-sulfotransferase. |
| 2.7.8.10 Sphingosine cholinephosphotransferase. | 2.8.2.6 Choline sulfotransferase. |
| 2.7.8.11 CDP-diacylglycerol--inositol 3-phosphatidyltransferase. | 2.8.2.7 UDP-N-acetylgalactosamine-4-sulfate sulfotransferase. |
| 2.7.8.12 CDP-glycerol glycerophosphotransferase. | 2.8.2.8 [Heparan sulfate]-glucosamine N-sulfotransferase. |
| 2.7.8.13 Phospho-N-acetylmuramoyl-pentapeptide-transferase. | 2.8.2.9 Tyrosine-ester sulfotransferase. |
| 2.7.8.14 CDP-ribitol ribitolphosphotransferase. | 2.8.2.10 Renilla-luciferin sulfotransferase. |
| 2.7.8.15 UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase. | 2.8.2.11 Galactosylceramide sulfotransferase. |
| 2.7.8.17 UDP-N-acetylglucosamine--lysosomal-enzyme N-acetylglucosaminephosphotransferase. | 2.8.2.13 Psychosine sulfotransferase. |
| 2.7.8.18 UDP-galactose--UDP-N-acetylglucosamine galactose phosphotransferase. | 2.8.2.14 Bile-salt sulfotransferase. |
| 2.7.8.19 UDP-glucose-glycoprotein glucose phosphotransferase. | 2.8.2.15 Steroid sulfotransferase. |
| 2.7.8.20 Phosphatidylglycerol--membrane-oligosaccharide glycerophosphotransferase. | 2.8.2.16 Thiol sulfotransferase. |
| 2.7.8.21 Membrane-oligosaccharide glycerophosphotransferase. | 2.8.2.17 Chondroitin 6-sulfotransferase. |

| | |
|---|--|
| 2.7.8.22 1-alkenyl-2-acylglycerol choline phosphotransferase. | 2.8.2.18 Cortisol sulfotransferase. |
| 2.7.8.23 Carboxyvinyl-carboxyphosphonate phosphorylmutase. | 2.8.2.19 Triglycosylalkylacylglycerol sulfotransferase. |
| 2.7.8.24 Phosphatidylcholine synthase. | 2.8.2.20 Protein-tyrosine sulfotransferase. |
| 2.7.8.25 Triphosphoribosyl-dephospho-CoA synthase. | 2.8.2.21 Keratan sulfotransferase. |
| 2.7.8.26 Adenosylcobinamide-GDP ribazoletransferase. | 2.8.2.22 Arylsulfate sulfotransferase. |
| 2.7.9.1 Pyruvate, phosphate dikinase. | 2.8.2.23 [Heparan sulfate]-glucosamine 3-sulfotransferase 1. |
| 2.7.9.2 Pyruvate, water dikinase. | 2.8.2.24 Desulfoglucosinolate sulfotransferase. |
| 2.7.9.3 Selenide, water dikinase. | 2.8.2.25 Flavonol 3-sulfotransferase. |
| 2.7.9.4 Alpha-glucan, water dikinase. | 2.8.2.26 Quercetin-3-sulfate 3'-sulfotransferase. |
| 2.8.1.1 Thiosulfate sulfur-transferase. | 2.8.2.27 Quercetin-3-sulfate 4'-sulfotransferase. |
| 2.8.1.2 3-mercaptopyruvate sulfur-transferase. | 2.8.2.28 Quercetin-3,3'-bissulfate 7-sulfotransferase. |
| 2.8.1.3 Thiosulfate--thiol sulfur-transferase. | 2.8.2.29 [Heparan sulfate]-glucosamine 3-sulfotransferase 2. |
| 2.8.1.4 tRNA sulfur-transferase. | 2.8.2.30 [Heparan sulfate]-glucosamine 3-sulfotransferase 3. |
| 2.8.1.5 Thiosulfate--dithiol sulfur-transferase. | 2.8.3.1 Propionate CoA-transferase. |
| 2.8.1.6 Biotin synthase. | 2.8.3.2 Oxalate CoA-transferase. |
| 2.8.1.7 Cysteine desulfurase. | 2.8.3.3 Malonate CoA-transferase. |

| | |
|---|---|
| 2.8.3.5 3-oxoacid CoA-transferase. | 3.1.1.34 Lipoprotein lipase. |
| 2.8.3.6 3-oxoadipate CoA-transferase. | 3.1.1.35 Dihydrocoumarin hydrolase. |
| 2.8.3.7 Succinate--citramalate CoA-transferase. | 3.1.1.36 Limonin-D-ring-lactonase. |
| 2.8.3.8 Acetate CoA-transferase. | 3.1.1.37 Steroid-lactonase. |
| 2.8.3.9 Butyrate--acetoacetate CoA-transferase. | 3.1.1.38 Triacetate-lactonase. |
| 2.8.3.10 Citrate CoA-transferase. | 3.1.1.39 Actinomycin lactonase. |
| 2.8.3.11 Citramalate CoA-transferase. | 3.1.1.40 Orsellinate-depside hydrolase. |
| 2.8.3.12 Glutaconate CoA-transferase. | 3.1.1.41 Cephalosporin-C deacetylase. |
| 2.8.3.13 Succinate--hydroxymethylglutarate CoA-transferase. | 3.1.1.42 Chlorogenate hydrolase. |
| 2.8.3.14 5-hydroxypentanoate CoA-transferase. | 3.1.1.43 Alpha-amino-acid esterase. |
| 2.8.3.15 Succinyl-CoA:(R)-benzylsuccinate CoA-transferase. | 3.1.1.44 4-methyloxaloacetate esterase. |
| 2.8.3.16 Formyl-CoA transferase. | 3.1.1.45 Carboxymethylenebutenolidase. |
| 2.8.3.17 Cinnamoyl-CoA:phenyllactate CoA-transferase. | 3.1.1.46 Deoxylimonate A-ring-lactonase. |
| 2.8.4.1 Coenzyme-B sulfoethylthiotransferase. | 3.1.1.47 1-alkyl-2-acetylgllycerophosphocholine esterase. |
| 2.9.1.1 L-seryl-tRNA(Sec) selenium transferase. | 3.1.1.48 Fusarinine-C ornithinesterase. |
| ENZYME: 3.-.-. | 3.1.1.49 Sinapine esterase. |
| 3.1.1.1 Carboxylesterase. | 3.1.1.50 Wax-ester hydrolase. |
| 3.1.1.2 Arylesterase. | 3.1.1.51 Phorbol-diester hydrolase. |
| 3.1.1.3 Triacylglycerol lipase. | 3.1.1.52 Phosphatidylinositol deacylase. |
| 3.1.1.4 Phospholipase A(2). | 3.1.1.53 Sialate O-acylesterase. |
| 3.1.1.5 Lysophospholipase. | 3.1.1.54 Acetoxybutynylbithiophene deacetylase. |
| 3.1.1.6 Acylesterase. | 3.1.1.55 Acetylsalicylate deacetylase. |
| 3.1.1.7 Acetylcholinesterase. | 3.1.1.56 Methylumbelliferyl-acetate deacetylase. |
| 3.1.1.8 Cholinesterase. | 3.1.1.57 2-pyrone-4,6-dicarboxylate lactonase. |
| | 3.1.1.58 N-acetylgalactosaminoglycan |

| | |
|---|--|
| | deacetylase. |
| 3.1.1.10 Tropinesterase. | 3.1.1.59 Juvenile-hormone esterase. |
| 3.1.1.11 Pectinesterase. | 3.1.1.60 Bis(2-ethylhexyl)phthalate esterase. |
| 3.1.1.13 Sterol esterase. | 3.1.1.61 Protein-glutamate methylesterase. |
| 3.1.1.14 Chlorophyllase. | 3.1.1.63 11-cis-retinyl-palmitate hydrolase. |
| 3.1.1.15 L-arabinonolactonase. | 3.1.1.64 All-trans-retinyl-palmitate hydrolase. |
| 3.1.1.17 Gluconolactonase. | 3.1.1.65 L-rhamnono-1,4-lactonase. |
| 3.1.1.19 Uronolactonase. | 3.1.1.66 5-(3,4-diacetoxybut-1-ynyl)-2,2'-bithiophene deacetylase. |
| 3.1.1.20 Tannase. | 3.1.1.67 Fatty-acyl-ethyl-ester synthase. |
| 3.1.1.21 Retinyl-palmitate esterase. | 3.1.1.68 Xylono-1,4-lactonase. |
| 3.1.1.22 Hydroxybutyrate-dimer hydrolase. | 3.1.1.70 Cetraxate benzylesterase. |
| 3.1.1.23 Acylglycerol lipase. | 3.1.1.71 Acetylalkylglycerol acetylhydrolase. |
| 3.1.1.24 3-oxoadipate enol-lactonase. | 3.1.1.72 Acetylxytan esterase. |
| 3.1.1.25 1,4-lactonase. | 3.1.1.73 Feruloyl esterase. |
| 3.1.1.26 Galactolipase. | 3.1.1.74 Cutinase. |
| 3.1.1.27 4-pyridoxolactonase. | 3.1.1.75 Poly(3-hydroxybutyrate) depolymerase. |
| 3.1.1.28 Acylcarnitine hydrolase. | 3.1.1.76 Poly(3-hydroxyoctanoate) depolymerase. |
| 3.1.1.29 Aminoacyl-tRNA hydrolase. | 3.1.1.77 Acyloxyacyl hydrolase. |
| 3.1.1.30 D-arabinonolactonase. | 3.1.1.78 Polyneuridine-aldehyde esterase. |
| 3.1.1.31 6-phosphogluconolactonase. | 3.1.1.79 Hormone-sensitive lipase. |
| 3.1.1.32 Phospholipase A(1). | 3.1.2.1 Acetyl-CoA hydrolase. |
| 3.1.1.33 6-acetylglucose deacetylase. | 3.1.2.2 Palmitoyl-CoA hydrolase. |

| | |
|---|--|
| 3.1.2.3 Succinyl-CoA hydrolase. | 3.1.3.23 Sugar-phosphatase. |
| 3.1.2.4 3-hydroxyisobutyryl-CoA hydrolase. | 3.1.3.24 Sucrose-phosphatase. |
| 3.1.2.5 Hydroxymethylglutaryl-CoA hydrolase. | 3.1.3.25 Inositol-1(or 4)-monophosphatase. |
| 3.1.2.6 Hydroxyacylglutathione hydrolase. | 3.1.3.26 4-phytase. |
| 3.1.2.7 Glutathione thioesterase. | 3.1.3.27 Phosphatidylglycerophosphatase. |
| 3.1.2.10 Formyl-CoA hydrolase. | 3.1.3.28 ADP-phosphoglycerate phosphatase. |
| 3.1.2.11 Acetoacetyl-CoA hydrolase. | 3.1.3.29 N-acylneuraminate-9-phosphatase. |
| 3.1.2.12 S-formylglutathione hydrolase. | 3.1.3.31 Nucleotidase. |
| 3.1.2.13 S-succinylglutathione hydrolase. | 3.1.3.32 Polynucleotide 3'-phosphatase. |
| 3.1.2.14 Oleoyl-[acyl-carrier-protein] hydrolase. | 3.1.3.33 Polynucleotide 5'-phosphatase. |
| 3.1.2.15 Ubiquitin thioesterase. | 3.1.3.34 Deoxynucleotide 3'-phosphatase. |
| 3.1.2.16 [Citrate-(pro-3S)-lyase] thioesterase. | 3.1.3.35 Thymidylate 5'-phosphatase. |
| 3.1.2.17 (S)-methylmalonyl-CoA hydrolase. | 3.1.3.36 Phosphoinositide 5-phosphatase. |
| 3.1.2.18 ADP-dependent short-chain-acyl-CoA hydrolase. | 3.1.3.37 Sedoheptulose-bisphosphatase. |
| 3.1.2.19 ADP-dependent medium-chain-acyl-CoA hydrolase. | 3.1.3.38 3-phosphoglycerate phosphatase. |
| 3.1.2.20 Acyl-CoA hydrolase. | 3.1.3.39 Streptomycin-6-phosphatase. |
| 3.1.2.21 Dodecanoyl-[acyl-carrier protein] hydrolase. | 3.1.3.40 Guanidinodeoxy-scylo-inositol-4-phosphatase. |
| 3.1.2.22 Palmitoyl-protein hydrolase. | 3.1.3.41 4-nitrophenylphosphatase. |
| 3.1.2.23 4-hydroxybenzoyl-CoA thioesterase. | 3.1.3.42 [Glycogen-synthase-D] phosphatase. |
| 3.1.2.24 2-(2-hydroxyphenyl)benzenesulfinate hydrolase. | 3.1.3.43 [Pyruvate dehydrogenase (lipoamide)]-phosphatase. |
| 3.1.2.25 Phenylacetyl-CoA hydrolase. | 3.1.3.44 [Acetyl-CoA carboxylase]-phosphatase. |
| 3.1.3.1 Alkaline phosphatase. | 3.1.3.45 3-deoxy-manno-octulosonate-8-phosphatase. |
| 3.1.3.2 Acid phosphatase. | 3.1.3.46 Fructose-2,6-bisphosphate 2- |

| | |
|--|---|
| | phosphatase. |
| 3.1.3.3 Phosphoserine phosphatase. | 3.1.3.47 [Hydroxymethylglutaryl-CoA reductase (NADPH)]-phosphatase. |
| 3.1.3.4 Phosphatidate phosphatase. | 3.1.3.48 Protein-tyrosine-phosphatase. |
| 3.1.3.5 5'-nucleotidase. | 3.1.3.49 [Pyruvate kinase]-phosphatase. |
| 3.1.3.6 3'-nucleotidase. | 3.1.3.50 Sorbitol-6-phosphatase. |
| 3.1.3.7 3'(2'),5'-bisphosphate nucleotidase. | 3.1.3.51 Dolichyl-phosphatase. |
| 3.1.3.8 3-phytase. | 3.1.3.52 [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)]-phosphatase. |
| 3.1.3.9 Glucose-6-phosphatase. | 3.1.3.53 [Myosin light-chain]-phosphatase. |
| 3.1.3.10 Glucose-1-phosphatase. | 3.1.3.54 Fructose-2,6-bisphosphate 6-phosphatase. |
| 3.1.3.11 Fructose-bisphosphatase. | 3.1.3.55 Caldesmon-phosphatase. |
| 3.1.3.12 Trehalose-phosphatase. | 3.1.3.56 Inositol-polyphosphate 5-phosphatase. |
| 3.1.3.13 Bisphosphoglycerate phosphatase. | 3.1.3.57 Inositol-1,4-bisphosphate 1-phosphatase. |
| 3.1.3.14 Methylphosphothioglycerate phosphatase. | 3.1.3.58 Sugar-terminal-phosphatase. |
| 3.1.3.15 Histidinol-phosphatase. | 3.1.3.59 Alkylacetylgllycerophosphatase. |
| 3.1.3.16 Phosphoprotein phosphatase. | 3.1.3.60 Phosphoenolpyruvate phosphatase. |
| 3.1.3.17 [Phosphorylase] phosphatase. | 3.1.3.62 Multiple inositol-polyphosphate phosphatase. |
| 3.1.3.18 Phosphoglycolate phosphatase. | 3.1.3.63 2-carboxy-D-arabinitol-1-phosphatase. |
| 3.1.3.19 Glycerol-2-phosphatase. | 3.1.3.64 Phosphatidylinositol-3-phosphatase. |
| 3.1.3.20 Phosphoglycerate phosphatase. | 3.1.3.66 Phosphatidylinositol-3,4-bisphosphate 4-phosphatase. |
| 3.1.3.21 Glycerol-1-phosphatase. | 3.1.3.67 Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase. |
| 3.1.3.22 Mannitol-1-phosphatase. | 3.1.3.68 2-deoxyglucose-6-phosphatase. |

| | |
|--|---|
| 3.1.3.69 Glucosylglycerol 3-phosphatase. | 3.1.13.3 Oligonucleotidase. |
| 3.1.3.70 Mannosyl-3-phosphoglycerate phosphatase. | 3.1.13.4 Poly(A)-specific ribonuclease. |
| 3.1.3.71 2-phosphosulfolactate phosphatase. | 3.1.14.1 Yeast ribonuclease. |
| 3.1.3.72 5-phytase. | 3.1.15.1 Venom exonuclease. |
| 3.1.3.73 Alpha-ribazole phosphatase. | 3.1.16.1 Spleen exonuclease. |
| 3.1.4.1 Phosphodiesterase I. | 3.1.21.1 Deoxyribonuclease I. |
| 3.1.4.2 Glycerophosphocholine phosphodiesterase. | 3.1.6.3 Glycosulfatase. |
| 3.1.4.3 Phospholipase C. | 3.1.6.4 N-acetylgalactosamine-6-sulfatase. |
| 3.1.4.4 Phospholipase D. | 3.1.6.6 Choline-sulfatase. |
| 3.1.4.11 Phosphoinositide phospholipase C. | 3.1.6.7 Cellulose-polysulfatase. |
| 3.1.4.12 Sphingomyelin phosphodiesterase. | 3.1.6.8 Cerebroside-sulfatase. |
| 3.1.4.13 Serine-ethanolaminophosphate phosphodiesterase. | 3.1.6.9 Chondro-4-sulfatase. |
| 3.1.4.14 [Acyl-carrier-protein] phosphodiesterase. | 3.1.6.10 Chondro-6-sulfatase. |
| 3.1.4.15 Adenyl-[glutamate--ammonia ligase] hydrolase. | 3.1.6.11 Disulfoglucosamine-6-sulfatase. |
| 3.1.4.16 2',3'-cyclic-nucleotide 2'-phosphodiesterase. | 3.1.6.12 N-acetylgalactosamine-4-sulfatase. |
| 3.1.4.17 3',5'-cyclic-nucleotide phosphodiesterase. | 3.1.6.13 Iduronate-2-sulfatase. |
| 3.1.4.35 3',5'-cyclic-GMP phosphodiesterase. | 3.1.6.14 N-acetylglucosamine-6-sulfatase. |
| 3.1.4.37 2',3'-cyclic-nucleotide 3'-phosphodiesterase. | 3.1.6.15 N-sulfoglucosamine-3-sulfatase. |

| | |
|--|--|
| 3.1.4.38 Glycerophosphocholine cholinephosphodiesterase. | 3.1.6.16 Monomethyl-sulfatase. |
| 3.1.4.39 Alkylglycerophosphoethanolamine phosphodiesterase. | 3.1.6.17 D-lactate-2-sulfatase. |
| 3.1.4.40 CMP-N-acylneuraminate phosphodiesterase. | 3.1.6.18 Glucuronate-2-sulfatase. |
| 3.1.4.41 Sphingomyelin phosphodiesterase D. | 3.1.7.1 Prenyl-diphosphatase. |
| 3.1.4.42 Glycerol-1,2-cyclic-phosphate 2-phosphodiesterase. | 3.1.7.2 Guanosine-3',5'-bis(diphosphate) 3'-diphosphatase. |
| 3.1.4.43 Glycerophosphoinositol inositolphosphodiesterase. | 3.1.7.3 Monoterpenyl-diphosphatase. |
| 3.1.4.44 Glycerophosphoinositol glycerophosphodiesterase. | 3.1.8.1 Aryldialkylphosphatase. |
| 3.1.4.45 N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase. | 3.1.8.2 Diisopropyl-fluorophosphatase. |
| 3.1.4.46 Glycerophosphodiester phosphodiesterase. | 3.1.11.1 Exodeoxyribonuclease I. |
| 3.1.4.48 Dolichylphosphate-glucose phosphodiesterase. | 3.1.11.2 Exodeoxyribonuclease III. |
| 3.1.4.49 Dolichylphosphate-mannose phosphodiesterase. | 3.1.11.3 Exodeoxyribonuclease (lambda-induced). |
| 3.1.4.50 Glycosylphosphatidylinositol phospholipase D. | 3.1.11.4 Exodeoxyribonuclease (phage Sp3-induced). |
| 3.1.4.51 Glucose-1-phospho-D-mannosylglycoprotein phosphodiesterase. | 3.1.11.5 Exodeoxyribonuclease V. |
| 3.1.5.1 dGTPase. | 3.1.11.6 Exodeoxyribonuclease VII. |
| 3.1.6.1 Arylsulfatase. | 3.1.13.1 Exoribonuclease II. |
| 3.1.6.2 Steryl-sulfatase. | 3.1.13.2 Exoribonuclease H. |

| | |
|---|--|
| 3.1.21.2 Deoxyribonuclease IV (phage-T(4)-induced). | 3.2.1.23 Beta-galactosidase. |
| 3.1.21.3 Type I site-specific deoxyribonuclease. | 3.2.1.24 Alpha-mannosidase. |
| 3.1.21.4 Type II site-specific deoxyribonuclease. | 3.2.1.25 Beta-mannosidase. |
| 3.1.21.5 Type III site-specific deoxyribonuclease. | 3.2.1.26 Beta-fructofuranosidase. |
| 3.1.21.6 CC-preferring endodeoxyribonuclease. | 3.2.1.28 Alpha, alpha-trehalase. |
| 3.1.21.7 Deoxyribonuclease V. | 3.2.1.31 Beta-glucuronidase. |
| 3.1.22.1 Deoxyribonuclease II. | 3.2.1.32 Xylan endo-1,3-beta-xylosidase. |
| 3.1.22.2 Aspergillus deoxyribonuclease K(1). | 3.2.1.33 Amylo-alpha-1,6-glucosidase. |
| 3.1.22.4 Crossover junction endoribonuclease. | 3.2.1.35 Hyaluronoglucosaminidase. |
| 3.1.22.5 Deoxyribonuclease X. | 3.2.1.36 Hyaluronoglucuronidase. |
| 3.1.25.1 Deoxyribonuclease (pyrimidine dimer). | 3.2.1.37 Xylan 1,4-beta-xylosidase. |
| 3.1.26.1 Physarum polycephalum ribonuclease. | 3.2.1.38 Beta-D-fucosidase. |
| 3.1.26.2 Ribonuclease alpha. | 3.2.1.39 Glucan endo-1,3-beta-D-glucosidase. |
| 3.1.26.3 Ribonuclease III. | 3.2.1.40 Alpha-L-rhamnosidase. |
| 3.1.26.4 Ribonuclease H. | 3.2.1.41 Pullulanase. |
| 3.1.26.5 Ribonuclease P. | 3.2.1.42 GDP-glucosidase. |
| 3.1.26.6 Ribonuclease IV. | 3.2.1.43 Beta-L-rhamnosidase. |
| 3.1.26.7 Ribonuclease P4. | 3.2.1.44 Fucoindase. |
| 3.1.26.8 Ribonuclease M5. | 3.2.1.45 Glucosylceramidase. |
| 3.1.26.9 Ribonuclease (poly-(U)-specific). | 3.2.1.46 Galactosylceramidase. |
| 3.1.26.10 Ribonuclease IX. | 3.2.1.47 Galactosylgalactosylglucosylceramidase. |
| 3.1.26.11 Ribonuclease Z. | 3.2.1.48 Sucrose alpha-glucosidase. |
| 3.1.27.1 Ribonuclease T(2). | 3.2.1.49 Alpha-N-acetylgalactosaminidase. |

| | | | |
|-----------|---------------------------------|----------|--|
| 3.1.27.2 | Bacillus subtilis ribonuclease. | 3.2.1.50 | Alpha-N-acetylglucosaminidase. |
| 3.1.27.3 | Ribonuclease T(1). | 3.2.1.51 | Alpha-L-fucosidase. |
| 3.1.27.4 | Ribonuclease U(2). | 3.2.1.52 | Beta-N-acetylhexosaminidase. |
| 3.1.27.5 | Pancreatic ribonuclease. | 3.2.1.53 | Beta-N-acetylgalactosaminidase. |
| 3.1.27.6 | Enterobacter ribonuclease. | 3.2.1.54 | Cyclomaltodextrinase. |
| 3.1.27.7 | Ribonuclease F. | 3.2.1.55 | Alpha-N-arabinofuranosidase. |
| 3.1.27.8 | Ribonuclease V. | 3.2.1.56 | Glucuronosyl-disulfoglucosamine glucuronidase. |
| 3.1.27.9 | tRNA-intron endonuclease. | 3.2.1.57 | Isopullulanase. |
| 3.1.27.10 | rRNA endonuclease. | 3.2.1.58 | Glucan 1,3-beta-glucosidase. |
| 3.1.30.1 | Aspergillus nuclease S(1). | 3.2.1.59 | Glucan endo-1,3-alpha-glucosidase. |
| 3.1.30.2 | Serratia marcescens nuclease. | 3.2.1.60 | Glucan 1,4-alpha-maltotetraohydrolase. |
| 3.1.31.1 | Micrococcal nuclease. | 3.2.1.61 | Mycodextranase. |
| 3.2.1.1 | Alpha-amylase. | 3.2.1.62 | Glycosylceramidase. |
| 3.2.1.2 | Beta-amylase. | 3.2.1.63 | 1,2-alpha-L-fucosidase. |
| 3.2.1.3 | Glucan 1,4-alpha-glucosidase. | 3.2.1.64 | 2,6-beta-fructan 6-levanbiohydrolase. |
| 3.2.1.4 | Cellulase. | 3.2.1.65 | Levanase. |
| 3.2.1.6 | Endo-1,3(4)-beta-glucanase. | 3.2.1.66 | Quercitrinase. |
| 3.2.1.7 | Inulinase. | 3.2.1.67 | Galacturan 1,4-alpha-galacturonidase. |
| 3.2.1.8 | Endo-1,4-beta-xylanase. | 3.2.1.68 | Isoamylase. |
| 3.2.1.10 | Oligo-1,6-glucosidase. | 3.2.1.70 | Glucan 1,6-alpha-glucosidase. |
| 3.2.1.11 | Dextranase. | 3.2.1.71 | Glucan endo-1,2-beta-glucosidase. |
| 3.2.1.14 | Chitinase. | 3.2.1.72 | Xylan 1,3-beta-xylosidase. |
| 3.2.1.15 | Polygalacturonase. | 3.2.1.73 | Licheninase. |
| 3.2.1.17 | Lysozyme. | 3.2.1.74 | Glucan 1,4-beta-glucosidase. |
| 3.2.1.18 | Exo-alpha-sialidase. | 3.2.1.75 | Glucan endo-1,6-beta-glucosidase. |
| 3.2.1.20 | Alpha-glucosidase. | 3.2.1.76 | L-iduronidase. |
| 3.2.1.21 | Beta-glucosidase. | 3.2.1.77 | Mannan 1,2-(1,3)-alpha-mannosidase. |
| 3.2.1.22 | Alpha-galactosidase. | 3.2.1.78 | Mannan endo-1,4-beta-mannosidase. |

| | | | |
|----------|--|-----------|---|
| 3.2.1.80 | Fructan beta-fructosidase. | 3.2.1.121 | Polymannuronate hydrolase. |
| 3.2.1.81 | Agarase. | 3.2.1.122 | Maltose-6'-phosphate glucosidase. |
| 3.2.1.82 | Exo-poly-alpha-galacturonosidase. | 3.2.1.123 | Endoglycosylceramidase. |
| 3.2.1.83 | Kappa-carrageenase. | 3.2.1.124 | 3-deoxy-2-octulosonidase. |
| 3.2.1.84 | Glucan 1,3-alpha-glucosidase. | 3.2.1.125 | Raucaffricine beta-glucosidase. |
| 3.2.1.85 | 6-phospho-beta-galactosidase. | 3.2.1.126 | Coniferin beta-glucosidase. |
| 3.2.1.86 | 6-phospho-beta-glucosidase. | 3.2.1.127 | 1,6-alpha-L-fucosidase. |
| 3.2.1.87 | Capsular-polysaccharide endo-1,3-alpha-galactosidase. | 3.2.1.128 | Glycyrrhizinate beta-glucuronidase. |
| 3.2.1.88 | Beta-L-arabinosidase. | 3.2.1.129 | Endo-alpha-sialidase. |
| 3.2.1.89 | Arabinogalactan endo-1,4-beta-galactosidase. | 3.2.1.130 | Glycoprotein endo-alpha-1,2-mannosidase. |
| 3.2.1.91 | Cellulose 1,4-beta-cellobiosidase. | 3.2.1.131 | Xylan alpha-1,2-glucuronosidase. |
| 3.2.1.92 | Peptidoglycan beta-N-acetylmuramidase. | 3.2.1.132 | Chitosanase. |
| 3.2.1.93 | Alpha, alpha-phosphotrehalase. | 3.2.1.133 | Glucan 1,4-alpha-maltohydrolase. |
| 3.2.1.94 | Glucan 1,6-alpha-isomaltosidase. | 3.2.1.134 | Difructose-anhydride synthase. |
| 3.2.1.95 | Dextran 1,6-alpha-isomaltotriosidase. | 3.2.1.135 | Neopullulanase. |
| 3.2.1.96 | Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase. | 3.2.1.136 | Glucuronoarabinoxylan endo-1,4-beta-xylanase. |
| 3.2.1.97 | Glycopeptide alpha-N-acetylgalactosaminidase. | 3.2.1.137 | Mannan exo-1,2-1,6-alpha-mannosidase. |
| 3.2.1.98 | Glucan 1,4-alpha-maltohexaosidase. | 3.2.1.139 | Alpha-glucuronidase. |

| | |
|--|---|
| 3.2.1.99 Arabinan endo-1,5- α -L-arabinosidase. | 3.2.1.140 Lacto-N-biosidase. |
| 3.2.1.100 Mannan 1,4-mannobiosidase. | 3.2.1.141 4- α -D- $\{(1\rightarrow4)\}$ - α -D-glucano}trehalose trehalohydrolase. |
| 3.2.1.101 Mannan endo-1,6- α -mannosidase. | 3.2.1.142 Limit dextrinase. |
| 3.2.1.102 Blood-group-substance endo-1,4- β -galactosidase. | 3.2.1.143 Poly(ADP-ribose) glycohydrolase. |
| 3.2.1.103 Keratan-sulfate endo-1,4- β -galactosidase. | 3.2.1.144 3-deoxyoctulosonase. |
| 3.2.1.104 Steryl- β -glucosidase. | 3.2.1.145 Galactan 1,3- β -galactosidase. |
| 3.2.1.105 Strictosidine β -glucosidase. | 3.2.1.146 β -galactofuranosidase. |
| 3.2.1.106 Mannosyl-oligosaccharide glucosidase. | 3.2.1.147 Thioglucosidase. |
| 3.2.1.107 Protein-glucosylgalactosylhydroxylysine glucosidase. | 3.2.1.148 Ribosylhomocysteinase. |
| 3.2.1.108 Lactase. | 3.2.1.149 β -primeverosidase. |
| 3.2.1.109 Endogalactosaminidase. | 3.2.1.150 Oligoxyloglucan reducing-end-specific cellobiohydrolase. |
| 3.2.1.110 Mucinaminyserine mucinaminidase. | 3.2.1.151 Xyloglucan-specific endo- β -1,4-glucanase. |
| 3.2.1.111 1,3- α -L-fucosidase. | 3.2.2.1 Purine nucleosidase. |
| 3.2.1.112 2-deoxyglucosidase. | 3.2.2.2 Inosine nucleosidase. |
| 3.2.1.113 Mannosyl-oligosaccharide 1,2- α -mannosidase. | 3.2.2.3 Uridine nucleosidase. |
| 3.2.1.114 Mannosyl-oligosaccharide 1,3-1,6- α -mannosidase. | 3.2.2.4 AMP nucleosidase. |
| 3.2.1.115 Branched-dextran exo-1,2- α -glucosidase. | 3.2.2.5 NAD(+) nucleosidase. |
| 3.2.1.116 Glucan 1,4- α -maltotriohydrolase. | 3.2.2.6 NAD(P)(+) nucleosidase. |
| 3.2.1.117 Amygdalin β -glucosidase. | 3.2.2.7 Adenosine nucleosidase. |
| 3.2.1.118 Prunasin β -glucosidase. | 3.2.2.8 Ribosylpyrimidine nucleosidase. |
| 3.2.1.119 Vicianin β -glucosidase. | 3.2.2.9 Adenosylhomocysteine nucleosidase. |
| 3.2.1.120 Oligoxyloglucan β -glycosidase. | 3.2.2.10 Pyrimidine-5'-nucleotide nucleosidase. |

| | |
|--|--|
| 3.2.2.11 β -aspartyl-N-acetylglucosaminidase. | 3.4.13.18 Cytosol nonspecific dipeptidase. |
| 3.2.2.12 Inosinate nucleosidase. | 3.4.13.19 Membrane dipeptidase. |
| 3.2.2.13 1-methyladenosine nucleosidase. | 3.4.13.20 β -Ala-His dipeptidase. |
| 3.2.2.14 NMN nucleosidase. | 3.4.13.21 Dipeptidase E. |
| 3.2.2.15 DNA-deoxyinosine glycosylase. | 3.4.14.1 Dipeptidyl-peptidase I. |
| 3.2.2.16 Methylthioadenosine nucleosidase. | 3.4.14.2 Dipeptidyl-peptidase II. |
| 3.2.2.17 Deoxyribodipyrimidine endonucleosidase. | 3.4.14.4 Dipeptidyl-peptidase III. |
| 3.2.2.19 [Protein ADP-ribosylarginine] hydrolase. | 3.4.14.5 Dipeptidyl-peptidase IV. |
| 3.2.2.20 DNA-3-methyladenine glycosylase I. | 3.4.14.6 Dipeptidyl-dipeptidase. |
| 3.2.2.21 DNA-3-methyladenine glycosylase II. | 3.4.14.9 Tripeptidyl-peptidase I. |
| 3.2.2.22 rRNA N-glycosylase. | 3.4.14.10 Tripeptidyl-peptidase II. |
| 3.2.2.23 DNA-formamidopyrimidine glycosylase. | 3.4.14.11 Xaa-Pro dipeptidyl-peptidase. |
| 3.2.2.24 ADP-ribosyl-[dinitrogen reductase] hydrolase. | 3.4.15.1 Peptidyl-dipeptidase A. |
| 3.3.1.1 Adenosylhomocysteinase. | 3.4.15.4 Peptidyl-dipeptidase B. |
| 3.3.1.2 Adenosylmethionine hydrolase. | 3.4.15.5 Peptidyl-dipeptidase Dcp. |
| 3.3.2.1 Isochorismatase. | 3.4.16.2 Lysosomal Pro-X carboxypeptidase. |
| 3.3.2.2 Alkenylglycerophosphocholine hydrolase. | 3.4.16.4 Serine-type D-Ala-D-Ala carboxypeptidase. |
| 3.3.2.3 Epoxide hydrolase. | 3.4.16.5 Carboxypeptidase C. |
| 3.3.2.4 Trans-epoxysuccinate hydrolase. | 3.4.16.6 Carboxypeptidase D. |

| | |
|--|--|
| 3.3.2.5 Alkenylglycerophosphoethanolamine hydrolase. | 3.4.17.1 Carboxypeptidase A. |
| 3.3.2.6 Leukotriene-A(4) hydrolase. | 3.4.17.2 Carboxypeptidase B. |
| 3.3.2.7 Hepoxilin-epoxide hydrolase. | 3.4.17.3 Lysine carboxypeptidase. |
| 3.3.2.8 Limonene-1,2-epoxide hydrolase. | 3.4.17.4 Gly-X carboxypeptidase. |
| 3.4.11.1 Leucyl aminopeptidase. | 3.4.17.6 Alanine carboxypeptidase. |
| 3.4.11.2 Membrane alanyl aminopeptidase. | 3.4.17.8 Muramoylpentapeptide carboxypeptidase. |
| 3.4.11.3 Cystinyl aminopeptidase. | 3.4.17.10 Carboxypeptidase E. |
| 3.4.11.4 Tripeptide aminopeptidase. | 3.4.17.11 Glutamate carboxypeptidase. |
| 3.4.11.5 Prolyl aminopeptidase. | 3.4.17.12 Carboxypeptidase M. |
| 3.4.11.6 Aminopeptidase B. | 3.4.17.13 Muramoyltetrapeptide carboxypeptidase. |
| 3.4.11.7 Glutamyl aminopeptidase. | 3.4.17.14 Zinc D-Ala-D-Ala carboxypeptidase. |
| 3.4.11.9 Xaa-Pro aminopeptidase. | 3.4.17.15 Carboxypeptidase A2. |
| 3.4.11.10 Bacterial leucyl aminopeptidase. | 3.4.17.16 Membrane Pro-X carboxypeptidase. |
| 3.4.11.13 Clostridial aminopeptidase. | 3.4.17.17 Tubuliny-Tyr carboxypeptidase. |
| 3.4.11.14 Cytosol alanyl aminopeptidase. | 3.4.17.18 Carboxypeptidase T. |
| 3.4.11.15 Aminopeptidase Y. | 3.4.17.19 Carboxypeptidase Taq. |
| 3.4.11.16 Xaa-Trp aminopeptidase. | 3.4.17.20 Carboxypeptidase U. |
| 3.4.11.17 Tryptophanyl aminopeptidase. | 3.4.17.21 Glutamate carboxypeptidase II. |
| 3.4.11.18 Methionyl aminopeptidase. | 3.4.17.22 Metallo-carboxypeptidase D. |
| 3.4.11.19 D-stereospecific aminopeptidase. | 3.4.18.1 Cathepsin X. |
| 3.4.11.20 Aminopeptidase Ey. | 3.4.19.1 Acylaminoacyl-peptidase. |
| 3.4.11.21 Aspartyl aminopeptidase. | 3.4.19.2 Peptidyl-glycinamidase. |
| 3.4.11.22 Aminopeptidase I. | 3.4.19.3 Pyroglutamyl-peptidase I. |
| 3.4.11.23 PepB aminopeptidase. | 3.4.19.5 Beta-aspartyl-peptidase. |
| 3.4.13.3 Xaa-His dipeptidase. | 3.4.19.6 Pyroglutamyl-peptidase II. |
| 3.4.13.4 Xaa-Arg dipeptidase. | 3.4.19.7 N-formylmethionyl-peptidase. |
| 3.4.13.5 Xaa-methyl-His dipeptidase. | 3.4.19.9 Gamma-glutamyl hydrolase. |
| 3.4.13.7 Glu-Glu dipeptidase. | 3.4.19.11 Gamma-D-glutamyl-meso-diaminopimelate peptidase. |
| 3.4.13.9 Xaa-Pro dipeptidase. | 3.4.19.12 Ubiquitinyl hydrolase 1. |
| 3.4.13.12 Met-Xaa dipeptidase. | 3.4.21.1 Chymotrypsin. |
| 3.4.13.17 Non-stereospecific dipeptidase. | 3.4.21.2 Chymotrypsin C. |

| | |
|--------------------------------------|--------------------------------------|
| 3.4.21.3 Metridin. | 3.4.21.74 Venombin A. |
| 3.4.21.4 Trypsin. | 3.4.21.75 Furin. |
| 3.4.21.5 Thrombin. | 3.4.21.76 Myeloblastin. |
| 3.4.21.6 Coagulation factor Xa. | 3.4.21.77 Semenogelase. |
| 3.4.21.7 Plasmin. | 3.4.21.78 Granzyme A. |
| 3.4.21.9 Enteropeptidase. | 3.4.21.79 Granzyme B. |
| 3.4.21.10 Acrosin. | 3.4.21.80 Streptogrisin A. |
| 3.4.21.12 Alpha-lytic endopeptidase. | 3.4.21.81 Streptogrisin B. |
| 3.4.21.19 Glutamyl endopeptidase. | 3.4.21.82 Glutamyl endopeptidase II. |
| 3.4.21.20 Cathepsin G. | 3.4.21.83 Oligopeptidase B. |
| 3.4.21.21 Coagulation factor VIIa. | 3.4.21.84 Limulus clotting factor C. |
| 3.4.21.22 Coagulation factor IXa. | 3.4.21.85 Limulus clotting factor B. |
| 3.4.21.25 Cucumisin. | 3.4.21.86 Limulus clotting enzyme. |
| 3.4.21.26 Prolyl oligopeptidase. | 3.4.21.87 Omptin. |
| 3.4.21.27 Coagulation factor XIa. | 3.4.21.88 Repressor lexA. |
| 3.4.21.32 Brachyurin. | 3.4.21.89 Signal peptidase I. |
| 3.4.21.34 Plasma kallikrein. | 3.4.21.90 Togavirin. |

| | | | |
|-----------|--|------------|----------------------------------|
| 3.4.21.35 | Tissue kallikrein. | 3.4.21.91 | Flavivirin. |
| 3.4.21.36 | Pancreatic elastase. | 3.4.21.92 | Endopeptidase Clp. |
| 3.4.21.37 | Leukocyte elastase. | 3.4.21.93 | Proprotein convertase 1. |
| 3.4.21.38 | Coagulation factor XIIa. | 3.4.21.94 | Proprotein convertase 2. |
| 3.4.21.39 | Chymase. | 3.4.21.95 | Snake venom factor V activator. |
| 3.4.21.41 | Complement subcomponent C1r. | 3.4.21.96 | Lactocypin. |
| 3.4.21.42 | Complement subcomponent C1s. | 3.4.21.97 | Assemblin. |
| 3.4.21.43 | Classical-complement-pathway C3/C5 convertase. | 3.4.21.98 | Hepacivirin. |
| 3.4.21.45 | Complement factor I. | 3.4.21.99 | Spermosin. |
| 3.4.21.46 | Complement factor D. | 3.4.21.100 | Pseudomonalisin. |
| 3.4.21.47 | Alternative-complement-pathway C3/C5 convertase. | 3.4.21.101 | Xanthomonalisin. |
| 3.4.21.48 | Cerevisin. | 3.4.21.102 | C-terminal processing peptidase. |
| 3.4.21.49 | Hypodermin C. | 3.4.21.103 | Physarolisin. |
| 3.4.21.50 | Lysyl endopeptidase. | 3.4.22.1 | Cathepsin B. |
| 3.4.21.53 | Endopeptidase La. | 3.4.22.2 | Papain. |
| 3.4.21.54 | Gamma-renin. | 3.4.22.3 | Ficain. |
| 3.4.21.55 | Venombin AB. | 3.4.22.6 | Chymopapain. |
| 3.4.21.57 | Leucyl endopeptidase. | 3.4.22.7 | Asclepain. |
| 3.4.21.59 | Tryptase. | 3.4.22.8 | Clostripain. |
| 3.4.21.60 | Scutellarin. | 3.4.22.10 | Streptopain. |
| 3.4.21.61 | Kexin. | 3.4.22.14 | Actinidain. |
| 3.4.21.62 | Subtilisin. | 3.4.22.15 | Cathepsin L. |
| 3.4.21.63 | Oryzin. | 3.4.22.16 | Cathepsin H. |
| 3.4.21.64 | Endopeptidase K. | 3.4.22.24 | Cathepsin T. |
| 3.4.21.65 | Thermomycolin. | 3.4.22.25 | Glycyl endopeptidase. |
| 3.4.21.66 | Thermitase. | 3.4.22.26 | Cancer procoagulant. |
| 3.4.21.67 | Endopeptidase So. | 3.4.22.27 | Cathepsin S. |
| 3.4.21.68 | T-plasminogen activator. | 3.4.22.28 | Picornain 3C. |
| 3.4.21.69 | Protein C (activated). | 3.4.22.29 | Picornain 2A. |
| 3.4.21.70 | Pancreatic endopeptidase E. | 3.4.22.30 | Caricain. |
| 3.4.21.71 | Pancreatic elastase II. | 3.4.22.31 | Ananain. |
| 3.4.21.72 | IgA-specific serine endopeptidase. | 3.4.22.32 | Stem bromelain. |
| 3.4.21.73 | U-plasminogen activator. | 3.4.22.33 | Fruit bromelain. |

| | | | |
|-----------|------------------------------------|-----------|------------------------------------|
| 3.4.22.34 | Legumain. | 3.4.23.44 | Nodavirus endopeptidase. |
| 3.4.22.35 | Histolysain. | 3.4.23.45 | Memapsin 1. |
| 3.4.22.36 | Caspase-1. | 3.4.23.46 | Memapsin 2. |
| 3.4.22.37 | Gingipain R. | 3.4.23.47 | HIV-2 retropepsin. |
| 3.4.22.38 | Cathepsin K. | 3.4.23.48 | Plasminogen activator Pla. |
| 3.4.22.39 | Adenain. | 3.4.24.1 | Atrolysin A. |
| 3.4.22.40 | Bleomycin hydrolase. | 3.4.24.3 | Microbial collagenase. |
| 3.4.22.41 | Cathepsin F. | 3.4.24.6 | Leucolysin. |
| 3.4.22.42 | Cathepsin O. | 3.4.24.7 | Interstitial collagenase. |
| 3.4.22.43 | Cathepsin V. | 3.4.24.11 | Neprilysin. |
| 3.4.22.44 | Nuclear-inclusion-a endopeptidase. | 3.4.24.12 | Envelysin. |
| 3.4.22.45 | Helper-component proteinase. | 3.4.24.13 | IgA-specific metalloendopeptidase. |
| 3.4.22.46 | L-peptidase. | 3.4.24.14 | Procollagen N-endopeptidase. |
| 3.4.22.47 | Gingipain K. | 3.4.24.15 | Thimet oligopeptidase. |
| 3.4.22.48 | Staphopain. | 3.4.24.16 | Neurolysin. |
| 3.4.22.49 | Separase. | 3.4.24.17 | Stromelysin 1. |
| 3.4.22.50 | V-cath endopeptidase. | 3.4.24.18 | Meprin A. |

| | | | |
|-----------|---|-----------|-------------------------------------|
| 3.4.22.51 | Cruzipain. | 3.4.24.19 | Procollagen C-endorpeptidase. |
| 3.4.22.52 | Calpain-1. | 3.4.24.20 | Peptidyl-Lys metalloendorpeptidase. |
| 3.4.22.53 | Calpain-2. | 3.4.24.21 | Astacin. |
| 3.4.23.1 | Pepsin A. | 3.4.24.22 | Stromelysin 2. |
| 3.4.23.2 | Pepsin B. | 3.4.24.23 | Matrilysin. |
| 3.4.23.3 | Gastricsin. | 3.4.24.24 | Gelatinase A. |
| 3.4.23.4 | Chymosin. | 3.4.24.25 | Vibriolysin. |
| 3.4.23.5 | Cathepsin D. | 3.4.24.26 | Pseudolysin. |
| 3.4.23.12 | Nepenthesin. | 3.4.24.27 | Thermolysin. |
| 3.4.23.15 | Renin. | 3.4.24.28 | Bacillolysin. |
| 3.4.23.16 | HIV-1 retropepsin. | 3.4.24.29 | Aureolysin. |
| 3.4.23.17 | Pro-opiomelanocortin converting enzyme. | 3.4.24.30 | Coccolysin. |
| 3.4.23.18 | Aspergillopepsin I. | 3.4.24.31 | Mycolysin. |
| 3.4.23.19 | Aspergillopepsin II. | 3.4.24.32 | Beta-lytic metalloendorpeptidase. |
| 3.4.23.20 | Penicillopepsin. | 3.4.24.33 | Peptidyl-Asp metalloendorpeptidase. |
| 3.4.23.21 | Rhizopuspepsin. | 3.4.24.34 | Neutrophil collagenase. |
| 3.4.23.22 | Endothiapepsin. | 3.4.24.35 | Gelatinase B. |
| 3.4.23.23 | Mucorpepsin. | 3.4.24.36 | Leishmanolysin. |
| 3.4.23.24 | Candidapepsin. | 3.4.24.37 | Saccharolysin. |
| 3.4.23.25 | Saccharopepsin. | 3.4.24.38 | Gametolysin. |
| 3.4.23.26 | Rhodotorulapepsin. | 3.4.24.39 | Deuterolysin. |
| 3.4.23.28 | Acrocylindropepsin. | 3.4.24.40 | Serralysin. |
| 3.4.23.29 | Polyporopepsin. | 3.4.24.41 | Atrolysin B. |
| 3.4.23.30 | Pycnoporopepsin. | 3.4.24.42 | Atrolysin C. |
| 3.4.23.31 | Scytalidopepsin A. | 3.4.24.43 | Atroxase. |
| 3.4.23.32 | Scytalidopepsin B. | 3.4.24.44 | Atrolysin E. |
| 3.4.23.34 | Cathepsin E. | 3.4.24.45 | Atrolysin F. |
| 3.4.23.35 | Barrierpepsin. | 3.4.24.46 | Adamalysin. |
| 3.4.23.36 | Signal peptidase II. | 3.4.24.47 | Horrolysin. |
| 3.4.23.38 | Plasmepsin I. | 3.4.24.48 | Ruberlysin. |
| 3.4.23.39 | Plasmepsin II. | 3.4.24.49 | Bothropasin. |
| 3.4.23.40 | Phytpepsin. | 3.4.24.50 | Bothrolysin. |
| 3.4.23.41 | Yapsin 1. | 3.4.24.51 | Ophiolysin. |
| 3.4.23.42 | Thermopsin. | 3.4.24.52 | Trimerelysin I. |
| 3.4.23.43 | Prepilin peptidase. | 3.4.24.53 | Trimerelysin II. |

| | | | |
|-----------|---------------------------------------|----------|--|
| 3.4.24.54 | Mucrolysin. | 3.5.1.16 | Acetylornithine deacetylase. |
| 3.4.24.55 | Pitrilysin. | 3.5.1.17 | Acyl-lysine deacylase. |
| 3.4.24.56 | Insulysin. | 3.5.1.18 | Succinyl-diaminopimelate desuccinylase. |
| 3.4.24.57 | O-sialoglycoprotein endopeptidase. | 3.5.1.19 | Nicotinamidase. |
| 3.4.24.58 | Russellysin. | 3.5.1.20 | Citrullinase. |
| 3.4.24.59 | Mitochondrial intermediate peptidase. | 3.5.1.21 | N-acetyl-beta-alanine deacetylase. |
| 3.4.24.60 | Dactylisin. | 3.5.1.22 | Pantothenase. |
| 3.4.24.61 | Nardilysin. | 3.5.1.23 | Ceramidase. |
| 3.4.24.62 | Magnolysin. | 3.5.1.24 | Choloylglycine hydrolase. |
| 3.4.24.63 | Mepri B. | 3.5.1.25 | N-acetylglucosamine-6-phosphate deacetylase. |
| 3.4.24.64 | Mitochondrial processing peptidase. | 3.5.1.26 | N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase. |
| 3.4.24.65 | Macrophage elastase. | 3.5.1.27 | N-formylmethionylaminoacyl-tRNA deformylase. |
| 3.4.24.66 | Choriolysin L. | 3.5.1.28 | N-acetylmuramoyl-L-alanine amidase. |

| | | | |
|-----------|---|----------|--|
| 3.4.24.67 | Choriolysin H. | 3.5.1.29 | 2-(acetamidomethylene)succinate hydrolase. |
| 3.4.24.68 | Tentoxilysin. | 3.5.1.30 | 5-aminopentanamidase. |
| 3.4.24.69 | Bontoxilysin. | 3.5.1.31 | Formylmethionine deformylase. |
| 3.4.24.70 | Oligopeptidase A. | 3.5.1.32 | Hippurate hydrolase. |
| 3.4.24.71 | Endothelin-converting enzyme 1. | 3.5.1.33 | N-acetylglucosamine deacetylase. |
| 3.4.24.72 | Fibrolase. | 3.5.1.35 | D-glutaminase. |
| 3.4.24.73 | Jararhagin. | 3.5.1.36 | N-methyl-2-oxoglutaramate hydrolase. |
| 3.4.24.74 | Fragilysin. | 3.5.1.38 | Glutamin-(asparagin-)ase. |
| 3.4.24.75 | Lysostaphin. | 3.5.1.39 | Alkylamidase. |
| 3.4.24.76 | Flavastacin. | 3.5.1.40 | Acylagmatine amidase. |
| 3.4.24.77 | Snapalysin. | 3.5.1.41 | Chitin deacetylase. |
| 3.4.24.78 | GPR endopeptidase. | 3.5.1.42 | Nicotinamide-nucleotide amidase. |
| 3.4.24.79 | Pappalysin-1. | 3.5.1.43 | Peptidyl-glutaminase. |
| 3.4.24.80 | Membrane-type matrix metalloproteinase-1. | 3.5.1.44 | Protein-glutamine glutaminase. |
| 3.4.24.81 | ADAM10 endopeptidase. | 3.5.1.46 | 6-aminohexanoate-dimer hydrolase. |
| 3.4.24.82 | ADAMTS-4 endopeptidase. | 3.5.1.47 | N-acetyldiaminopimelate deacetylase. |
| 3.4.24.83 | Anthrax lethal factor endopeptidase. | 3.5.1.48 | Acetylspermidine deacetylase. |
| 3.4.24.84 | Ste24 endopeptidase. | 3.5.1.49 | Formamidase. |
| 3.4.24.85 | S2P endopeptidase. | 3.5.1.50 | Pentanamidase. |
| 3.4.24.86 | ADAM 17 endopeptidase. | 3.5.1.51 | 4-acetamidobutyryl-CoA deacetylase. |
| 3.4.25.1 | Proteasome endopeptidase complex. | 3.5.1.52 | Peptide-N(4)-(N-acetyl-beta-glucosaminy)asparagine amidase. |
| 3.5.1.1 | Asparaginase. | 3.5.1.53 | N-carbamoylputrescine amidase. |
| 3.5.1.2 | Glutaminase. | 3.5.1.54 | Allophanate hydrolase. |
| 3.5.1.3 | Omega-amidase. | 3.5.1.55 | Long-chain-fatty-acyl-glutamate deacylase. |
| 3.5.1.4 | Amidase. | 3.5.1.56 | N,N-dimethylformamidase. |
| 3.5.1.5 | Urease. | 3.5.1.57 | Tryptophanamidase. |
| 3.5.1.6 | Beta-ureidopropionase. | 3.5.1.58 | N-benzoyloxycarbonylglycine hydrolase. |
| 3.5.1.7 | Ureidosuccinase. | 3.5.1.59 | N-carbamoylsarcosine amidase. |
| 3.5.1.8 | Formylaspartate deformylase. | 3.5.1.60 | N-(long-chain-acyl)ethanolamine deacylase. |
| 3.5.1.9 | Arylformamidase. | 3.5.1.61 | Mimosinase. |
| 3.5.1.10 | Formyltetrahydrofolate deformylase. | 3.5.1.62 | Acetylputrescine deacetylase. |
| 3.5.1.11 | Penicillin amidase. | 3.5.1.63 | 4-acetamidobutyrate deacetylase. |
| 3.5.1.12 | Biotinidase. | 3.5.1.64 | N(alpha)-benzoyloxycarbonylleucine hydrolase. |
| 3.5.1.13 | Aryl-acylamidase. | 3.5.1.65 | Theanine hydrolase. |
| 3.5.1.14 | Aminoacylase. | 3.5.1.66 | 2-(hydroxymethyl)-3-(acetamidomethylene)succinate hydrolase. |
| 3.5.1.15 | Aspartoacylase. | 3.5.1.67 | 4-methyleneglutaminase. |

| | | | |
|----------|---|----------|---------------------------------|
| 3.5.1.68 | N-formylglutamate deformylase. | 3.5.3.9 | Allantoate deiminase. |
| 3.5.1.69 | Glycosphingolipid deacylase. | 3.5.3.10 | D-arginase. |
| 3.5.1.70 | Aculeacin-A deacylase. | 3.5.3.11 | Agmatinase. |
| 3.5.1.71 | N-feruloylglycine deacylase. | 3.5.3.12 | Agmatine deiminase. |
| 3.5.1.72 | D-benzoylarginine-4-nitroanilide amidase. | 3.5.3.13 | Formimidoylglutamate deiminase. |
| 3.5.1.73 | Carnitinamidase. | 3.5.3.14 | Amidinoaspartase. |
| 3.5.1.74 | Chenodeoxycholytaurine hydrolase. | 3.5.3.15 | Protein-arginine deiminase. |
| 3.5.1.75 | Urethanase. | 3.5.3.16 | Methylguanidinase. |
| 3.5.1.76 | Arylalkyl acylamidase. | 3.5.3.17 | Guanidinopropionase. |
| 3.5.1.77 | N-carbamoyl-D-amino acid hydrolase. | 3.5.3.18 | Dimethylargininase. |
| 3.5.1.78 | Glutathionylspermidine amidase. | 3.5.3.19 | Ureidoglycolate hydrolase. |

| | | | |
|----------|---|----------|--|
| 3.5.1.79 | Phthalyl amidase. | 3.5.3.20 | Diguanidinobutanase. |
| 3.5.1.81 | N-acyl-D-amino-acid deacylase. | 3.5.3.21 | Methylenediurea deaminase. |
| 3.5.1.82 | N-acyl-D-glutamate deacylase. | 3.5.3.22 | Proclavamate amidohydrolase. |
| 3.5.1.83 | N-acyl-D-aspartate deacylase. | 3.5.4.1 | Cytosine deaminase. |
| 3.5.1.84 | Biuret amidohydrolase. | 3.5.4.2 | Adenine deaminase. |
| 3.5.1.85 | (S)-N-acetyl-1-phenylethylamine hydrolase. | 3.5.4.3 | Guanine deaminase. |
| 3.5.1.86 | Mandelamide amidase. | 3.5.4.4 | Adenosine deaminase. |
| 3.5.1.87 | N-carbamoyl-L-amino-acid hydrolase. | 3.5.4.5 | Cytidine deaminase. |
| 3.5.1.88 | Peptide deformylase. | 3.5.4.6 | AMP deaminase. |
| 3.5.1.89 | N-acetylglucosaminylphosphatidylinositol deacetylase. | 3.5.4.7 | ADP deaminase. |
| 3.5.1.90 | Adenosylcobinamide hydrolase. | 3.5.4.8 | Aminoimidazole. |
| 3.5.2.1 | Barbiturase. | 3.5.4.9 | Methenyltetrahydrofolate cyclohydrolase. |
| 3.5.2.2 | Dihydropyrimidinase. | 3.5.4.10 | IMP cyclohydrolase. |
| 3.5.2.3 | Dihydroorotase. | 3.5.4.11 | Pterin deaminase. |
| 3.5.2.4 | Carboxymethylhydantoinase. | 3.5.4.12 | dCMP deaminase. |
| 3.5.2.5 | Allantoinase. | 3.5.4.13 | dCTP deaminase. |
| 3.5.2.6 | Beta-lactamase. | 3.5.4.14 | Deoxycytidine deaminase. |
| 3.5.2.7 | Imidazolonepropionase. | 3.5.4.15 | Guanosine deaminase. |
| 3.5.2.9 | 5-oxoprolinase (ATP-hydrolyzing). | 3.5.4.16 | GTP cyclohydrolase I. |
| 3.5.2.10 | Creatininase. | 3.5.4.17 | Adenosine-phosphate deaminase. |
| 3.5.2.11 | L-lysine-lactamase. | 3.5.4.18 | ATP deaminase. |
| 3.5.2.12 | 6-aminohexanoate-cyclic-dimer hydrolase. | 3.5.4.19 | Phosphoribosyl-AMP cyclohydrolase. |
| 3.5.2.13 | 2,5-dioxopiperazine hydrolase. | 3.5.4.20 | Pyriithamine deaminase. |
| 3.5.2.14 | N-methylhydantoinase (ATP-hydrolyzing). | 3.5.4.21 | Creatinine deaminase. |
| 3.5.2.15 | Cyanuric acid amidohydrolase. | 3.5.4.22 | 1-pyrroline-4-hydroxy-2-carboxylate deaminase. |
| 3.5.2.16 | Maleimide hydrolase. | 3.5.4.23 | Blasticidin-S deaminase. |
| 3.5.2.17 | Hydroxyisourate hydrolase. | 3.5.4.24 | Sepiapterin deaminase. |
| 3.5.3.1 | Arginase. | 3.5.4.25 | GTP cyclohydrolase II. |
| 3.5.3.2 | Guanidinoacetase. | 3.5.4.26 | Diaminohydroxyphosphoribosylaminopyrimidine deaminase. |
| 3.5.3.3 | Creatinase. | 3.5.4.27 | Methenyltetrahydromethanopterin cyclohydrolase. |
| 3.5.3.4 | Allantoicase. | 3.5.4.28 | S-adenosylhomocysteine deaminase. |
| 3.5.3.5 | Formimidoylaspartate deiminase. | 3.5.4.29 | GTP cyclohydrolase IIa. |
| 3.5.3.6 | Arginine deiminase. | 3.5.4.30 | dCTP deaminase (dUMP-forming). |
| 3.5.3.7 | Guanidinobutyrase. | 3.5.5.1 | Nitrilase. |
| 3.5.3.8 | Formimidoylglutamate. | 3.5.5.2 | Ricinine nitrilase. |

| | | | |
|----------|-------------------------|----------|---|
| 3.5.5.4 | Cyanoalanine nitrilase. | 3.6.1.40 | Guanosine-5'-triphosphate,3'-diphosphate diphosphatase. |
| 3.5.5.5 | Arylacetone nitrilase. | 3.6.1.41 | Bis(5'-nucleosyl)-tetraphosphatase (symmetrical). |
| 3.5.5.6 | Bromoxynil nitrilase. | 3.6.1.42 | Guanosine-diphosphatase. |
| 3.5.5.7 | Aliphatic nitrilase. | 3.6.1.43 | Dolichyldiphosphatase. |
| 3.5.5.8 | Thiocyanate hydrolase. | 3.6.1.44 | Oligosaccharide-diphosphodolichol diphosphatase. |
| 3.5.99.1 | Riboflavinase. | 3.6.1.45 | UDP-sugar diphosphatase. |

| | |
|---|---|
| 3.5.99.2 Thiaminase. | 3.6.1.52 Diphosphoinositol-polyphosphate diphosphatase. |
| 3.5.99.3 Hydroxydechloroatrazine ethylaminohydrolase. | 3.6.2.1 Adenylylsulfatase. |
| 3.5.99.4 N-isopropylammelide isopropylaminohydrolase. | 3.6.2.2 Phosphoadenylylsulfatase. |
| 3.5.99.5 2-aminomuconate deaminase. | 3.6.3.1 Phospholipid-translocating ATPase. |
| 3.5.99.6 Glucosamine-6-phosphate deaminase. | 3.6.3.2 Magnesium-importing ATPase. |
| 3.5.99.7 1-aminocyclopropane-1-carboxylate deaminase. | 3.6.3.3 Cadmium-exporting ATPase. |
| 3.6.1.1 Inorganic diphosphatase. | 3.6.3.4 Copper-exporting ATPase. |
| 3.6.1.2 Trimetaphosphatase. | 3.6.3.5 Zinc-exporting ATPase. |
| 3.6.1.3 Adenosinetriphosphatase. | 3.6.3.6 Proton-exporting ATPase. |
| 3.6.1.5 Apyrase. | 3.6.3.7 Sodium-exporting ATPase. |
| 3.6.1.6 Nucleoside-diphosphatase. | 3.6.3.8 Calcium-transporting ATPase. |
| 3.6.1.7 Acylphosphatase. | 3.6.3.9 Sodium/potassium-exchanging ATPase. |
| 3.6.1.8 ATP diphosphatase. | 3.6.3.10 Hydrogen/potassium-exchanging ATPase. |
| 3.6.1.9 Nucleotide diphosphatase. | 3.6.3.11 Chloride-transporting ATPase. |
| 3.6.1.10 Endopolyphosphatase. | 3.6.3.12 Potassium-transporting ATPase. |
| 3.6.1.11 Exopolyphosphatase. | 3.6.3.14 H(+)-transporting two-sector ATPase. |
| 3.6.1.12 dCTP diphosphatase. | 3.6.3.15 Sodium-transporting two-sector ATPase. |
| 3.6.1.13 ADP-ribose diphosphatase. | 3.6.3.16 Arsenite-transporting ATPase. |
| 3.6.1.14 Adenosine-tetraphosphatase. | 3.6.3.17 Monosaccharide-transporting ATPase. |
| 3.6.1.15 Nucleoside-triphosphatase. | 3.6.3.18 Oligosaccharide-transporting ATPase. |
| 3.6.1.16 CDP-glycerol diphosphatase. | 3.6.3.19 Maltose-transporting ATPase. |
| 3.6.1.17 Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical). | 3.6.3.20 Glycerol-3-phosphate-transporting ATPase. |
| 3.6.1.18 FAD diphosphatase. | 3.6.3.21 Polar-amino-acid-transporting ATPase. |
| 3.6.1.19 Nucleoside-triphosphate diphosphatase. | 3.6.3.22 Nonpolar-amino-acid-transporting ATPase. |
| 3.6.1.20 5'-acylphosphoadenosine hydrolase. | 3.6.3.23 Oligopeptide-transporting ATPase. |
| 3.6.1.21 ADP-sugar diphosphatase. | 3.6.3.24 Nickel-transporting ATPase. |
| 3.6.1.22 NAD ⁺ diphosphatase. | 3.6.3.25 Sulfate-transporting ATPase. |
| 3.6.1.23 dUTP diphosphatase. | 3.6.3.26 Nitrate-transporting ATPase. |
| 3.6.1.24 Nucleoside phosphoacylhydrolase. | 3.6.3.27 Phosphate-transporting ATPase. |
| 3.6.1.25 Triphosphatase. | 3.6.3.28 Phosphonate-transporting ATPase. |
| 3.6.1.26 CDP-diacylglycerol diphosphatase. | 3.6.3.29 Molybdate-transporting ATPase. |
| 3.6.1.27 Undecaprenyl-diphosphatase. | 3.6.3.30 Fe(3+)-transporting ATPase. |
| 3.6.1.28 Thiamine-triphosphatase. | 3.6.3.31 Polyamine-transporting ATPase. |
| 3.6.1.29 Bis(5'-adenosyl)-triphosphatase. | 3.6.3.32 Quaternary-amine-transporting ATPase. |
| 3.6.1.30 M(7)G(5')pppN diphosphatase. | 3.6.3.33 Vitamin B12-transporting ATPase. |
| 3.6.1.31 Phosphoribosyl-ATP diphosphatase. | 3.6.3.34 Iron-chelate-transporting ATPase. |
| 3.6.1.39 Thymidine-triphosphatase. | 3.6.3.35 Manganese-transporting ATPase. |

| | |
|---|--------------------------------------|
| 3.6.3.36 Taurine-transporting ATPase. | 3.8.1.1 Alkylhalidase. |
| 3.6.3.37 Guanine-transporting ATPase. | 3.8.1.2 (S)-2-haloacid dehalogenase. |
| 3.6.3.38 Capsular-polysaccharide-transporting ATPase. | 3.8.1.3 Haloacetate dehalogenase. |
| 3.6.3.39 Lipopolysaccharide-transporting | 3.8.1.5 Haloalkane dehalogenase. |

| | |
|---|---|
| ATPase. | |
| 3.6.3.40 Teichoic-acid-transporting ATPase. | 3.8.1.6 4-chlorobenzoate dehalogenase. |
| 3.6.3.41 Heme-transporting ATPase. | 3.8.1.7 4-chlorobenzoyl-CoA dehalogenase. |
| 3.6.3.42 Beta-glucan-transporting ATPase. | 3.8.1.8 Atrazine chlorohydrolase. |
| 3.6.3.43 Peptide-transporting ATPase. | 3.8.1.9 (R)-2-haloacid dehalogenase. |
| 3.6.3.44 Xenobiotic-transporting ATPase. | 3.8.1.10 2-haloacid dehalogenase (configuration-inverting). |
| 3.6.3.45 Stéroid-transporting ATPase. | 3.8.1.11 2-haloacid dehalogenase (configuration-retaining). |
| 3.6.3.46 Cadmium-transporting ATPase. | 3.9.1.1 Phosphoamidase. |
| 3.6.3.47 Fatty-acyl-CoA-transporting ATPase. | 3.10.1.1 N-sulfoglucosamine sulfohydrolase. |
| 3.6.3.48 Alpha-factor-transporting ATPase. | 3.10.1.2 Cyclamate sulfohydrolase. |
| 3.6.3.49 Channel-conductance-controlling ATPase. | 3.11.1.1 Phosphonoacetaldehyde hydrolase. |
| 3.6.3.50 Protein-secreting ATPase. | 3.11.1.2 Phosphonoacetate hydrolase. |
| 3.6.3.51 Mitochondrial protein-transporting ATPase. | 3.12.1.1 Trithionate hydrolase. |
| 3.6.3.52 Chloroplast protein-transporting ATPase. | 3.13.1.1 UDP-sulfoquinovose synthase. |
| 3.6.3.53 Ag(+)-exporting ATPase. | |
| 3.6.4.1 Myosin ATPase. | ENZYME: 4.-.-.- |
| 3.6.4.2 Dynein ATPase. | 4.1.1.1 Pyruvate decarboxylase. |
| 3.6.4.3 Microtubule-severing ATPase. | 4.1.1.2 Oxalate decarboxylase. |
| 3.6.4.4 Plus-end-directed kinesin ATPase. | 4.1.1.3 Oxaloacetate decarboxylase. |
| 3.6.4.5 Minus-end-directed kinesin ATPase. | 4.1.1.4 Acetoacetate decarboxylase. |
| 3.6.4.6 Vesicle-fusing ATPase. | 4.1.1.5 Acetolactate decarboxylase. |
| 3.6.4.7 Peroxisome-assembly ATPase. | 4.1.1.6 Aconitate decarboxylase. |
| 3.6.4.8 Proteasome ATPase. | 4.1.1.7 Benzoylformate decarboxylase. |
| 3.6.4.9 Chaperonin ATPase. | 4.1.1.8 Oxalyl-CoA decarboxylase. |
| 3.6.4.10 Non-chaperonin molecular chaperone ATPase. | 4.1.1.9 Malonyl-CoA decarboxylase. |
| 3.6.4.11 Nucleoplasmin ATPase. | 4.1.1.11 Aspartate 1-decarboxylase. |
| 3.6.5.1 Heterotrimeric G-protein GTPase. | 4.1.1.12 Aspartate 4-decarboxylase. |
| 3.6.5.2 Small monomeric GTPase. | 4.1.1.14 Valine decarboxylase. |
| 3.6.5.3 Protein-synthesizing GTPase. | 4.1.1.15 Glutamate decarboxylase. |
| 3.6.5.4 Signal-recognition-particle GTPase. | 4.1.1.16 Hydroxyglutamate decarboxylase. |
| 3.6.5.5 Dynammin GTPase. | 4.1.1.17 Ornithine decarboxylase. |
| 3.6.5.6 Tubulin GTPase. | 4.1.1.18 Lysine decarboxylase. |
| 3.7.1.1 Oxaloacetase. | 4.1.1.19 Arginine decarboxylase. |
| 3.7.1.2 Fumarylacetoacetase. | 4.1.1.20 Diaminopimelate decarboxylase. |
| 3.7.1.3 Kynureninase. | 4.1.1.21 Phosphoribosylaminoimidazole carboxylase. |
| 3.7.1.4 Phloretin hydrolase. | 4.1.1.22 Histidine decarboxylase. |
| 3.7.1.5 Acylpyruvate hydrolase. | 4.1.1.23 Orotidine-5'-phosphate decarboxylase. |
| 3.7.1.6 Acetylpyruvate hydrolase. | 4.1.1.24 Aminobenzoate decarboxylase. |
| 3.7.1.7 Beta-diketone hydrolase. | 4.1.1.25 Tyrosine decarboxylase. |
| 3.7.1.8 2,6-dioxo-6-phenylhexa-3-enoate hydrolase. | 4.1.1.28 Aromatic-L-amino-acid decarboxylase. |
| 3.7.1.9 2-hydroxymuconate-semialdehyde hydrolase. | 4.1.1.29 Sulfinolalanine decarboxylase. |
| 3.7.1.10 Cyclohexane-1,3-dione hydrolase. | 4.1.1.30 Pantothenoylcysteine decarboxylase. |
| 4.1.1.31 Phosphoenolpyruvate carboxylase. | 4.1.1.74 Indolepyruvate decarboxylase. |

| | |
|--|---|
| 4.1.1.32 Phosphoenolpyruvate carboxykinase (GTP). | 4.1.1.75 5-guanidino-2-oxopentanoate decarboxylase. |
| 4.1.1.33 Diphosphomevalonate decarboxylase. | 4.1.1.76 Arylmalonate decarboxylase. |
| 4.1.1.34 Dehydro-L-gulonate decarboxylase. | 4.1.1.77 4-oxalocrotonate decarboxylase. |
| 4.1.1.35 UDP-glucuronate decarboxylase. | 4.1.1.78 Acetylenedicarboxylate decarboxylase. |
| 4.1.1.36 Phosphopantothenoylcysteine decarboxylase. | 4.1.1.79 Sulfopyruvate decarboxylase. |
| 4.1.1.37 Uroporphyrinogen decarboxylase. | 4.1.1.80 4-hydroxyphenylpyruvate decarboxylase. |
| 4.1.1.38 Phosphoenolpyruvate carboxykinase (diphosphate). | 4.1.1.81 Threonine-phosphate decarboxylase. |
| 4.1.1.39 Ribulose-bisphosphate carboxylase. | 4.1.2.2 Ketotetrose-phosphate aldolase. |
| 4.1.1.40 Hydroxypyruvate decarboxylase. | 4.1.2.4 Deoxyribose-phosphate aldolase. |
| 4.1.1.41 Methylmalonyl-CoA decarboxylase. | 4.1.2.5 Threonine aldolase. |
| 4.1.1.42 Carnitine decarboxylase. | 4.1.2.9 Phosphoketolase. |
| 4.1.1.43 Phenylpyruvate decarboxylase. | 4.1.2.10 Mandelonitrile lyase. |
| 4.1.1.44 4-carboxymuconolactone decarboxylase. | 4.1.2.11 Hydroxymandelonitrile lyase. |
| 4.1.1.45 Aminocarboxymuconate-semialdehyde decarboxylase. | 4.1.2.12 2-dehydropantoate aldolase. |
| 4.1.1.46 O-pyrocatechuate decarboxylase. | 4.1.2.13 Fructose-bisphosphate aldolase. |
| 4.1.1.47 Tartronate-semialdehyde synthase. | 4.1.2.14 2-dehydro-3-deoxy-phosphogluconate aldolase. |
| 4.1.1.48 Indole-3-glycerol-phosphate synthase. | 4.1.2.17 L-fucose-phosphate aldolase. |
| 4.1.1.49 Phosphoenolpyruvate carboxykinase (ATP). | 4.1.2.18 2-dehydro-3-deoxy-L-pentionate aldolase. |
| 4.1.1.50 Adenosylmethionine decarboxylase. | 4.1.2.19 Rhamnulose-1-phosphate aldolase. |
| 4.1.1.51 3-hydroxy-2-methylpyridine-4,5-dicarboxylate 4-decarboxylase. | 4.1.2.20 2-dehydro-3-deoxyglucarate aldolase. |
| 4.1.1.52 6-methylsalicylate decarboxylase. | 4.1.2.21 2-dehydro-3-deoxy-6-phosphogalactonate aldolase. |
| 4.1.1.53 Phenylalanine decarboxylase. | 4.1.2.22 Fructose-6-phosphate phosphoketolase. |
| 4.1.1.54 Dihydroxyfumarate decarboxylase. | 4.1.2.23 3-deoxy-D-manno-octulosonate aldolase. |
| 4.1.1.55 4,5-dihydroxyphthalate decarboxylase. | 4.1.2.24 Dimethylaniline-N-oxide aldolase. |
| 4.1.1.56 3-oxolaurate decarboxylase. | 4.1.2.25 Dihydroneopterin aldolase. |
| 4.1.1.57 Methionine decarboxylase. | 4.1.2.26 Phenylserine aldolase. |
| 4.1.1.58 Orsellinate decarboxylase. | 4.1.2.27 Sphinganine-1-phosphate aldolase. |
| 4.1.1.59 Gallate decarboxylase. | 4.1.2.28 2-dehydro-3-deoxy-D-pentionate aldolase. |
| 4.1.1.60 Stipitatonate decarboxylase. | 4.1.2.29 5-dehydro-2-deoxyphosphogluconate aldolase. |
| 4.1.1.61 4-hydroxybenzoate decarboxylase. | 4.1.2.30 17-alpha-hydroxyprogesterone aldolase. |
| 4.1.1.62 Gentisate decarboxylase. | 4.1.2.32 Trimethylamine-oxide aldolase. |
| 4.1.1.63 Protocatechuate decarboxylase. | 4.1.2.33 Fucosterol-epoxide lyase. |
| 4.1.1.64 2,2-dialkylglycine decarboxylase (pyruvate). | 4.1.2.34 4-(2-carboxyphenyl)-2-oxobut-3-enoate aldolase. |
| 4.1.1.65 Phosphatidylserine decarboxylase. | 4.1.2.35 Propioin synthase. |
| 4.1.1.66 Uracil-5-carboxylate decarboxylase. | 4.1.2.36 Lactate aldolase. |
| 4.1.1.67 UDP-galacturonate decarboxylase. | 4.1.2.37 Acetone-cyanohydrin lyase. |
| 4.1.1.68 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase. | 4.1.2.38 Benzoin aldolase. |
| 4.1.1.69 3,4-dihydroxyphthalate decarboxylase. | 4.1.2.39 Hydroxynitrilase. |
| 4.1.1.70 Glutaconyl-CoA decarboxylase. | 4.1.2.40 Tagatose-bisphosphate aldolase. |
| 4.1.1.71 2-oxoglutarate decarboxylase. | 4.1.2.41 Vanillin synthase. |
| 4.1.1.72 Branched-chain-2-oxoacid decarboxylase. | 4.1.3.1 Isocitrate lyase. |

| | |
|--|---|
| 4.1.1.73 Tartrate decarboxylase. | 4.1.3.3 N-acetylneuraminate lyase. |
| 4.1.3.4 Hydroxymethylglutaryl-CoA lyase. | 4.2.1.32 L(+)-tartrate dehydratase. |
| 4.1.3.6 Citrate (pro-3S)-lyase. | 4.2.1.33 3-isopropylmalate dehydratase. |
| 4.1.3.13 Oxalomalate lyase. | 4.2.1.34 (S)-2-methylmalate dehydratase. |
| 4.1.3.14 3-hydroxyaspartate aldolase. | 4.2.1.35 (R)-2-methylmalate dehydratase. |
| 4.1.3.16 4-hydroxy-2-oxoglutarate aldolase. | 4.2.1.36 Homoaconitate hydratase. |
| 4.1.3.17 4-hydroxy-4-methyl-2-oxoglutarate aldolase. | 4.2.1.39 Gluconate dehydratase. |
| 4.1.3.22 Citramalate lyase. | 4.2.1.40 Glucarate dehydratase. |
| 4.1.3.24 Maltol-CoA lyase. | 4.2.1.41 5-dehydro-4-deoxyglucarate dehydratase. |
| 4.1.3.25 Citramalyl-CoA lyase. | 4.2.1.42 Galactarate dehydratase. |
| 4.1.3.26 3-hydroxy-3-isohexenylglutaryl-CoA lyase. | 4.2.1.43 2-dehydro-3-deoxy-L-arabinonate dehydratase. |
| 4.1.3.27 Anthranilate synthase. | 4.2.1.44 Myo-inosose-2 dehydratase. |
| 4.1.3.30 Methylisocitrate lyase. | 4.2.1.45 CDP-glucose 4,6-dehydratase. |
| 4.1.3.32 2,3-dimethylmalate lyase. | 4.2.1.46 dTDP-glucose 4,6-dehydratase. |
| 4.1.3.34 Citryl-CoA lyase. | 4.2.1.47 GDP-mannose 4,6-dehydratase. |
| 4.1.3.35 (1-hydroxycyclohexan-1-yl)acetyl-CoA lyase. | 4.2.1.48 D-glutamate cyclase. |
| 4.1.3.36 Naphthoate synthase. | 4.2.1.49 Urocanate hydratase. |
| 4.1.3.38 Aminodeoxychorismate lyase. | 4.2.1.50 Pyrazolylalanine synthase. |
| 4.1.99.1 Tryptophanase. | 4.2.1.51 Prephenate dehydratase. |
| 4.1.99.2 Tyrosine phenol-lyase. | 4.2.1.52 Dihydrodipicolinate synthase. |
| 4.1.99.3 Deoxyribodipyrimidine photo-lyase. | 4.2.1.53 Oleate hydratase. |
| 4.1.99.5 Octadecanal decarbonylase. | 4.2.1.54 Lactoyl-CoA dehydratase. |
| 4.1.99.11 Benzylsuccinate synthase. | 4.2.1.55 3-hydroxybutyryl-CoA dehydratase. |
| 4.2.1.1 Carbonate dehydratase. | 4.2.1.56 Itaconyl-CoA hydratase. |
| 4.2.1.2 Fumarate hydratase. | 4.2.1.57 Isohexenylglutaconyl-CoA hydratase. |
| 4.2.1.3 Aconitate hydratase. | 4.2.1.58 Crotonoyl-[acyl-carrier-protein] hydratase. |
| 4.2.1.4 Citrate dehydratase. | 4.2.1.59 3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase. |
| 4.2.1.5 Arabinonate dehydratase. | 4.2.1.60 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase. |
| 4.2.1.6 Galactonate dehydratase. | 4.2.1.61 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase. |
| 4.2.1.7 Altronate dehydratase. | 4.2.1.62 5-alpha-hydroxysteroid dehydratase. |
| 4.2.1.8 Mannonate dehydratase. | 4.2.1.65 3-cyanoalanine hydratase. |
| 4.2.1.9 Dihydroxy-acid dehydratase. | 4.2.1.66 Cyanide hydratase. |
| 4.2.1.10 3-dehydroquinone dehydratase. | 4.2.1.67 D-fuconate dehydratase. |
| 4.2.1.11 Phosphopyruvate hydratase. | 4.2.1.68 L-fuconate dehydratase. |
| 4.2.1.12 Phosphogluconate dehydratase. | 4.2.1.69 Cyanamide hydratase. |
| 4.2.1.17 Enoyl-CoA hydratase. | 4.2.1.70 Pseudouridylate synthase. |
| 4.2.1.18 Methylglutaconyl-CoA hydratase. | 4.2.1.73 Protoaphin-aglucone dehydratase (cyclizing). |
| 4.2.1.19 Imidazoleglycerol-phosphate dehydratase. | 4.2.1.74 Long-chain-enoil-CoA hydratase. |
| 4.2.1.20 Tryptophan synthase. | 4.2.1.75 Uroporphyrinogen-III synthase. |
| 4.2.1.22 Cystathionine beta-synthase. | 4.2.1.76 UDP-glucose 4,6-dehydratase. |
| 4.2.1.24 Porphobilinogen synthase. | 4.2.1.77 Trans-L-3-hydroxyproline dehydratase. |
| 4.2.1.25 L-arabinonate dehydratase. | 4.2.1.78 (S)-norcoclaurine synthase. |

| | | | |
|----------|---------------------------------|----------|-------------------------------|
| 4.2.1.27 | Acetylenecarboxylate hydratase. | 4.2.1.79 | 2-methylcitrate dehydratase. |
| 4.2.1.28 | Propanediol dehydratase. | 4.2.1.80 | 2-oxopent-4-enoate hydratase. |
| 4.2.1.30 | Glycerol dehydratase. | 4.2.1.81 | D(-)-tartrate dehydratase. |
| 4.2.1.31 | Maleate hydratase. | 4.2.1.82 | Xylonate dehydratase. |

| | | | |
|-----------|--|-----------|---|
| 4.2.1.83 | 4-oxalmesaconate hydratase. | 4.2.3.6 | Trichodiene synthase. |
| 4.2.1.84 | Nitrile hydratase. | 4.2.3.7 | Pentalenene synthase. |
| 4.2.1.85 | Dimethylmaleate hydratase. | 4.2.3.8 | Casbene synthase. |
| 4.2.1.86 | 16-dehydropregesterone hydratase. | 4.2.3.9 | Aristolochene synthase. |
| 4.2.1.87 | Octopamine dehydratase. | 4.2.3.10 | (-)-endo-fenchol synthase. |
| 4.2.1.88 | Synephrine dehydratase. | 4.2.3.11 | Sabinene-hydrate synthase. |
| 4.2.1.89 | Carnitine dehydratase. | 4.2.3.12 | 6-pyruvoyltetrahydropterin synthase. |
| 4.2.1.90 | L-rhamnonate dehydratase. | 4.2.3.13 | (+)-delta-cadinene synthase. |
| 4.2.1.91 | Carboxycyclohexadienyl dehydratase. | 4.2.3.14 | Pinene synthase. |
| 4.2.1.92 | Hydroperoxide dehydratase. | 4.2.3.15 | Myrcene synthase. |
| 4.2.1.93 | ATP-dependent NAD(P)H-hydrate dehydratase. | 4.2.3.16 | (4S)-limonene synthase. |
| 4.2.1.94 | Scytalone dehydratase. | 4.2.3.17 | Taxadiene synthase. |
| 4.2.1.95 | Kievitone hydratase. | 4.2.3.18 | Abietadiene synthase. |
| 4.2.1.96 | 4a-hydroxytetrahydrobiopterin dehydratase. | 4.2.3.19 | Ent-kaurene synthase. |
| 4.2.1.97 | Phaseollidin hydratase. | 4.2.3.20 | (+)-limonene synthase. |
| 4.2.1.98 | 16-alpha-hydroxyprogesterone dehydratase. | 4.2.3.21 | Vetispiradiene synthase. |
| 4.2.1.99 | 2-methylisocitrate dehydratase. | 4.2.99.12 | Carboxymethyloxysuccinate lyase. |
| 4.2.1.100 | Cyclohexa-1,5-dienecarbonyl-CoA hydratase. | 4.2.99.18 | DNA-(apurinic or apyrimidinic site) lyase. |
| 4.2.1.101 | Trans-feruloyl-CoA hydratase. | 4.2.99.19 | 2-hydroxypropyl-CoM lyase. |
| 4.2.1.103 | Cyclohexyl-isocyanide hydratase. | 4.3.1.1 | Aspartate ammonia-lyase. |
| 4.2.1.104 | Cyanate hydratase. | 4.3.1.2 | Methylaspartate ammonia-lyase. |
| 4.2.2.1 | Hyaluronate lyase. | 4.3.1.3 | Histidine ammonia-lyase. |
| 4.2.2.2 | Pectate lyase. | 4.3.1.4 | Formimidoyltetrahydrofolate cyclodeaminase. |
| 4.2.2.3 | Poly(beta-D-mannuronate) lyase. | 4.3.1.5 | Phenylalanine ammonia-lyase. |
| 4.2.2.4 | Chondroitin ABC lyase. | 4.3.1.6 | Beta-alanyl-CoA ammonia-lyase. |
| 4.2.2.5 | Chondroitin AC lyase. | 4.3.1.7 | Ethanolamine ammonia-lyase. |
| 4.2.2.6 | Oligogalacturonide lyase. | 4.3.1.9 | Glucosaminase ammonia-lyase. |
| 4.2.2.7 | Heparin lyase. | 4.3.1.10 | Serine-sulfate ammonia-lyase. |
| 4.2.2.8 | Heparin-sulfate lyase. | 4.3.1.11 | Dihydroxyphenylalanine ammonia-lyase. |
| 4.2.2.9 | Pectate disaccharide-lyase. | 4.3.1.12 | Ornithine cyclodeaminase. |
| 4.2.2.10 | Pectin lyase. | 4.3.1.13 | Carbamoyl-serine ammonia-lyase. |
| 4.2.2.11 | Poly(alpha-L-guluronate) lyase. | 4.3.1.14 | 3-aminobutyryl-CoA ammonia-lyase. |
| 4.2.2.12 | Xanthan lyase. | 4.3.1.15 | Diaminopropionate ammonia-lyase. |
| 4.2.2.13 | Exo-(1->4)-alpha-D-glucan lyase. | 4.3.1.16 | Threo-3-hydroxyaspartate ammonia-lyase. |
| 4.2.2.14 | Glucuronan lyase. | 4.3.1.17 | L-serine ammonia-lyase. |
| 4.2.2.15 | Anhydrosialidase. | 4.3.1.18 | D-serine ammonia-lyase. |
| 4.2.2.16 | Levan fructotransferase (DFA-IV-forming). | 4.3.1.19 | Threonine ammonia-lyase. |
| 4.2.2.17 | Inulin fructotransferase (DFA-I-forming). | 4.3.1.20 | Erythro-3-hydroxyaspartate ammonia-lyase. |

| | | | |
|----------|---|---------|---------------------------------|
| 4.2.2.18 | Inulin fructotransferase (DFA-III-forming). | 4.3.2.1 | Argininosuccinate lyase. |
| 4.2.3.1 | Threonine synthase. | 4.3.2.2 | Adenylosuccinate lyase. |
| 4.2.3.2 | Ethanolamine-phosphate phospho-lyase. | 4.3.2.3 | Ureidoglycolate lyase. |
| 4.2.3.3 | Methylglyoxal synthase. | 4.3.2.4 | Purine imidazole-ring cyclase. |
| 4.2.3.4 | 3-dehydroquininate synthase. | 4.3.2.5 | Peptidylamidoglycolate lyase. |
| 4.2.3.5 | Chorismate synthase. | 4.3.3.1 | 3-ketovalidoxylamine C-N-lyase. |

| | | | |
|----------|--|----------|--|
| 4.3.3.2 | Strictosidine synthase. | 5.1.1.7 | Diaminopimelate epimerase. |
| 4.3.3.3 | Deacetylisopecoside synthase. | 5.1.1.8 | 4-hydroxyproline epimerase. |
| 4.3.3.4 | Deacetylpecoside synthase. | 5.1.1.9 | Arginine racemase. |
| 4.4.1.1 | Cystathionine gamma-lyase. | 5.1.1.10 | Amino-acid racemase. |
| 4.4.1.2 | Homocysteine desulfhydrase. | 5.1.1.11 | Phenylalanine racemase (ATP-hydrolyzing). |
| 4.4.1.3 | Dimethylpropiothetin dethiomethylase. | 5.1.1.12 | Ornithine racemase. |
| 4.4.1.4 | Alliin lyase. | 5.1.1.13 | Aspartate racemase. |
| 4.4.1.5 | Lactoylgutathione lyase. | 5.1.1.14 | Nocardicin-A epimerase. |
| 4.4.1.6 | S-alkylcysteine lyase. | 5.1.1.15 | 2-aminohexano-6-lactam racemase. |
| 4.4.1.8 | Cystathionine beta-lyase. | 5.1.1.16 | Protein-serine epimerase. |
| 4.4.1.9 | L-3-cyanoalanine synthase. | 5.1.1.17 | Isopenicillin-N epimerase. |
| 4.4.1.10 | Cysteine lyase. | 5.1.2.1 | Lactate racemase. |
| 4.4.1.11 | Methionine gamma-lyase. | 5.1.2.2 | Mandelate racemase. |
| 4.4.1.13 | Cysteine-S-conjugate beta-lyase. | 5.1.2.3 | 3-hydroxybutyryl-CoA epimerase. |
| 4.4.1.14 | 1-aminocyclopropane-1-carboxylate synthase. | 5.1.2.4 | Acetoin racemase. |
| 4.4.1.15 | D-cysteine desulfhydrase. | 5.1.2.5 | Tartrate epimerase. |
| 4.4.1.16 | Selenocysteine lyase. | 5.1.2.6 | Isocitrate epimerase. |
| 4.4.1.17 | Holocytochrome-c synthase. | 5.1.3.1 | Ribulose-phosphate 3-epimerase. |
| 4.4.1.19 | Phosphosulfolactate synthase. | 5.1.3.2 | UDP-glucose 4-epimerase. |
| 4.4.1.20 | Leukotriene-C(4) synthase. | 5.1.3.3 | Aldose 1-epimerase. |
| 4.5.1.1 | DDT-dehydrochlorinase. | 5.1.3.4 | L-ribulose-phosphate 4-epimerase. |
| 4.5.1.2 | 3-chloro-D-alanine dehydrochlorinase. | 5.1.3.5 | UDP-arabinose 4-epimerase. |
| 4.5.1.3 | Dichloromethane dehalogenase. | 5.1.3.6 | UDP-glucuronate 4-epimerase. |
| 4.5.1.4 | L-2-amino-4-chloropent-4-enoate dehydrochlorinase. | 5.1.3.7 | UDP-N-acetylglucosamine 4-epimerase. |
| 4.5.1.5 | S-carboxymethylcysteine synthase. | 5.1.3.8 | N-acylglucosamine 2-epimerase. |
| 4.6.1.1 | Adenylate cyclase. | 5.1.3.9 | N-acylglucosamine-6-phosphate 2-epimerase. |
| 4.6.1.2 | Guanylate cyclase. | 5.1.3.10 | CDP-abequose epimerase. |
| 4.6.1.6 | Cytidylate cyclase. | 5.1.3.11 | Cellobiose epimerase. |
| 4.6.1.12 | 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase. | 5.1.3.12 | UDP-glucuronate 5'-epimerase. |
| 4.6.1.13 | Phosphatidylinositol diacylglycerol-lyase. | 5.1.3.13 | dTDP-4-dehydrorhamnose 3,5-epimerase. |
| 4.6.1.14 | Glycosylphosphatidylinositol diacylglycerol-lyase. | 5.1.3.14 | UDP-N-acetylglucosamine 2-epimerase. |
| 4.6.1.15 | FAD-AMP lyase (cyclizing). | 5.1.3.15 | Glucose-6-phosphate 1-epimerase. |
| 4.99.1.1 | Ferrochelataase. | 5.1.3.16 | UDP-glucosamine 4-epimerase. |
| 4.99.1.2 | Alkylmercury lyase. | 5.1.3.17 | Heparosan-N-sulfate-glucuronate 5-epimerase. |
| 4.99.1.3 | Sirohydrochlorin cobaltochelataase. | 5.1.3.18 | GDP-mannose 3,5-epimerase. |
| 4.99.1.4 | Sirohydrochlorin ferrochelataase. | 5.1.3.19 | Chondroitin-glucuronate 5-epimerase. |
| 4.99.1.5 | Aliphatic aldoxime dehydratase. | 5.1.3.20 | ADP-glyceromanno-heptose 6-epimerase. |

| | | | |
|-----------------|---------------------------------|----------|--------------------------------|
| 4.99.1.6 | Indoleacetaldoxime dehydratase. | 5.1.3.21 | Maltose epimerase. |
| ENZYME: 5.-.-.- | | 5.1.99.1 | Methylmalonyl-CoA epimerase. |
| 5.1.1.1 | Alanine racemase. | 5.1.99.2 | 16-hydroxysteroid epimerase. |
| 5.1.1.2 | Methionine racemase. | 5.1.99.3 | Allantoin racemase. |
| 5.1.1.3 | Glutamate racemase. | 5.1.99.4 | Alpha-methylacyl-CoA racemase. |
| 5.1.1.4 | Proline racemase. | 5.2.1.1 | Maleate isomerase. |
| 5.1.1.5 | Lysine racemase. | 5.2.1.2 | Maleylacetoacetate isomerase. |
| 5.1.1.6 | Threonine racemase. | 5.2.1.3 | Retinal isomerase. |
| | | 5.2.1.4 | Maleylpyruvate isomerase. |

| | | | |
|----------|--|----------|---|
| 5.2.1.5 | Linoleate isomerase. | 5.3.4.1 | Protein disulfide-isomerase. |
| 5.2.1.6 | Furylfuramide isomerase. | 5.3.99.2 | Prostaglandin-D synthase. |
| 5.2.1.7 | Retinol isomerase. | 5.3.99.3 | Prostaglandin-E synthase. |
| 5.2.1.8 | Peptidylprolyl isomerase. | 5.3.99.4 | Prostaglandin-I synthase. |
| 5.2.1.9 | Farnesol 2-isomerase. | 5.3.99.5 | Thromboxane-A synthase. |
| 5.2.1.10 | 2-chloro-4-carboxymethylenebut-2-en-1,4-olide isomerase. | 5.3.99.6 | Allene-oxide cyclase. |
| 5.2.1.11 | 4-hydroxyphenylacetaldehyde-oxime isomerase. | 5.3.99.7 | Styrene-oxide isomerase. |
| 5.3.1.1 | Triose-phosphate isomerase. | 5.4.1.1 | Lysolecithin acylmutase. |
| 5.3.1.3 | Arabinose isomerase. | 5.4.1.2 | Precorrin-8X methylmutase. |
| 5.3.1.4 | L-arabinose isomerase. | 5.4.2.1 | Phosphoglycerate mutase. |
| 5.3.1.5 | Xylose isomerase. | 5.4.2.2 | Phosphoglucomutase. |
| 5.3.1.6 | Ribose-5-phosphate isomerase. | 5.4.2.3 | Phosphoacetylglucosamine mutase. |
| 5.3.1.7 | Mannose isomerase. | 5.4.2.4 | Bisphosphoglycerate mutase. |
| 5.3.1.8 | Mannose-6-phosphate isomerase. | 5.4.2.5 | Phosphoglucomutase (glucose-cofactor). |
| 5.3.1.9 | Glucose-6-phosphate isomerase. | 5.4.2.6 | Beta-phosphoglucomutase. |
| 5.3.1.12 | Glucuronate isomerase. | 5.4.2.7 | Phosphopentomutase. |
| 5.3.1.13 | Arabinose-5-phosphate isomerase. | 5.4.2.8 | Phosphomannomutase. |
| 5.3.1.14 | L-rhamnose isomerase. | 5.4.2.9 | Phosphoenolpyruvate mutase. |
| 5.3.1.15 | D-lyxose ketol-isomerase. | 5.4.2.10 | Phosphoglucosamine mutase. |
| 5.3.1.16 | 1-(5-phosphoribosyl)-5-((5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase. | 5.4.3.2 | Lysine 2,3-aminomutase. |
| 5.3.1.17 | 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase. | 5.4.3.3 | Beta-lysine 5,6-aminomutase. |
| 5.3.1.20 | Ribose isomerase. | 5.4.3.4 | D-lysine 5,6-aminomutase. |
| 5.3.1.21 | Corticosteroid side-chain-isomerase. | 5.4.3.5 | D-ornithine 4,5-aminomutase. |
| 5.3.1.22 | Hydroxypyruvate isomerase. | 5.4.3.6 | Tyrosine 2,3-aminomutase. |
| 5.3.1.23 | S-methyl-5-thioribose-1-phosphate isomerase. | 5.4.3.7 | Leucine 2,3-aminomutase. |
| 5.3.1.24 | Phosphoribosylanthranilate isomerase. | 5.4.3.8 | Glutamate-1-semialdehyde 2,1-aminomutase. |
| 5.3.1.25 | L-fucose isomerase. | 5.4.4.1 | (Hydroxyamino)benzene mutase. |
| 5.3.1.26 | Galactose-6-phosphate isomerase. | 5.4.4.2 | Isochorismate synthase. |
| 5.3.2.1 | Phenylpyruvate tautomerase. | 5.4.4.3 | 3-(hydroxyamino)phenol mutase. |
| 5.3.2.2 | Oxaloacetate tautomerase. | 5.4.99.1 | Methylaspartate mutase. |
| 5.3.3.1 | Steroid delta-isomerase. | 5.4.99.2 | Methylmalonyl-CoA mutase. |
| 5.3.3.2 | Isopentenyl-diphosphate delta-isomerase. | 5.4.99.3 | 2-acetolactate mutase. |
| 5.3.3.3 | Vinylacetyl-CoA delta-isomerase. | 5.4.99.4 | 2-methyleneglutarate mutase. |
| 5.3.3.4 | Muconolactone delta-isomerase. | 5.4.99.5 | Chorismate mutase. |
| 5.3.3.5 | Cholestenol delta-isomerase. | 5.4.99.7 | Lanosterol synthase. |
| 5.3.3.6 | Methylitaconate delta-isomerase. | 5.4.99.8 | Cycloartenol synthase. |

| | |
|---|---|
| 5.3.3.7 Aconitate delta-isomerase. | 5.4.99.9 UDP-galactopyranose mutase. |
| 5.3.3.8 Dodecenoyl-CoA delta-isomerase. | 5.4.99.11 Isomaltulose synthase. |
| 5.3.3.9 Prostaglandin-A(1) delta-isomerase. | 5.4.99.12 tRNA-pseudouridine synthase I. |
| 5.3.3.10 5-carboxymethyl-2-hydroxymuconate delta-isomerase. | 5.4.99.13 Isobutyryl-CoA mutase. |
| 5.3.3.11 Isopiperitenone delta-isomerase. | 5.4.99.14 4-carboxymethyl-4-methylbutenolide mutase. |
| 5.3.3.12 Dopachrome isomerase. | 5.4.99.15 (1->4)-alpha-D-glucan 1-alpha-D-glucosylmutase. |
| 5.3.3.13 Polyenoic fatty acid isomerase. | 5.4.99.16 Maltose alpha-D-glucosyltransferase. |

| | |
|--|---|
| 5.4.99.17 Squalene--hopene cyclase. | 6.2.1.5 Succinate--CoA ligase (ADP-forming). |
| 5.5.1.1 Muconate cycloisomerase. | 6.2.1.6 Glutarate--CoA ligase. |
| 5.5.1.2 3-carboxy-cis,cis-muconate cycloisomerase. | 6.2.1.7 Cholate--CoA ligase. |
| 5.5.1.3 Tetrahydroxypteridine cycloisomerase. | 6.2.1.8 Oxalate--CoA ligase. |
| 5.5.1.4 Inositol-3-phosphate synthase. | 6.2.1.9 Malate--CoA ligase. |
| 5.5.1.5 Carboxy-cis,cis-muconate cyclase. | 6.2.1.10 Acid--CoA ligase (GDP-forming). |
| 5.5.1.6 Chalcone isomerase. | 6.2.1.11 Biotin--CoA ligase. |
| 5.5.1.7 Chloromuconate cycloisomerase. | 6.2.1.12 4-coumarate--CoA ligase. |
| 5.5.1.8 Geranyl-diphosphate cyclase. | 6.2.1.13 Acetate--CoA ligase (ADP-forming). |
| 5.5.1.9 Cycloeucalenol cycloisomerase. | 6.2.1.14 6-carboxyhexanoate--CoA ligase. |
| 5.5.1.10 Alpha-pinene-oxide decyclase. | 6.2.1.15 Arachidonate--CoA ligase. |
| 5.5.1.11 Dichloromuconate cycloisomerase. | 6.2.1.16 Acetoacetate--CoA ligase. |
| 5.5.1.12 Copalyl diphosphate synthase. | 6.2.1.17 Propionate--CoA ligase. |
| 5.5.1.13 Ent-copalyl diphosphate synthase. | 6.2.1.18 Citrate--CoA ligase. |
| 5.99.1.1 Thiocyanate isomerase. | 6.2.1.19 Long-chain-fatty-acid--luciferin-component ligase. |
| 5.99.1.2 DNA topoisomerase. | 6.2.1.20 Long-chain-fatty-acid--[acyl-carrier-protein] ligase. |
| 5.99.1.3 DNA topoisomerase (ATP-hydrolyzing). | 6.2.1.22 [Citrate (pro-3S)-lyase] ligase. |
| ENZYME: 6.-.-. | 6.2.1.23 Dicarboxylate--CoA ligase. |
| 6.1.1.1 Tyrosine--tRNA ligase. | 6.2.1.24 Phytanate--CoA ligase. |
| 6.1.1.2 Tryptophan--tRNA ligase. | 6.2.1.25 Benzoate--CoA ligase. |
| 6.1.1.3 Threonine--tRNA ligase. | 6.2.1.26 O-succinylbenzoate--CoA ligase. |
| 6.1.1.4 Leucine--tRNA ligase. | 6.2.1.27 4-hydroxybenzoate--CoA ligase. |
| 6.1.1.5 Isoleucine--tRNA ligase. | 6.2.1.28 3-alpha,7-alpha-dihydroxy-5-beta-cholestanate--CoA ligase. |
| 6.1.1.6 Lysine--tRNA ligase. | 6.2.1.29 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanate--CoA ligase. |
| 6.1.1.7 Alanine--tRNA ligase. | 6.2.1.30 Phenylacetate--CoA ligase. |
| 6.1.1.9 Valine--tRNA ligase. | 6.2.1.31 2-furoate--CoA ligase. |
| 6.1.1.10 Methionine--tRNA ligase. | 6.2.1.32 Anthranilate--CoA ligase. |
| 6.1.1.11 Serine--tRNA ligase. | 6.2.1.33 4-chlorobenzoate--CoA ligase. |
| 6.1.1.12 Aspartate--tRNA ligase. | 6.2.1.34 Trans-feruloyl--CoA synthase. |
| 6.1.1.13 D-alanine--poly(phosphoribitol) ligase. | 6.3.1.1 Aspartate--ammonia ligase. |
| 6.1.1.14 Glycine--tRNA ligase. | 6.3.1.2 Glutamate--ammonia ligase. |
| 6.1.1.15 Proline--tRNA ligase. | 6.3.1.4 Aspartate--ammonia ligase (ADP-forming). |
| 6.1.1.16 Cysteine--tRNA ligase. | 6.3.1.5 NAD(+) synthase. |
| 6.1.1.17 Glutamate--tRNA ligase. | 6.3.1.6 Glutamate--ethylamine ligase. |
| 6.1.1.18 Glutamine--tRNA ligase. | 6.3.1.7 4-methyleneglutamate--ammonia |

| | |
|--|---|
| | ligase. |
| 6.1.1.19 Arginine--tRNA ligase. | 6.3.1.8 Glutathionylspermidine synthase. |
| 6.1.1.20 Phenylalanine--tRNA ligase. | 6.3.1.9 Trypanothione synthase. |
| 6.1.1.21 Histidine--tRNA ligase. | 6.3.1.10 Adenosylcobinamide-phosphate synthase. |
| 6.1.1.22 Asparagine--tRNA ligase. | 6.3.2.1 Pantoate--beta-alanine ligase. |
| 6.1.1.23 Aspartate--tRNA(Asn) ligase. | 6.3.2.2 Glutamate--cysteine ligase. |
| 6.1.1.24 Glutamate--tRNA(Gln) ligase. | 6.3.2.3 Glutathione synthase. |
| 6.1.1.25 Lysine--tRNA(Pyl) ligase. | 6.3.2.4 D-alanine--D-alanine ligase. |
| 6.2.1.1 Acetate--CoA ligase. | 6.3.2.5 Phosphopantothenate--cysteine ligase. |
| 6.2.1.2 Butyrate--CoA ligase. | 6.3.2.6 Phosphoribosylaminoimidazolesuccinocarboxamide synthase. |
| 6.2.1.3 Long-chain-fatty-acid--CoA ligase. | 6.3.2.7 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L-lysine ligase. |
| 6.2.1.4 Succinate--CoA ligase (GDP-forming). | 6.3.2.8 UDP-N-acetylmuramate--L-alanine ligase. |

| | |
|--|---|
| 6.3.2.9 UDP-N-acetylmuramoylalanine--D-glutamate ligase. | 6.3.4.14 Biotin carboxylase. |
| 6.3.2.10 UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase. | 6.3.4.15 Biotin--[acetyl-CoA-carboxylase] ligase. |
| 6.3.2.11 Carnosine synthase. | 6.3.4.16 Carbamoyl-phosphate synthase (ammonia). |
| 6.3.2.12 Dihydrofolate synthase. | 6.3.4.17 Formate--dihydrofolate ligase. |
| 6.3.2.13 UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase. | 6.3.5.1 NAD(+) synthase (glutamine-hydrolyzing). |
| 6.3.2.14 2,3-dihydroxybenzoate--serine ligase. | 6.3.5.2 GMP synthase (glutamine-hydrolyzing). |
| 6.3.2.16 D-alanine--alanyl-poly(glycerolphosphate) ligase. | 6.3.5.3 Phosphoribosylformylglycinamidine synthase. |
| 6.3.2.17 Tetrahydrofolylpolyglutamate synthase. | 6.3.5.4 Asparagine synthase (glutamine-hydrolyzing). |
| 6.3.2.18 Gamma-glutamylhistamine synthase. | 6.3.5.5 Carbamoyl-phosphate synthase (glutamine-hydrolyzing). |
| 6.3.2.19 Ubiquitin--protein ligase. | 6.3.5.6 Asparaginyl-tRNA synthase (glutamine-hydrolyzing). |
| 6.3.2.20 Indoleacetate-lysine synthetase. | 6.3.5.7 Glutaminyl-tRNA synthase (glutamine-hydrolyzing). |
| 6.3.2.21 Ubiquitin--calmodulin ligase. | 6.3.5.8 Aminodeoxychorismate synthase. |
| 6.3.2.22 Diphthine--ammonia ligase. | 6.3.5.9 Hydrogenobyrinic acid a,c-diamide synthase (glutamine-hydrolyzing). |
| 6.3.2.23 Homoglutathione synthase. | 6.3.5.10 Adenosylcobyric acid synthase (glutamine-hydrolyzing). |
| 6.3.2.24 Tyrosine--arginine ligase. | 6.4.1.1 Pyruvate carboxylase. |
| 6.3.2.25 Tubulin--tyrosine ligase. | 6.4.1.2 Acetyl-CoA carboxylase. |
| 6.3.2.26 N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase. | 6.4.1.3 Propionyl-CoA carboxylase. |
| 6.3.2.27 Aerobactin synthase. | 6.4.1.4 Methylcrotonoyl-CoA carboxylase. |
| 6.3.3.1 Phosphoribosylformylglycinamidine cyclo-ligase. | 6.4.1.5 Geranoyl-CoA carboxylase. |
| 6.3.3.2 5-formyltetrahydrofolate cyclo-ligase. | 6.4.1.6 Acetone carboxylase. |
| 6.3.3.3 Dethiobiotin synthase. | 6.5.1.1 DNA ligase (ATP). |

| | |
|--|---|
| 6.3.3.4 (Carboxyethyl)arginine beta-lactam-synthase. | 6.5.1.2 DNA ligase (NAD+). |
| 6.3.4.1 GMP synthase. | 6.5.1.3 RNA ligase (ATP). |
| 6.3.4.2 CTP synthase. | 6.5.1.4 RNA-3'-phosphate cyclase. |
| 6.3.4.3 Formate--tetrahydrofolate ligase. | 6.6.1.1 Magnesium chelatase. |
| 6.3.4.4 Adenylosuccinate synthase. | 6.6.1.2 Cobaltochelataase. |
| 6.3.4.5 Argininosuccinate synthase. | 6.3.4.17 Formate--dihydrofolate ligase. |
| 6.3.4.6 Urea carboxylase. | 6.3.5.1 NAD(+) synthase (glutamine-hydrolyzing). |
| 6.3.4.7 Ribose-5-phosphate--ammonia ligase. | 6.3.5.2 GMP synthase (glutamine-hydrolyzing). |
| 6.3.4.8 Imidazoleacetate--phosphoribosyldiphosphate ligase. | 6.3.5.3 Phosphoribosylformylglycinamide synthase. |
| 6.3.4.9 Biotin--[methylmalonyl-CoA-carboxytransferase] ligase. | 6.3.5.4 Asparagine synthase (glutamine-hydrolyzing). |
| 6.3.4.10 Biotin--[propionyl-CoA-carboxylase (ATP-hydrolyzing)] ligase. | 6.3.5.5 Carbamoyl-phosphate synthase (glutamine-hydrolyzing). |
| 6.3.4.11 Biotin--[methylcrotonoyl-CoA-carboxylase] ligase. | 6.3.5.6 Asparaginyl-tRNA synthase (glutamine-hydrolyzing). |
| 6.3.4.12 Glutamate--methylamine ligase. | 6.3.5.7 Glutaminyl-tRNA synthase (glutamine-hydrolyzing). |
| 6.3.4.13 Phosphoribosylamine- glycine ligase. | 6.3.5.8 Aminodeoxychorismate synthase. |

| | |
|---|-----------------------------------|
| 6.3.5.9 Hydrogenobyrinic acid a,c-diamide synthase (glutamine-hydrolyzing). | 6.4.1.6 Acetone carboxylase. |
| 6.3.5.10 Adenosylcobyric acid synthase (glutamine-hydrolyzing). | 6.5.1.1 DNA ligase (ATP). |
| 6.4.1.1 Pyruvate carboxylase. | 6.5.1.2 DNA ligase (NAD+). |
| 6.4.1.2 Acetyl-CoA carboxylase. | 6.5.1.3 RNA ligase (ATP). |
| 6.4.1.3 Propionyl-CoA carboxylase. | 6.5.1.4 RNA-3'-phosphate cyclase. |
| 6.4.1.4 Methylcrotonoyl-CoA carboxylase. | 6.6.1.1 Magnesium chelatase. |
| 6.4.1.5 Geranoyl-CoA carboxylase. | 6.6.1.2 Cobaltochelataase. |

Table 3 summarizes exemplary functions of exemplary enzymes of the invention; these enzyme functions were determined using sequence identity comparison analysis using closest BLAST hits to the exemplary polypeptides and polynucleotides of the invention.

The invention also provides isolated and recombinant nucleic acids encoding polypeptides, e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, etc., and all additional nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897 (the exemplary polynucleotides of the invention). The invention also provides isolated and recombinant polypeptides, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include

all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898 (the exemplary polypeptides of the invention).

In another embodiment, the polypeptides of the invention can be expressed in any expression system, in vitro or in vivo, e.g., any microorganism or other cell system (e.g., eukaryotic, such as yeast or mammalian cells) using procedures known in the art. In other aspects, the polypeptides of the invention can be immobilized on a solid support prior to use in the methods of the invention. Methods for immobilizing enzymes on solid supports are commonly known in the art, for example J. Mol. Cat. B: Enzymatic 6 (1999) 29-39; Chivata et al. Biocatalysis: Immobilized cells and enzymes, J Mol. Cat. 37 (1986) 1-24; Sharma et al., Immobilized Biomaterials Techniques and Applications, Angew. Chem. Int. Ed. Engl. 21 (1982) 837-54; Laskin (Ed.), Enzymes and Immobilized Cells in Biotechnology.

Definitions

A "coding sequence of" or a "sequence encodes" a particular polypeptide or protein, is a nucleic acid sequence which is transcribed and translated into a polypeptide or protein when placed under the control of appropriate regulatory sequences.

A promoter sequence is "operably linked to" a coding sequence when RNA polymerase which initiates transcription at the promoter will transcribe the coding sequence into mRNA.

The phrase "substantially identical" in the context of two nucleic acids or polypeptides, refers to two or more sequences that have, e.g., at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more nucleotide or amino acid residue (sequence) identity, when compared and aligned for maximum correspondence, as measured using one of the known sequence comparison algorithms or by visual inspection. In alternative aspects, the substantial identity exists over a region of at least about 100 or more residues and most commonly the sequences are substantially identical over at least about 150 to 200 or more residues. In some aspects, the sequences are substantially identical over the entire length of the coding regions.

Additionally a "substantially identical" amino acid sequence is a sequence that differs from a reference sequence by one or more conservative or non-conservative amino acid substitutions, deletions, or insertions. In one aspect, the substitution occurs at

a site that is not the active site of the molecule, or, alternatively the substitution occurs at a site that is the active site of the molecule, provided that the polypeptide essentially retains its functional (enzymatic) properties. A conservative amino acid substitution, for example, substitutes one amino acid for another of the same class (e.g., substitution of one hydrophobic amino acid, such as isoleucine, valine, leucine, or methionine, for another, or substitution of one polar amino acid for another, such as substitution of arginine for lysine, glutamic acid for aspartic acid or glutamine for asparagine). One or more amino acids can be deleted, for example, from a polypeptide, resulting in modification of the structure of the polypeptide, without significantly altering its biological activity. For example, amino- or carboxyl-terminal amino acids that are not required for a polypeptide, enzyme, protein, e.g. structural or binding protein, biological activity can be removed. Modified polypeptide sequences of the invention can be assayed for enzyme, structural or binding activity by any number of methods, including contacting the modified polypeptide sequence with a substrate and determining whether the modified polypeptide decreases the amount of specific substrate in the assay or increases the bioproducts of the reaction of a functional polypeptide, enzyme, protein, e.g. structural or binding protein, with the substrate. Assays for enzyme activity are well known in the art.

“Fragments” as used herein are a portion of a naturally occurring protein which can exist in at least two different conformations. Fragments can have the same or substantially the same amino acid sequence as the naturally occurring protein. Fragments which have different three dimensional structures as the naturally occurring protein are also included. An example of this, is a “pro-form” molecule, such as a low activity proprotein that can be modified by cleavage to produce a mature enzyme with significantly higher activity.

The term “variant” refers to polynucleotides or polypeptides of the invention modified at one or more base pairs, codons, introns, exons, or amino acid residues (respectively) yet still retain the biological activity of a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention. Variants can be produced by any number of means included methods such as, for example, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, GSSM and any combination thereof.

The term "saturation mutagenesis", Gene Site Saturation Mutagenesis, or "GSSM" includes a method that uses degenerate oligonucleotide primers to introduce point mutations into a polynucleotide, as described in detail, below.

The term "optimized directed evolution system" or "optimized directed evolution" includes a method for reassembling fragments of related nucleic acid sequences, e.g., related genes, and explained in detail, below.

The term "synthetic ligation reassembly" or "SLR" includes a method of ligating oligonucleotide fragments in a non-stochastic fashion, and explained in detail, below.

Nucleic Acids

The invention provides nucleic acids (e.g., the exemplary SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, etc., including all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897), including expression cassettes such as expression vectors, encoding polypeptides (e.g., enzymes) of the invention. The invention also includes methods for discovering new polypeptide (e.g., enzyme) sequences using the nucleic acids of the invention. The invention also includes methods for inhibiting the expression of enzymes, genes, transcripts and polypeptides using the nucleic acids of the invention. Also provided are methods for modifying the nucleic acids of the invention by, e.g., synthetic ligation reassembly, optimized directed evolution system and/or saturation mutagenesis.

The nucleic acids of the invention can be made, isolated and/or manipulated by, e.g., cloning and expression of cDNA libraries, amplification of message or genomic DNA by PCR, and the like. For example, exemplary sequences of the invention were initially derived from environmental sources.

In one aspect, the invention provides nucleic acids, and the polypeptides encoded by them, with a common novelty in that they are derived from a common source, e.g., an environmental or a bacterial source.

In practicing the methods of the invention, homologous genes can be modified by manipulating a template nucleic acid, as described herein. The invention can be practiced in conjunction with any method or protocol or device known in the art, which are well described in the scientific and patent literature.

The phrases "nucleic acid" or "nucleic acid sequence" as used herein refer to an oligonucleotide, nucleotide, polynucleotide, or to a fragment of any of these, to DNA or

RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent a sense or antisense (complementary) strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material, natural or synthetic in origin. The phrases "nucleic acid" or "nucleic acid sequence" includes oligonucleotide, nucleotide, polynucleotide, or to a fragment of any of these, to DNA or RNA (e.g., mRNA, rRNA, tRNA, iRNA) of genomic or synthetic origin which may be single-stranded or double-stranded and may represent a sense or antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material, natural or synthetic in origin, including, e.g., iRNA, ribonucleoproteins (e.g., e.g., double stranded iRNAs, e.g., iRNPs). The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogues of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones, see e.g., Mata (1997) *Toxicol. Appl. Pharmacol.* 144:189-197; Strauss-Soukup (1997) *Biochemistry* 36:8692-8698; Samstag (1996) *Antisense Nucleic Acid Drug Dev* 6:153-156. "Oligonucleotide" includes either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide can ligate to a fragment that has not been dephosphorylated.

A "coding sequence of" or a "nucleotide sequence encoding" a particular polypeptide or protein, is a nucleic acid sequence which is transcribed and translated into a polypeptide or protein when placed under the control of appropriate regulatory sequences. The term "gene" means the segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as, where applicable, intervening sequences (introns) between individual coding segments (exons). "Operably linked" as used herein refers to a functional relationship between two or more nucleic acid (e.g., DNA) segments. Typically, it refers to the functional relationship of transcriptional regulatory sequence to a transcribed sequence. For example, a promoter is operably linked to a coding sequence, such as a nucleic acid of the invention, if it stimulates or modulates the transcription of the coding sequence in an appropriate host cell or other expression system. Generally, promoter transcriptional regulatory sequences that are operably linked to a transcribed sequence are physically contiguous to the transcribed sequence, i.e., they are cis-acting. However, some transcriptional regulatory sequences, such as enhancers, need not be

physically contiguous or located in close proximity to the coding sequences whose transcription they enhance.

As used herein, the term "promoter" includes all sequences capable of driving transcription of a coding sequence in a cell, e.g., a plant cell. Thus, promoters used in the constructs of the invention include *cis*-acting transcriptional control elements and regulatory sequences that are involved in regulating or modulating the timing and/or rate of transcription of a gene. For example, a promoter can be a *cis*-acting transcriptional control element, including an enhancer, a promoter, a transcription terminator, an origin of replication, a chromosomal integration sequence, 5' and 3' untranslated regions, or an intronic sequence, which are involved in transcriptional regulation. These *cis*-acting sequences typically interact with proteins or other biomolecules to carry out (turn on/off, regulate, modulate, etc.) transcription. "Constitutive" promoters are those that drive expression continuously under most environmental conditions and states of development or cell differentiation. "Inducible" or "regulatable" promoters direct expression of the nucleic acid of the invention under the influence of environmental conditions or developmental conditions. Examples of environmental conditions that may affect transcription by inducible promoters include anaerobic conditions, elevated temperature, drought, or the presence of light.

"Plasmids" can be commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. Equivalent plasmids to those described herein are known in the art and will be apparent to the ordinarily skilled artisan.

In one aspect, the term "recombinant" means that the nucleic acid is adjacent to a "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the nucleic acids will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Typically, the enriched nucleic acids represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More typically, the enriched nucleic acids represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a one aspect, the enriched nucleic acids represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

One aspect of the invention is an isolated nucleic acid comprising one of the sequences of the invention, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 or more consecutive bases of a nucleic acid of the invention. The isolated, nucleic acids may comprise DNA, including cDNA, genomic DNA and synthetic DNA. The DNA may be double-stranded or single-stranded and if single stranded may be the coding strand or non-coding (anti-sense) strand. Alternatively, the isolated nucleic acids may comprise RNA.

The isolated nucleic acids of the invention may be used to prepare one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids of one of the polypeptides of the invention. Accordingly, another aspect of the invention is an isolated nucleic acid which encodes one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids of one of the polypeptides of the invention. The coding sequences of these nucleic acids may be identical to one of the coding sequences of one of the nucleic acids of the invention or may be different coding sequences which encode one of the of the invention having at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids of one of the polypeptides of the invention, as a result of the redundancy or degeneracy of the genetic code. The genetic code is well known to those of skill in the art and can be obtained, e.g., on page 214 of B. Lewin, *Genes VI*, Oxford University Press, 1997.

The isolated nucleic acid which encodes one of the polypeptides of the invention, but is not limited to: only the coding sequence of a nucleic acid of the invention and additional coding sequences, such as leader sequences or proprotein sequences and non-coding sequences, such as introns or non-coding sequences 5' and/or 3' of the coding sequence. Thus, as used herein, the term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only the coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

Alternatively, the nucleic acid sequences of the invention, may be mutagenized using conventional techniques, such as site directed mutagenesis, or other techniques familiar to those skilled in the art, to introduce silent changes into the polynucleotides of the invention. As used herein, "silent changes" include, for example, changes which do not alter the amino acid sequence encoded by the polynucleotide. Such changes may be desirable in order to increase the level of the

polypeptide produced by host cells containing a vector encoding the polypeptide by introducing codons or codon pairs which occur frequently in the host organism.

The invention also relates to polynucleotides which have nucleotide changes which result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptides of the invention. Such nucleotide changes may be introduced using techniques such as site directed mutagenesis, random chemical mutagenesis, exonuclease III deletion and other recombinant DNA techniques. Alternatively, such nucleotide changes may be naturally occurring allelic variants which are isolated by identifying nucleic acids which specifically hybridize to probes comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the invention (or the sequences complementary thereto) under conditions of high, moderate, or low stringency as provided herein.

General Techniques

The nucleic acids used to practice this invention, whether RNA, iRNA, antisense nucleic acid, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed/generated recombinantly. Recombinant polypeptides generated from these nucleic acids can be individually isolated or cloned and tested for a desired activity. Any recombinant expression system can be used, including bacterial, mammalian, yeast, insect or plant cell expression systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, e.g., Adams (1983) J. Am. Chem. Soc. 105:661; Belousov (1997) Nucleic Acids Res. 25:3440-3444; Frenkel (1995) Free Radic. Biol. Med. 19:373-380; Blommers (1994) Biochemistry 33:7886-7896; Narang (1979) Meth. Enzymol. 68:90; Brown (1979) Meth. Enzymol. 68:109; Beaucage (1981) Tetra. Lett. 22:1859; U.S. Patent No. 4,458,066.

Techniques for the manipulation of nucleic acids, such as, e.g., subcloning, labeling probes (e.g., random-primer labeling using Klenow polymerase, nick translation, amplification), sequencing, hybridization and the like are well described in the scientific and patent literature, see, e.g., Sambrook, ed., MOLECULAR CLONING: A LABORATORY MANUAL (2ND ED.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989); CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); LABORATORY TECHNIQUES IN

BIOCHEMISTRY AND MOLECULAR BIOLOGY: HYBRIDIZATION WITH NUCLEIC ACID PROBES, Part I. Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Another useful means of obtaining and manipulating nucleic acids used to practice the methods of the invention is to clone from genomic samples, and, if desired, screen and re-clone inserts isolated or amplified from, e.g., genomic clones or cDNA clones. Sources of nucleic acid used in the methods of the invention include genomic or cDNA libraries contained in, e.g., mammalian artificial chromosomes (MACs), see, e.g., U.S. Patent Nos. 5,721,118; 6,025,155; human artificial chromosomes, see, e.g., Rosenfeld (1997) *Nat. Genet.* 15:333-335; yeast artificial chromosomes (YAC); bacterial artificial chromosomes (BAC); P1 artificial chromosomes, see, e.g., Woon (1998) *Genomics* 50:306-316; P1-derived vectors (PACs), see, e.g., Kern (1997) *Biotechniques* 23:120-124; cosmids, recombinant viruses, phages or plasmids.

In one aspect, a nucleic acid encoding a polypeptide of the invention is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof.

The invention provides fusion proteins and nucleic acids encoding them. A polypeptide of the invention can be fused to a heterologous peptide or polypeptide, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification. Peptides and polypeptides of the invention can also be synthesized and expressed as fusion proteins with one or more additional domains linked thereto for, e.g., producing a more immunogenic peptide, to more readily isolate a recombinantly synthesized peptide, to identify and isolate antibodies and antibody-expressing B cells, and the like. Detection and purification facilitating domains include, e.g., metal chelating peptides such as polyhistidine tracts and histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA). The inclusion of a cleavable linker sequences such as Factor Xa or enterokinase (Invitrogen, San Diego CA) between a purification domain and the motif-comprising peptide or polypeptide to facilitate purification. For example, an expression vector can include an epitope-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin and an enterokinase cleavage site (see e.g., Williams (1995) *Biochemistry* 34:1787-1797; Dobeli (1998) *Protein Expr. Purif.* 12:404-414). The histidine residues

facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the epitope from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, see e.g., Kroll (1993) *DNA Cell. Biol.*, 12:441-53.

Transcriptional and translational control sequences

The invention provides nucleic acid (e.g., DNA) sequences of the invention operatively linked to expression (e.g., transcriptional or translational) control sequence(s), e.g., promoters or enhancers, to direct or modulate RNA synthesis/expression. The expression control sequence can be in an expression vector. Exemplary bacterial promoters include *lacI*, *lacZ*, T3, T7, *gpt*, *lambda PR*, *PL* and *trp*. Exemplary eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein I.

Promoters suitable for expressing a polypeptide in bacteria include the *E. coli lac* or *trp* promoters, the *lacI* promoter, the *lacZ* promoter, the T3 promoter, the T7 promoter, the *gpt* promoter, the *lambda PR* promoter, the *lambda PL* promoter, promoters from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), and the acid phosphatase promoter. Eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, heat shock promoters, the early and late SV40 promoter, LTRs from retroviruses, and the mouse metallothionein-I promoter. Other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses may also be used. Promoters suitable for expressing the polypeptide or fragment thereof in bacteria include the *E. coli lac* or *trp* promoters, the *lacI* promoter, the *lacZ* promoter, the T3 promoter, the T7 promoter, the *gpt* promoter, the *lambda PR* promoter, the *lambda PL* promoter, promoters from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK) and the acid phosphatase promoter. Fungal promoters include the α -factor promoter. Eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, heat shock promoters, the early and late SV40 promoter, LTRs from retroviruses and the mouse metallothionein-I promoter. Other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses may also be used.

Tissue-Specific Promoters

The invention provides expression cassettes that can be expressed in a tissue-specific manner, e.g., that can express a polypeptide, enzyme, protein, e.g. structural or

binding protein, of the invention in a tissue-specific manner. The invention also provides plants or seeds that express a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention in a tissue-specific manner. The tissue-specificity can be seed specific, stem specific, leaf specific, root specific, fruit specific and the like.

The term "expression cassette" as used herein refers to a nucleotide sequence which is capable of affecting expression of a structural gene (i.e., a protein coding sequence, such as a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention) in a host compatible with such sequences. Expression cassettes include at least a promoter operably linked with the polypeptide coding sequence; and, optionally, with other sequences, e.g., transcription termination signals. Additional factors necessary or helpful in effecting expression may also be used, e.g., enhancers, alpha-factors. Thus, expression cassettes also include plasmids, expression vectors, recombinant viruses, any form of recombinant "naked DNA" vector, and the like. A "vector" comprises a nucleic acid which can infect, transfect, transiently or permanently transduce a cell. It will be recognized that a vector can be a naked nucleic acid, or a nucleic acid complexed with protein or lipid. The vector optionally comprises viral or bacterial nucleic acids and/or proteins, and/or membranes (e.g., a cell membrane, a viral lipid envelope, etc.). Vectors include, but are not limited to replicons (e.g., RNA replicons, bacteriophages) to which fragments of DNA may be attached and become replicated. Vectors thus include, but are not limited to RNA, autonomous self-replicating circular or linear DNA or RNA (e.g., plasmids, viruses, and the like, see, e.g., U.S. Patent No. 5,217,879), and include both the expression and non-expression plasmids. Where a recombinant microorganism or cell culture is described as hosting an "expression vector" this includes both extra-chromosomal circular and linear DNA and DNA that has been incorporated into the host chromosome(s). Where a vector is being maintained by a host cell, the vector may either be stably replicated by the cells during mitosis as an autonomous structure, or is incorporated within the host's genome.

"Tissue-specific" promoters are transcriptional control elements that are only active in particular cells or tissues or organs, e.g., in plants or animals. Tissue-specific regulation may be achieved by certain intrinsic factors which ensure that genes encoding proteins specific to a given tissue are expressed. Such factors are known to exist in mammals and plants so as to allow for specific tissues to develop.

The term "plant" includes whole plants, plant parts (e.g., leaves, stems, flowers, roots, etc.), plant protoplasts, seeds and plant cells and progeny of same. The class of

plants which can be used in the method of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), as well as gymnosperms. It includes plants of a variety of ploidy levels, including polyploid, diploid, haploid and hemizygous states. As used herein, the term "transgenic plant" includes plants or plant cells into which a heterologous nucleic acid sequence has been inserted, e.g., the nucleic acids and various recombinant constructs (e.g., expression cassettes) of the invention.

In one aspect, a constitutive promoter such as the CaMV 35S promoter can be used for expression in specific parts of the plant or seed or throughout the plant. For example, for overexpression, a plant promoter fragment can be employed which will direct expression of a nucleic acid in some or all tissues of a plant, e.g., a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'- promoter derived from T-DNA of *Agrobacterium tumefaciens*, and other transcription initiation regions from various plant genes known to those of skill. Such genes include, e.g., *ACT11* from *Arabidopsis* (Huang (1996) *Plant Mol. Biol.* 33:125-139); *Cat3* from *Arabidopsis* (GenBank No. U43147, Zhong (1996) *Mol. Gen. Genet.* 251:196-203); the gene encoding stearyl-acyl carrier protein desaturase from *Brassica napus* (Genbank No. X74782, Solcombe (1994) *Plant Physiol.* 104:1167-1176); *GPc1* from maize (GenBank No. X15596; Martinez (1989) *J. Mol. Biol.* 208:551-565); the *Gpc2* from maize (GenBank No. U45855, Manjunath (1997) *Plant Mol. Biol.* 33:97-112); plant promoters described in U.S. Patent Nos. 4,962,028; 5,633,440.

The invention uses tissue-specific or constitutive promoters derived from viruses which can include, e.g., the tobamovirus subgenomic promoter (Kumagai (1995) *Proc. Natl. Acad. Sci. USA* 92:1679-1683; the rice tungro bacilliform virus (RTBV), which replicates only in phloem cells in infected rice plants, with its promoter which drives strong phloem-specific reporter gene expression; the cassava vein mosaic virus (CVMV) promoter, with highest activity in vascular elements, in leaf mesophyll cells, and in root tips (Verdaguer (1996) *Plant Mol. Biol.* 31:1129-1139).

Alternatively, the plant promoter may direct expression of a polypeptide, enzyme, protein, e.g. structural or binding protein-expressing nucleic acid in a specific tissue, organ or cell type (*i.e.* tissue-specific promoters) or may be otherwise under more precise

environmental or developmental control or under the control of an inducible promoter. Examples of environmental conditions that may affect transcription include anaerobic conditions, elevated temperature, the presence of light, or sprayed with chemicals/hormones. For example, the invention incorporates the drought-inducible promoter of maize (Busk (1997) *supra*); the cold, drought, and high salt inducible promoter from potato (Kirch (1997) *Plant Mol. Biol.* 33:897-909).

Tissue-specific promoters can promote transcription only within a certain time frame of developmental stage within that tissue. See, e.g., Blazquez (1998) *Plant Cell* 10:791-800, characterizing the *Arabidopsis* LEAFY gene promoter. See also Cardon (1997) *Plant J* 12:367-77, describing the transcription factor SPL3, which recognizes a conserved sequence motif in the promoter region of the *A. thaliana* floral meristem identity gene AP1; and Mandel (1995) *Plant Molecular Biology*, Vol. 29, pp 995-1004, describing the meristem promoter eIF4. Tissue specific promoters which are active throughout the life cycle of a particular tissue can be used. In one aspect, the nucleic acids of the invention are operably linked to a promoter active primarily only in cotton fiber cells. In one aspect, the nucleic acids of the invention are operably linked to a promoter active primarily during the stages of cotton fiber cell elongation, e.g., as described by Rinehart (1996) *supra*. The nucleic acids can be operably linked to the Fb12A gene promoter to be preferentially expressed in cotton fiber cells (*Ibid*). See also, John (1997) *Proc. Natl. Acad. Sci. USA* 89:5769-5773; John, et al., U.S. Patent Nos. 5,608,148 and 5,602,321, describing cotton fiber-specific promoters and methods for the construction of transgenic cotton plants. Root-specific promoters may also be used to express the nucleic acids of the invention. Examples of root-specific promoters include the promoter from the alcohol dehydrogenase gene (DeLisle (1990) *Int. Rev. Cytol.* 123:39-60). Other promoters that can be used to express the nucleic acids of the invention include, e.g., ovule-specific, embryo-specific, endosperm-specific, integument-specific, seed coat-specific promoters, or some combination thereof; a leaf-specific promoter (see, e.g., Busk (1997) *Plant J.* 11:1285 1295, describing a leaf-specific promoter in maize); the ORF13 promoter from *Agrobacterium rhizogenes* (which exhibits high activity in roots, see, e.g., Hansen (1997) *supra*); a maize pollen specific promoter (see, e.g., Guerrero (1990) *Mol. Gen. Genet.* 224:161 168); a tomato promoter active during fruit ripening, senescence and abscission of leaves and, to a lesser extent, of flowers can be used (see, e.g., Blume (1997) *Plant J.* 12:731 746); a pistil-specific promoter from the potato SK2 gene (see, e.g., Ficker (1997) *Plant Mol. Biol.* 35:425

431); the Blec4 gene from pea, which is active in epidermal tissue of vegetative and floral shoot apices of transgenic alfalfa making it a useful tool to target the expression of foreign genes to the epidermal layer of actively growing shoots or fibers; the ovule-specific BEL1 gene (see, e.g., Reiser (1995) Cell 83:735-742, GenBank No. U39944); and/or, the promoter in Klee, U.S. Patent No. 5,589,583, describing a plant promoter region is capable of conferring high levels of transcription in meristematic tissue and/or rapidly dividing cells.

Alternatively, plant promoters which are inducible upon exposure to plant hormones, such as auxins, are used to express the nucleic acids of the invention. For example, the invention can use the auxin-response elements E1 promoter fragment (AuxREs) in the soybean (*Glycine max* L.) (Liu (1997) Plant Physiol. 115:397-407); the auxin-responsive *Arabidopsis* GST6 promoter (also responsive to salicylic acid and hydrogen peroxide) (Chen (1996) Plant J. 10: 955-966); the auxin-inducible parC promoter from tobacco (Sakai (1996) 37:906-913); a plant biotin response element (Streit (1997) Mol. Plant Microbe Interact. 10:933-937); and, the promoter responsive to the stress hormone abscisic acid (Sheen (1996) Science 274:1900-1902).

The nucleic acids of the invention can also be operably linked to plant promoters which are inducible upon exposure to chemicals reagents which can be applied to the plant, such as herbicides or antibiotics. For example, the maize In2-2 promoter, activated by benzenesulfonamide herbicide safeners, can be used (De Veylder (1997) Plant Cell Physiol. 38:568-577); application of different herbicide safeners induces distinct gene expression patterns, including expression in the root, hydathodes, and the shoot apical meristem. Coding sequence can be under the control of, e.g., a tetracycline-inducible promoter, e.g., as described with transgenic tobacco plants containing the *Avena sativa* L. (oat) arginine decarboxylase gene (Masgrau (1997) Plant J. 11:465-473); or, a salicylic acid-responsive element (Stange (1997) Plant J. 11:1315-1324). Using chemically- (e.g., hormone- or pesticide-) induced promoters, i.e., promoter responsive to a chemical which can be applied to the transgenic plant in the field, expression of a polypeptide of the invention can be induced at a particular stage of development of the plant. Thus, the invention also provides for transgenic plants containing an inducible gene encoding for polypeptides of the invention whose host range is limited to target plant species, such as corn, rice, barley, wheat, potato or other crops, inducible at any stage of development of the crop.

One of skill will recognize that a tissue-specific plant promoter may drive expression of operably linked sequences in tissues other than the target tissue. Thus, a tissue-specific promoter is one that drives expression preferentially in the target tissue or cell type, but may also lead to some expression in other tissues as well.

The nucleic acids of the invention can also be operably linked to plant promoters which are inducible upon exposure to chemicals reagents. These reagents include, e.g., herbicides, synthetic auxins, or antibiotics which can be applied, e.g., sprayed, onto transgenic plants. Inducible expression of the polypeptide, enzyme, protein, e.g. structural or binding protein-producing nucleic acids of the invention will allow the grower to select plants with the optimal polypeptide, enzyme, protein, e.g. structural or binding protein, expression and/or activity. The development of plant parts can thus be controlled. In this way the invention provides the means to facilitate the harvesting of plants and plant parts. For example, in various embodiments, the maize In2-2 promoter, activated by benzenesulfonamide herbicide safeners, is used (De Veylder (1997) *Plant Cell Physiol.* 38:568-577); application of different herbicide safeners induces distinct gene expression patterns, including expression in the root, hydathodes, and the shoot apical meristem. Coding sequences of the invention are also under the control of a tetracycline-inducible promoter, e.g., as described with transgenic tobacco plants containing the *Avena sativa* L. (oat) arginine decarboxylase gene (Masgrau (1997) *Plant J.* 11:465-473); or, a salicylic acid-responsive element (Stange (1997) *Plant J.* 11:1315-1324).

In some aspects, proper polypeptide expression may require polyadenylation region at the 3'-end of the coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant (or animal or other) genes, or from genes in the *Agrobacterium* T-DNA.

Expression vectors and cloning vehicles

The invention provides expression vectors and cloning vehicles comprising nucleic acids of the invention, e.g., sequences encoding the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention. Expression vectors and cloning vehicles of the invention can comprise viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA (e.g., vaccinia, adenovirus, fowl pox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for specific hosts of interest (such as bacillus, *Aspergillus* and yeast).

Vectors of the invention can include chromosomal, non-chromosomal and synthetic DNA sequences. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. Exemplary vectors are include: bacterial: pQE vectors (Qiagen), pBLUESCRIPT plasmids, pNH vectors, (lambda-ZAP vectors (Stratagene); ptc99a, pKK223-3, pDR540, pRIT2T (Pharmacia); Eukaryotic: pXT1, pSG5 (Stratagene), pSVK3, pBPV, pMSG, pSVLSV40 (Pharmacia). However, any other plasmid or other vector may be used so long as they are replicable and viable in the host. Low copy number or high copy number vectors may be employed with the present invention.

The expression vector can comprise a promoter, a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Mammalian expression vectors can comprise an origin of replication, any necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking non-transcribed sequences. In some aspects, DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required non-transcribed genetic elements.

In one aspect, the expression vectors contain one or more selectable marker genes to permit selection of host cells containing the vector. Such selectable markers include genes encoding dihydrofolate reductase or genes conferring neomycin resistance for eukaryotic cell culture, genes conferring tetracycline or ampicillin resistance in *E. coli*, and the *S. cerevisiae* TRP1 gene. Promoter regions can be selected from any desired gene using chloramphenicol transferase (CAT) vectors or other vectors with selectable markers.

Vectors for expressing the polypeptide or fragment thereof in eukaryotic cells can also contain enhancers to increase expression levels. Enhancers are cis-acting elements of DNA that can be from about 10 to about 300 bp in length. They can act on a promoter to increase its transcription. Exemplary enhancers include the SV40 enhancer on the late side of the replication origin bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and the adenovirus enhancers.

A nucleic acid sequence can be inserted into a vector by a variety of procedures. In general, the sequence is ligated to the desired position in the vector following digestion of the insert and the vector with appropriate restriction

endonucleases. Alternatively, blunt ends in both the insert and the vector may be ligated. A variety of cloning techniques are known in the art, e.g., as described in Ausubel and Sambrook. Such procedures and others are deemed to be within the scope of those skilled in the art.

The vector can be in the form of a plasmid, a viral particle, or a phage. Other vectors include chromosomal, non-chromosomal and synthetic DNA sequences, derivatives of SV40; bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. A variety of cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by, e.g., Sambrook.

Particular bacterial vectors which can be used include the commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017), pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden), GEM1 (Promega Biotec, Madison, WI, USA) pQE70, pQE60, pQE-9 (Qiagen), pD10, psiX174 pBLUESCRIPT II KS, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene), ptrc99a, pKK223-3, pKK233-3, DR540, pRIT5 (Pharmacia), pKK232-8 and pCM7. Particular eukaryotic vectors include pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). However, any other vector may be used as long as it is replicable and viable in the host cell.

The nucleic acids of the invention can be expressed in expression cassettes, vectors or viruses and transiently or stably expressed in plant cells and seeds. One exemplary transient expression system uses episomal expression systems, e.g., cauliflower mosaic virus (CaMV) viral RNA generated in the nucleus by transcription of an episomal mini-chromosome containing supercoiled DNA, see, e.g., Covey (1990) Proc. Natl. Acad. Sci. USA 87:1633-1637. Alternatively, coding sequences, i.e., all or sub-fragments of sequences of the invention can be inserted into a plant host cell genome becoming an integral part of the host chromosomal DNA. Sense or antisense transcripts can be expressed in this manner. A vector comprising the sequences (e.g., promoters or coding regions) from nucleic acids of the invention can comprise a marker gene that confers a selectable phenotype on a plant cell or a seed. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

Expression vectors capable of expressing nucleic acids and proteins in plants are well known in the art, and can include, *e.g.*, vectors from *Agrobacterium* spp., potato virus X (see, *e.g.*, Angell (1997) EMBO J. 16:3675-3684), tobacco mosaic virus (see, *e.g.*, Casper (1996) Gene 173:69-73), tomato bushy stunt virus (see, *e.g.*, Hillman (1989) Virology 169:42-50), tobacco etch virus (see, *e.g.*, Dolja (1997) Virology 234:243-252), bean golden mosaic virus (see, *e.g.*, Morinaga (1993) Microbiol Immunol. 37:471-476), cauliflower mosaic virus (see, *e.g.*, Cecchini (1997) Mol. Plant Microbe Interact. 10:1094-1101), maize Ac/Ds transposable element (see, *e.g.*, Rubin (1997) Mol. Cell. Biol. 17:6294-6302; Kunze (1996) Curr. Top. Microbiol. Immunol. 204:161-194), and the maize suppressor-mutator (Spm) transposable element (see, *e.g.*, Schlappi (1996) Plant Mol. Biol. 32:717-725); and derivatives thereof.

In one aspect, the expression vector can have two replication systems to allow it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector can contain at least one sequence homologous to the host cell genome. It can contain two homologous sequences which flank the expression construct. The integrating vector can be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

Expression vectors of the invention may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed, *e.g.*, genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers can also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct RNA synthesis. Particular named bacterial promoters include *lacI*, *lacZ*, *T3*, *T7*, *gpt*, *lambda P_R*, *P_L* and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Promoter regions can be selected from any desired gene using

chloramphenicol transferase (CAT) vectors or other vectors with selectable markers. In addition, the expression vectors in one aspect contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

Mammalian expression vectors may also comprise an origin of replication, any necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. In some aspects, DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Vectors for expressing the polypeptide or fragment thereof in eukaryotic cells may also contain enhancers to increase expression levels. Enhancers are cis-acting elements of DNA, usually from about 10 to about 300 bp in length that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin and the adenovirus enhancers.

In addition, the expression vectors typically contain one or more selectable marker genes to permit selection of host cells containing the vector. Such selectable markers include genes encoding dihydrofolate reductase or genes conferring neomycin resistance for eukaryotic cell culture, genes conferring tetracycline or ampicillin resistance in *E. coli* and the *S. cerevisiae* *TRP1* gene.

In some aspects, the nucleic acid encoding one of the polypeptides of the invention, or fragments comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof. Optionally, the nucleic acid can encode a fusion polypeptide in which one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is fused to heterologous peptides or polypeptides, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is ligated to the desired position in the vector following digestion of the insert and the vector with appropriate restriction endonucleases. Alternatively, blunt ends in both the insert and the vector may be ligated.

A variety of cloning techniques are disclosed in Ausubel *et al.* Current Protocols in Molecular Biology, John Wiley 503 Sons, Inc. 1997 and Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2nd Ed., Cold Spring Harbor Laboratory Press (1989). Such procedures and others are deemed to be within the scope of those skilled in the art.

The vector may be, for example, in the form of a plasmid, a viral particle, or a phage. Other vectors include chromosomal, nonchromosomal and synthetic DNA sequences, derivatives of SV40; bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus and pseudorabies. A variety of cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, N.Y., (1989).

Host cells and transformed cells

The invention also provides a transformed cell comprising a nucleic acid sequence of the invention, e.g., a sequence encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, or a vector of the invention. The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, such as bacterial cells, fungal cells, yeast cells, mammalian cells, insect cells, or plant cells. Exemplary bacterial cells include *E. coli*, *Streptomyces*, *Bacillus subtilis*, *Bacillus cereus*, *Salmonella typhimurium* and various species within the genera *Streptomyces* and *Staphylococcus*. Exemplary insect cells include *Drosophila S2* and *Spodoptera Sf9*. Exemplary animal cells include CHO, COS or Bowes melanoma or any mouse or human cell line. The selection of an appropriate host is within the abilities of those skilled in the art. Techniques for transforming a wide variety of higher plant species are well known and described in the technical and scientific literature. See, e.g., Weising (1988) Ann. Rev. Genet. 22:421-477; U.S. Patent No. 5,750,870.

The vector can be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

In one aspect, the nucleic acids or vectors of the invention are introduced into the cells for screening, thus, the nucleic acids enter the cells in a manner suitable for subsequent expression of the nucleic acid. The method of introduction is largely dictated

by the targeted cell type. Exemplary methods include CaPO_4 precipitation, liposome fusion, lipofection (e.g., LIPOFECTIN™), electroporation, viral infection, etc. The candidate nucleic acids may stably integrate into the genome of the host cell (for example, with retroviral introduction) or may exist either transiently or stably in the cytoplasm (i.e. through the use of traditional plasmids, utilizing standard regulatory sequences, selection markers, etc.). As many pharmaceutically important screens require human or model mammalian cell targets, retroviral vectors capable of transfecting such targets can be used.

Where appropriate, the engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired polypeptide or fragment thereof.

Cells can be harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Depending upon the host employed in a recombinant production procedure, the polypeptides produced by host cells containing the vector may be glycosylated or may be non-glycosylated. Polypeptides of the invention may or may not also include an initial methionine amino acid residue.

Cell-free translation systems can also be employed to produce a polypeptide of the invention. Cell-free translation systems can use mRNAs transcribed from a DNA construct comprising a promoter operably linked to a nucleic acid encoding the polypeptide or fragment thereof. In some aspects, the DNA construct may be linearized prior to conducting an *in vitro* transcription reaction. The transcribed mRNA is then incubated with an appropriate cell-free translation extract, such as a rabbit reticulocyte extract, to produce the desired polypeptide or fragment thereof.

The expression vectors can contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

Host cells containing the polynucleotides of interest, e.g., nucleic acids of the invention, can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression and will be apparent to the ordinarily skilled artisan. The clones which are identified as having the specified enzyme activity may then be sequenced to identify the polynucleotide sequence encoding an enzyme having the enhanced activity.

The invention provides a method for overexpressing a recombinant polypeptide, enzyme, protein, e.g. structural or binding protein, in a cell comprising expressing a vector comprising a nucleic acid of the invention, e.g., a nucleic acid comprising a nucleic acid sequence with at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to an exemplary sequence of the invention over a region of at least about 100 residues, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection, or, a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence of the invention. The overexpression can be effected by any means, e.g., use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

The nucleic acids of the invention can be expressed, or overexpressed, in any *in vitro* or *in vivo* expression system. Any cell culture systems can be employed to

express, or over-express, recombinant protein, including bacterial, insect, yeast, fungal or mammalian cultures. Over-expression can be effected by appropriate choice of promoters, enhancers, vectors (e.g., use of replicon vectors, dicistronic vectors (see, e.g., Gurtu (1996) *Biochem. Biophys. Res. Commun.* 229:295-8), media, culture systems and the like. In one aspect, gene amplification using selection markers, e.g., glutamine synthetase (see, e.g., Sanders (1987) *Dev. Biol. Stand.* 66:55-63), in cell systems are used to overexpress the polypeptides of the invention.

The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, mammalian cells, insect cells, or plant cells. As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Bacillus subtilis*, *Bacillus cereus*, *Salmonella typhimurium* and various species within the genera *Streptomyces* and *Staphylococcus*, fungal cells, such as yeast, insect cells such as *Drosophila S2* and *Spodoptera Sf9*, animal cells such as CHO, COS or Bowes melanoma and adenoviruses. The selection of an appropriate host is within the abilities of those skilled in the art.

The vector may be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation (Davis, L., Dibner, M., Battey, I., *Basic Methods in Molecular Biology*, (1986)).

Where appropriate, the engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired polypeptide or fragment thereof.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction,

anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts (described by Gluzman, *Cell*, 23:175, 1981) and other cell lines capable of expressing proteins from a compatible vector, such as the C127, 3T3, CHO, HeLa and BHK cell lines.

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Depending upon the host employed in a recombinant production procedure, the polypeptides produced by host cells containing the vector may be glycosylated or may be non-glycosylated. Polypeptides of the invention may or may not also include an initial methionine amino acid residue.

Alternatively, the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof can be synthetically produced by conventional peptide synthesizers. In other aspects, fragments or portions of the polypeptides may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, the fragments may be employed as intermediates for producing the full-length polypeptides.

Cell-free translation systems can also be employed to produce one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof using mRNAs transcribed from a DNA construct comprising a promoter operably linked to a nucleic acid encoding the polypeptide or fragment thereof. In some aspects, the DNA construct may be linearized prior to conducting an *in vitro* transcription reaction. The transcribed mRNA is then incubated with an appropriate cell-free translation extract, such as a rabbit reticulocyte extract, to produce the desired polypeptide or fragment thereof.

Amplification of Nucleic Acids

In practicing the invention, nucleic acids encoding the polypeptides of the invention, or modified nucleic acids, can be reproduced by, e.g., amplification. The invention provides amplification primer sequence pairs for amplifying nucleic acids encoding polypeptides (e.g., enzymes) of the invention. In one aspect, the primer pairs

are capable of amplifying nucleic acid sequences of the invention, e.g., including the exemplary SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, etc., including all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, or a subsequence thereof, etc. One of skill in the art can design amplification primer sequence pairs for any part of or the full length of these sequences.

In one aspect, the invention provides a nucleic acid amplified by a primer pair of the invention, e.g., a primer pair as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of a nucleic acid of the invention, and about the first (the 5') 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of the complementary strand.

The invention provides an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence of the invention, or fragments or subsequences thereof. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising at least about 10 to 50 or more consecutive bases of the sequence, or about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more consecutive bases of the sequence. The invention provides amplification primer pairs, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of a nucleic acid of the invention, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of the complementary strand of the first member. The invention provides a polypeptide, enzyme, protein, e.g. structural or binding protein, generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides methods of making a polypeptide, enzyme, protein, e.g. structural or binding protein, by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. In one aspect, the amplification primer pair amplifies a nucleic acid from a library, e.g., a gene library, such as an environmental library.

Amplification reactions can also be used to quantify the amount of nucleic acid in a sample (such as the amount of message in a cell sample), label the nucleic acid (e.g., to apply it to an array or a blot), detect the nucleic acid, or quantify the amount of a

specific nucleic acid in a sample. In one aspect of the invention, message isolated from a cell or a cDNA library are amplified.

The skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (see, e.g., PCR PROTOCOLS, A GUIDE TO METHODS AND APPLICATIONS, ed. Innis, Academic Press, N.Y. (1990) and PCR STRATEGIES (1995), ed. Innis, Academic Press, Inc., N.Y., ligase chain reaction (LCR) (see, e.g., Wu (1989) Genomics 4:560; Landegren (1988) Science 241:1077; Barringer (1990) Gene 89:117); transcription amplification (see, e.g., Kwoh (1989) Proc. Natl. Acad. Sci. USA 86:1173); and, self-sustained sequence replication (see, e.g., Guatelli (1990) Proc. Natl. Acad. Sci. USA 87:1874); Q Beta replicase amplification (see, e.g., Smith (1997) J. Clin. Microbiol. 35:1477-1491), automated Q-beta replicase amplification assay (see, e.g., Burg (1996) Mol. Cell. Probes 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger (1987) Methods Enzymol. 152:307-316; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Söcknanan (1995) Biotechnology 13:563-564.

Determining the degree of sequence identity

The invention provides nucleic acids comprising sequences having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, etc., including all nucleic acids disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, and nucleic acids encoding SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898) over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550 or more, residues. The invention provides polypeptides comprising sequences having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%,

79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary polypeptide of the invention. The extent of sequence identity (homology) may be determined using any computer program and associated parameters, including those described herein, such as BLAST 2.2.2. or FASTA version 3.0t78, with the default parameters.

As used herein, the terms "computer," "computer program" and "processor" are used in their broadest general contexts and incorporate all such devices, as described in detail, below.

Nucleic acid sequences of the invention can comprise at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 or more consecutive nucleotides of an exemplary sequence of the invention and sequences substantially identical thereto. Homologous sequences and fragments of nucleic acid sequences of the invention can refer to a sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity (homology) to these sequences. Homology (sequence identity) may be determined using any of the computer programs and parameters described herein, including FASTA version 3.0t78 with the default parameters. Homologous sequences also include RNA sequences in which uridines replace the thymines in the nucleic acid sequences of the invention. The homologous sequences may be obtained using any of the procedures described herein or may result from the correction of a sequencing error. It will be appreciated that the nucleic acid sequences of the invention can be represented in the traditional single character format (See the inside back cover of Stryer, Lubert. Biochemistry, 3rd Ed., W. H Freeman & Co., New York.) or in any other format which records the identity of the nucleotides in a sequence.

Various sequence comparison programs identified elsewhere in this patent specification are particularly contemplated for use in this aspect of the invention. Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA and CLUSTALW (see, e.g., Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85(8):2444-2448, 1988; Altschul *et al.*, J. Mol. Biol. 215(3):403-410, 1990; Thompson

Nucleic Acids Res. 22(2):4673-4680, 1994; Higgins *et al.*, Methods Enzymol. 266:383-402, 1996; Altschul *et al.*, J. Mol. Biol. 215(3):403-410, 1990; Altschul *et al.*, Nature Genetics 3:266-272, 1993).

Homology or identity is often measured using sequence analysis software (*e.g.*, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). Such software matches similar sequences by assigning degrees of homology to various deletions, substitutions and other modifications. The terms "homology" and "identity" in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same when compared and aligned for maximum correspondence over a comparison window or designated region as measured using any number of sequence comparison algorithms or by manual alignment and visual inspection.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443, 1970, by the search for similarity method of person & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, in addition to a BLAST program (Basic Local Alignment Search Tool at the National Center

for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLocks IMProved Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction & Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-IF. Such alignment programs can also be used to screen genome databases to identify polynucleotide sequences having substantially identical sequences. A number of genome databases are available, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project (Gibbs, 1995). At least twenty-one other genomes have already been sequenced, including, for example, *M. genitalium* (Fraser *et al.*, 1995), *M. jannaschii* (Bult *et al.*, 1996), *H. influenzae* (Fleischmann *et al.*, 1995), *E. coli* (Blattner *et al.*, 1997) and yeast (*S. cerevisiae*) (Mewes *et al.*, 1997) and *D. melanogaster* (Adams *et al.*, 2000). Significant progress has also been made in sequencing the genomes of model organism, such as mouse, *C. elegans* and *Arabidopsis sp.* Several databases containing genomic information annotated with some functional information are maintained by different organizations and may be accessible via internet.

One example of a useful algorithm is BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, Nuc. Acids Res. 25:3389-3402, 1997 and Altschul *et al.*, J. Mol. Biol. 215:403-410, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along

each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3 and expectations (E) of 10 and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N= -4 and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin & Altschul, Proc. Natl. Acad. Sci. USA 90:5873, 1993). One measure of similarity provided by BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a references sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more in one aspect less than about 0.01 and most in one aspect less than about 0.001.

In one aspect, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") In particular, five specific BLAST programs are used to perform the following task:

- (1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- (2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;

(4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and

(5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is in one aspect obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are in one aspect identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. In one aspect, the scoring matrix used is the BLOSUM62 matrix (Gonnet (1992) *Science* 256:1443-1445; Henikoff and Henikoff (1993) *Proteins* 17:49-61). Less in one aspect, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation). BLAST programs are accessible through the U.S. National Library of Medicine.

The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some aspects, the parameters may be the default parameters used by the algorithms in the absence of instructions from the user.

Computer systems and computer program products

To determine and identify sequence identities, structural homologies, motifs and the like *in silico*, a nucleic acid or polypeptide sequence of the invention can be stored, recorded, and manipulated on any medium which can be read and accessed by a computer.

Accordingly, the invention provides computers, computer systems, computer readable mediums, computer programs products and the like recorded or stored thereon the nucleic acid and polypeptide sequences of the invention. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid and/or polypeptide sequences of the invention.

The polypeptides of the invention include the polypeptide sequences of the invention, e.g., the exemplary sequences of the invention, and sequences substantially identical thereto, and fragments of any of the preceding sequences. Substantially identical, or homologous, polypeptide sequences refer to a polypeptide sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity (homology) to an exemplary sequence of the invention.

Homology (sequence identity) may be determined using any of the computer programs and parameters described herein. A nucleic acid or polypeptide sequence of the invention can be stored, recorded and manipulated on any medium which can be read and accessed by a computer. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any of the presently known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid sequences of the invention, one or more of the polypeptide sequences of the invention. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, or 20 or more nucleic acid or polypeptide sequences of the invention.

Another aspect of the invention is a computer readable medium having recorded thereon one or more of the nucleic acid sequences of the invention. Another aspect of the invention is a computer readable medium having recorded thereon one or more of the polypeptide sequences of the invention. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, or 20 or more of the nucleic acid or polypeptide sequences as set forth above.

Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

Aspects of the invention include systems (e.g., internet based systems), particularly computer systems which store and manipulate the sequence information described herein. One example of a computer system 100 is illustrated in block diagram form in Figure 1. As used herein, "a computer system" refers to the hardware components,

software components and data storage components used to analyze a nucleotide sequence of a nucleic acid sequence of the invention, or a polypeptide sequence of the invention. The computer system 100 typically includes a processor for processing, accessing and manipulating the sequence data. The processor 105 can be any well-known type of central processing unit, such as, for example, the Pentium III from Intel Corporation, or similar processor from Sun, Motorola, Compaq, AMD or International Business Machines.

Typically the computer system 100 is a general purpose system that comprises the processor 105 and one or more internal data storage components 110 for storing data and one or more data retrieving devices for retrieving the data stored on the data storage components. A skilled artisan can readily appreciate that any one of the currently available computer systems are suitable.

In one particular aspect, the computer system 100 includes a processor 105 connected to a bus which is connected to a main memory 115 (in one aspect implemented as RAM) and one or more internal data storage devices 110, such as a hard drive and/or other computer readable media having data recorded thereon. In some aspects, the computer system 100 further includes one or more data retrieving device 118 for reading the data stored on the internal data storage devices 110.

The data retrieving device 118 may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, or a modem capable of connection to a remote data storage system (e.g., via internet) etc. In some aspects, the internal data storage device 110 is a removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system 100 may advantageously include or be programmed by appropriate software for reading the control logic and/or the data from the data storage component once inserted in the data retrieving device.

The computer system 100 includes a display 120 which is used to display output to a computer user. It should also be noted that the computer system 100 can be linked to other computer systems 125a-c in a network or wide area network to provide centralized access to the computer system 100.

Software for accessing and processing the nucleotide sequences of a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, (such as search tools, compare tools and modeling tools etc.) may reside in main memory 115 during execution.

In some aspects, the computer system 100 may further comprise a sequence comparison algorithm for comparing a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, stored on a computer readable medium to a reference nucleotide or polypeptide sequence(s) stored on a computer readable medium. A "sequence comparison algorithm" refers to one or more programs which are implemented (locally or remotely) on the computer system 100 to compare a nucleotide sequence with other nucleotide sequences and/or compounds stored within a data storage means. For example, the sequence comparison algorithm may compare the nucleotide sequences of a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, stored on a computer readable medium to reference sequences stored on a computer readable medium to identify homologies or structural motifs.

Figure 2 is a flow diagram illustrating one aspect of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database. The database of sequences can be a private database stored within the computer system 100, or a public database such as GENBANK that is available through the Internet.

The process 200 begins at a start state 201 and then moves to a state 202 wherein the new sequence to be compared is stored to a memory in a computer system 100. As discussed above, the memory could be any type of memory, including RAM or an internal storage device.

The process 200 then moves to a state 204 wherein a database of sequences is opened for analysis and comparison. The process 200 then moves to a state 206 wherein the first sequence stored in the database is read into a memory on the computer. A comparison is then performed at a state 210 to determine if the first sequence is the same as the second sequence. It is important to note that this step is not limited to performing an exact comparison between the new sequence and the first sequence in the database. Well-known methods are known to those of skill in the art for comparing two nucleotide or protein sequences, even if they are not identical. For example, gaps can be introduced into one sequence in order to raise the homology level between the two tested sequences. The parameters that control whether gaps or other features are introduced into a sequence during comparison are normally entered by the user of the computer system.

Once a comparison of the two sequences has been performed at the state 210, a determination is made at a decision state 210 whether the two sequences are the same. Of course, the term "same" is not limited to sequences that are absolutely identical. Sequences

that are within the homology parameters entered by the user will be marked as "same" in the process 200.

If a determination is made that the two sequences are the same, the process 200 moves to a state 214 wherein the name of the sequence from the database is displayed to the user. This state notifies the user that the sequence with the displayed name fulfills the homology constraints that were entered. Once the name of the stored sequence is displayed to the user, the process 200 moves to a decision state 218 wherein a determination is made whether more sequences exist in the database. If no more sequences exist in the database, then the process 200 terminates at an end state 220. However, if more sequences do exist in the database, then the process 200 moves to a state 224 wherein a pointer is moved to the next sequence in the database so that it can be compared to the new sequence. In this manner, the new sequence is aligned and compared with every sequence in the database.

It should be noted that if a determination had been made at the decision state 212 that the sequences were not homologous, then the process 200 would move immediately to the decision state 218 in order to determine if any other sequences were available in the database for comparison.

Accordingly, one aspect of the invention is a computer system comprising a processor, a data storage device having stored thereon a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, a data storage device having retrievably stored thereon reference nucleotide sequences or polypeptide sequences to be compared to a nucleic acid sequence of the invention, or a polypeptide sequence of the invention and a sequence comparer for conducting the comparison. The sequence comparer may indicate a homology level between the sequences compared or identify structural motifs in the above described nucleic acid code a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, or it may identify structural motifs in sequences which are compared to these nucleic acid codes and polypeptide codes. In some aspects, the data storage device may have stored thereon the sequences of at least 2, 5, 10, 15, 20, 25, 30 or 40 or more of the nucleic acid sequences of the invention, or the polypeptide sequences of the invention.

Another aspect of the invention is a method for determining the level of homology between a nucleic acid sequence of the invention, or a polypeptide sequence of the invention and a reference nucleotide sequence. The method including reading the nucleic acid code or the polypeptide code and the reference nucleotide or polypeptide sequence through the use of a computer program which determines homology levels and

determining homology between the nucleic acid code or polypeptide code and the reference nucleotide or polypeptide sequence with the computer program. The computer program may be any of a number of computer programs for determining homology levels, including those specifically enumerated herein, (e.g., BLAST2N with the default parameters or with any modified parameters). The method may be implemented using the computer systems described above. The method may also be performed by reading at least 2, 5, 10, 15, 20, 25, 30 or 40 or more of the above described nucleic acid sequences of the invention, or the polypeptide sequences of the invention through use of the computer program and determining homology between the nucleic acid codes or polypeptide codes and reference nucleotide sequences or polypeptide sequences.

Figure 3 is a flow diagram illustrating one aspect of a process 250 in a computer for determining whether two sequences are homologous. The process 250 begins at a start state 252 and then moves to a state 254 wherein a first sequence to be compared is stored to a memory. The second sequence to be compared is then stored to a memory at a state 256. The process 250 then moves to a state 260 wherein the first character in the first sequence is read and then to a state 262 wherein the first character of the second sequence is read. It should be understood that if the sequence is a nucleotide sequence, then the character would normally be either A, T, C, G or U. If the sequence is a protein sequence, then it is in one aspect in the single letter amino acid code so that the first and sequence sequences can be easily compared.

A determination is then made at a decision state 264 whether the two characters are the same. If they are the same, then the process 250 moves to a state 268 wherein the next characters in the first and second sequences are read. A determination is then made whether the next characters are the same. If they are, then the process 250 continues this loop until two characters are not the same. If a determination is made that the next two characters are not the same, the process 250 moves to a decision state 274 to determine whether there are any more characters either sequence to read.

If there are not any more characters to read, then the process 250 moves to a state 276 wherein the level of homology between the first and second sequences is displayed to the user. The level of homology is determined by calculating the proportion of characters between the sequences that were the same out of the total number of sequences in the first sequence. Thus, if every character in a first 100 nucleotide sequence aligned with a every character in a second sequence, the homology level would be 100%.

Alternatively, the computer program may be a computer program which compares the nucleotide sequences of a nucleic acid sequence as set forth in the invention, to one or more reference nucleotide sequences in order to determine whether the nucleic acid code of the invention, differs from a reference nucleic acid sequence at one or more positions. Optionally such a program records the length and identity of inserted, deleted or substituted nucleotides with respect to the sequence of either the reference polynucleotide or a nucleic acid sequence of the invention. In one aspect, the computer program may be a program which determines whether a nucleic acid sequence of the invention, contains a single nucleotide polymorphism (SNP) with respect to a reference nucleotide sequence.

Accordingly, another aspect of the invention is a method for determining whether a nucleic acid sequence of the invention, differs at one or more nucleotides from a reference nucleotide sequence comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through use of a computer program which identifies differences between nucleic acid sequences and identifying differences between the nucleic acid code and the reference nucleotide sequence with the computer program. In some aspects, the computer program is a program which identifies single nucleotide polymorphisms. The method may be implemented by the computer systems described above and the method illustrated in Figure 3. The method may also be performed by reading at least 2, 5, 10, 15, 20, 25, 30, or 40 or more of the nucleic acid sequences of the invention and the reference nucleotide sequences through the use of the computer program and identifying differences between the nucleic acid codes and the reference nucleotide sequences with the computer program.

In other aspects the computer based system may further comprise an identifier for identifying features within a nucleic acid sequence of the invention or a polypeptide sequence of the invention.

An "identifier" refers to one or more programs which identifies certain features within a nucleic acid sequence of the invention, or a polypeptide sequence of the invention. In one aspect, the identifier may comprise a program which identifies an open reading frame in a nucleic acid sequence of the invention.

Figure 4 is a flow diagram illustrating one aspect of an identifier process 300 for detecting the presence of a feature in a sequence. The process 300 begins at a start state 302 and then moves to a state 304 wherein a first sequence that is to be checked for features is stored to a memory 115 in the computer system 100. The process 300 then moves to a state 306 wherein a database of sequence features is opened. Such a database

would include a list of each feature's attributes along with the name of the feature. For example, a feature name could be "Initiation Codon" and the attribute would be "ATG". Another example would be the feature name "TAATAA Box" and the feature attribute would be "TAATAA". An example of such a database is produced by the University of Wisconsin Genetics Computer Group. Alternatively, the features may be structural polypeptide motifs such as alpha helices, beta sheets, or functional polypeptide motifs such as enzymatic active sites, helix-turn-helix motifs or other motifs known to those skilled in the art.

Once the database of features is opened at the state 306, the process 300 moves to a state 308 wherein the first feature is read from the database. A comparison of the attribute of the first feature with the first sequence is then made at a state 310. A determination is then made at a decision state 316 whether the attribute of the feature was found in the first sequence. If the attribute was found, then the process 300 moves to a state 318 wherein the name of the found feature is displayed to the user.

The process 300 then moves to a decision state 320 wherein a determination is made whether more features exist in the database. If no more features do exist, then the process 300 terminates at an end state 324. However, if more features do exist in the database, then the process 300 reads the next sequence feature at a state 326 and loops back to the state 310 wherein the attribute of the next feature is compared against the first sequence. It should be noted, that if the feature attribute is not found in the first sequence at the decision state 316, the process 300 moves directly to the decision state 320 in order to determine if any more features exist in the database.

Accordingly, another aspect of the invention is a method of identifying a feature within a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, comprising reading the nucleic acid code(s) or polypeptide code(s) through the use of a computer program which identifies features therein and identifying features within the nucleic acid code(s) with the computer program. In one aspect, computer program comprises a computer program which identifies open reading frames. The method may be performed by reading a single sequence or at least 2, 5, 10, 15, 20, 25, 30, or 40 of the nucleic acid sequences of the invention, or the polypeptide sequences of the invention, through the use of the computer program and identifying features within the nucleic acid codes or polypeptide codes with the computer program.

A nucleic acid sequence of the invention, or a polypeptide sequence of the invention, may be stored and manipulated in a variety of data processor programs in a

variety of formats. For example, a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, may be stored as text in a word processing file, such as Microsoft WORD™ or WORDPERFECT™ or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2™, SYBASE™, or ORACLE™. In addition, many computer programs and databases may be used as sequence comparison algorithms, identifiers, or sources of reference nucleotide sequences or polypeptide sequences to be compared to a nucleic acid sequence of the invention, or a polypeptide sequence of the invention. The following list is intended not to limit the invention but to provide guidance to programs and databases which are useful with the nucleic acid sequences of the invention, or the polypeptide sequences of the invention.

The programs and databases which may be used include, but are not limited to: MacPattern (EMBL), DiscoveryBase (Molecular Applications Group), GeneMine (Molecular Applications Group), Look (Molecular Applications Group), MacLook (Molecular Applications Group), BLAST and BLAST2 (NCBI), BLASTN and BLASTX (Altschul et al, J. Mol. Biol. 215: 403, 1990), FASTA (Pearson and Lipman, Proc. Natl. Acad. Sci. USA, 85: 2444, 1988), FASTDB (Brutlag *et al.* Comp. App. Biosci. 6:237-245, 1990), Catalyst (Molecular Simulations Inc.), Catalyst/SHAPE (Molecular Simulations Inc.), Cerius².DBAccess (Molecular Simulations Inc.), HypoGen (Molecular Simulations Inc.), Insight II, (Molecular Simulations Inc.), Discover (Molecular Simulations Inc.), CHARMm (Molecular Simulations Inc.), Felix (Molecular Simulations Inc.), DelPhi, (Molecular Simulations Inc.), QuanteMM, (Molecular Simulations Inc.), Homology (Molecular Simulations Inc.), Modeler (Molecular Simulations Inc.), ISIS (Molecular Simulations Inc.), Quanta/Protein Design (Molecular Simulations Inc.), WebLab (Molecular Simulations Inc.), WebLab Diversity Explorer (Molecular Simulations Inc.), Gene Explorer (Molecular Simulations Inc.), SeqFold (Molecular Simulations Inc.), the MDL Available Chemicals Directory database, the MDL Drug Data Report data base, the Comprehensive Medicinal Chemistry database, Derwents's World Drug Index database, the BioByteMasterFile database, the Genbank database and the Genseqn database. Many other programs and data bases would be apparent to one of skill in the art given the present disclosure.

Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in

transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites and enzymatic cleavage sites.

Hybridization of nucleic acids

The invention provides isolated or recombinant nucleic acids that hybridize under stringent conditions to an exemplary sequence of the invention (e.g., SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9). The stringent conditions can be highly stringent conditions, medium stringent conditions and/or low stringent conditions, including the high and reduced stringency conditions described herein. In one aspect, it is the stringency of the wash conditions that set forth the conditions which determine whether a nucleic acid is within the scope of the invention, as discussed below.

"Hybridization" refers to the process by which a nucleic acid strand joins with a complementary strand through base pairing. Hybridization reactions can be sensitive and selective so that a particular sequence of interest can be identified even in samples in which it is present at low concentrations. Suitably stringent conditions can be defined by, for example, the concentrations of salt or formamide in the prehybridization and hybridization solutions, or by the hybridization temperature and are well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature. In alternative aspects, nucleic acids of the invention are defined by their ability to hybridize under various stringency conditions (e.g., high, medium, and low), as set forth herein.

For example, hybridization under high stringency conditions could occur in about 50% formamide at about 37°C to 42°C. Hybridization could occur under reduced stringency conditions in about 35% to 25% formamide at about 30°C to 35°C. In one aspect, hybridization occurs under high stringency conditions, e.g., at 42°C in 50% formamide, 5X SSPE, 0.3% SDS and 200 n/ml sheared and denatured salmon sperm DNA. Hybridization could occur under these reduced stringency conditions, but in 35% formamide at a reduced temperature of 35°C. The temperature range corresponding to a particular level of stringency can be further narrowed by calculating the purine to pyrimidine ratio of the nucleic acid of interest and adjusting the temperature accordingly. Variations on the above ranges and conditions are well known in the art.

In alternative aspects, nucleic acids of the invention as defined by their ability to hybridize under stringent conditions can be between about five residues and the full length of nucleic acid of the invention; e.g., they can be at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 55, 60, 65, 70, 75, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600,

650, 700, 750, 800, 850, 900, 950, 1000, or more, residues in length. Nucleic acids shorter than full length are also included. These nucleic acids can be useful as, e.g., hybridization probes, labeling probes, PCR oligonucleotide probes, iRNA (single or double stranded), antisense or sequences encoding antibody binding peptides (epitopes), motifs, active sites and the like.

In one aspect, nucleic acids of the invention are defined by their ability to hybridize under high stringency comprising conditions of about 50% formamide at about 37°C to 42°C. In one aspect, nucleic acids of the invention are defined by their ability to hybridize under reduced stringency comprising conditions in about 35% to 25% formamide at about 30°C to 35°C.

Alternatively, nucleic acids of the invention are defined by their ability to hybridize under high stringency comprising conditions at 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and a repetitive sequence blocking nucleic acid, such as cot-1 or salmon sperm DNA (e.g., 200 n/ml sheared and denatured salmon sperm DNA). In one aspect, nucleic acids of the invention are defined by their ability to hybridize under reduced stringency conditions comprising 35% formamide at a reduced temperature of 35°C.

In nucleic acid hybridization reactions, the conditions used to achieve a particular level of stringency will vary, depending on the nature of the nucleic acids being hybridized. For example, the length, degree of complementarity, nucleotide sequence composition (e.g., GC v. AT content) and nucleic acid type (e.g., RNA v. DNA) of the hybridizing regions of the nucleic acids can be considered in selecting hybridization conditions. An additional consideration is whether one of the nucleic acids is immobilized, for example, on a filter.

Hybridization may be carried out under conditions of low stringency, moderate stringency or high stringency. As an example of nucleic acid hybridization, a polymer membrane containing immobilized denatured nucleic acids is first prehybridized for 30 minutes at 45°C in a solution consisting of 0.9 M NaCl, 50 mM NaH₂PO₄, pH 7.0, 5.0 mM Na₂EDTA, 0.5% SDS, 10X Denhardt's and 0.5 mg/ml polyriboadenylic acid. Approximately 2×10^7 cpm (specific activity $4-9 \times 10^8$ cpm/ug) of ³²P end-labeled oligonucleotide probe are then added to the solution. After 12-16 hours of incubation, the membrane is washed for 30 minutes at room temperature in 1X SET (150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na₂EDTA) containing 0.5% SDS, followed by a 30 minute wash in fresh 1X SET at T_m-10°C for the oligonucleotide probe. The

membrane is then exposed to auto-radiographic film for detection of hybridization signals.

All of the foregoing hybridizations would be considered to be under conditions of high stringency.

Following hybridization, a filter can be washed to remove any non-specifically bound detectable probe. The stringency used to wash the filters can also be varied depending on the nature of the nucleic acids being hybridized, the length of the nucleic acids being hybridized, the degree of complementarity, the nucleotide sequence composition (*e.g.*, GC v. AT content) and the nucleic acid type (*e.g.*, RNA v. DNA). Examples of progressively higher stringency condition washes are as follows: 2X SSC, 0.1% SDS at room temperature for 15 minutes (low stringency); 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour (moderate stringency); 0.1X SSC, 0.5% SDS for 15 to 30 minutes at between the hybridization temperature and 68°C (high stringency); and 0.15M NaCl for 15 minutes at 72°C (very high stringency). A final low stringency wash can be conducted in 0.1X SSC at room temperature. The examples above are merely illustrative of one set of conditions that can be used to wash filters. One of skill in the art would know that there are numerous recipes for different stringency washes. Some other examples are given below.

In one aspect, hybridization conditions comprise a wash step comprising a wash for 30 minutes at room temperature in a solution comprising 1X 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na₂EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution.

Nucleic acids which have hybridized to the probe are identified by autoradiography or other conventional techniques.

The above procedure may be modified to identify nucleic acids having decreasing levels of homology to the probe sequence. For example, to obtain nucleic acids of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a Na⁺ concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C. A specific example of "moderate" hybridization conditions is when the above hybridization is conducted at 55°C. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 45°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide. A specific example of "moderate" hybridization conditions is when the above hybridization is conducted at 30% formamide. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 10% formamide.

However, the selection of a hybridization format is not critical - it is the stringency of the wash conditions that set forth the conditions which determine whether a nucleic acid is within the scope of the invention. Wash conditions used to identify nucleic acids within the scope of the invention include, e.g.: a salt concentration of about 0.02 molar at pH 7 and a temperature of at least about 50°C or about 55°C to about 60°C; or, a salt concentration of about 0.15 M NaCl at 72°C for about 15 minutes; or, a salt concentration of about 0.2X SSC at a temperature of at least about 50°C or about 55°C to about 60°C for about 15 to about 20 minutes; or, the hybridization complex is washed twice with a solution with a salt concentration of about 2X SSC containing 0.1% SDS at room temperature for 15 minutes and then washed twice by 0.1X SSC containing 0.1% SDS at 68°C for 15 minutes; or, equivalent conditions. See Sambrook, Tijssen and Ausubel for a description of SSC buffer and equivalent conditions.

These methods may be used to isolate nucleic acids of the invention. For example, the preceding methods may be used to isolate nucleic acids having a sequence with at least about 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, or at least 50% sequence identity (homology) to a nucleic acid sequence selected from the group consisting of one of the sequences of the invention, or fragments comprising at least about 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases thereof and the sequences complementary thereto. Sequence identity (homology) may be measured using the alignment algorithm. For example, the homologous polynucleotides may have a coding sequence which is a naturally occurring allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to the nucleic acids of the invention. Additionally, the above procedures may be used to isolate nucleic acids which encode

polypeptides having at least about 99%, 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, or at least 50% sequence identity (homology) to a polypeptide of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using a sequence alignment algorithm (e.g., such as the FASTA version 3.0t78 algorithm with the default parameters).

Oligonucleotides probes and methods for using them

The invention also provides nucleic acid probes that can be used, e.g., for identifying nucleic acids encoding a polypeptide with an enzyme, structural or binding activity or fragments thereof or for identifying polypeptide, enzyme, protein, e.g. structural or binding protein, genes. In one aspect, the probe comprises at least 10 consecutive bases of a nucleic acid of the invention. Alternatively, a probe of the invention can be at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 150 or about 10 to 50, about 20 to 60 about 30 to 70, consecutive bases of a sequence as set forth in a nucleic acid of the invention. The probes identify a nucleic acid by binding and/or hybridization. The probes can be used in arrays of the invention, see discussion below, including, e.g., capillary arrays. The probes of the invention can also be used to isolate other nucleic acids or polypeptides.

The isolated nucleic acids of the invention, the sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the invention, or the sequences complementary thereto may also be used as probes to determine whether a biological sample, such as a soil sample, contains an organism having a nucleic acid sequence of the invention or an organism from which the nucleic acid was obtained. In such procedures, a biological sample potentially harboring the organism from which the nucleic acid was isolated is obtained and nucleic acids are obtained from the sample. The nucleic acids are contacted with the probe under conditions which permit the probe to specifically hybridize to any complementary sequences from which are present therein.

Where necessary, conditions which permit the probe to specifically hybridize to complementary sequences may be determined by placing the probe in contact with complementary sequences from samples known to contain the complementary sequence as well as control sequences which do not contain the complementary sequence. Hybridization conditions, such as the salt concentration of the hybridization buffer, the

formamide concentration of the hybridization buffer, or the hybridization temperature, may be varied to identify conditions which allow the probe to hybridize specifically to complementary nucleic acids.

If the sample contains the organism from which the nucleic acid was isolated, specific hybridization of the probe is then detected. Hybridization may be detected by labeling the probe with a detectable agent such as a radioactive isotope, a fluorescent dye or an enzyme capable of catalyzing the formation of a detectable product.

Many methods for using the labeled probes to detect the presence of complementary nucleic acids in a sample are familiar to those skilled in the art. These include Southern Blots, Northern Blots, colony hybridization procedures and dot blots. Protocols for each of these procedures are provided in Ausubel *et al.* *Current Protocols in Molecular Biology*, John Wiley 503 Sons, Inc. (1997) and Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* 2nd Ed., Cold Spring Harbor Laboratory Press (1989).

Alternatively, more than one probe (at least one of which is capable of specifically hybridizing to any complementary sequences which are present in the nucleic acid sample), may be used in an amplification reaction to determine whether the sample contains an organism containing a nucleic acid sequence of the invention (e.g., an organism from which the nucleic acid was isolated). Typically, the probes comprise oligonucleotides. In one aspect, the amplification reaction may comprise a PCR reaction. PCR protocols are described in Ausubel and Sambrook, *supra*. Alternatively, the amplification may comprise a ligase chain reaction, 3SR, or strand displacement reaction. (See Barany, F., "The Ligase Chain Reaction in a PCR World", *PCR Methods and Applications* 1:5-16, 1991; E. Fahy *et al.*, "Self-sustained Sequence Replication (3SR): An Isothermal Transcription-based Amplification System Alternative to PCR", *PCR Methods and Applications* 1:25-33, 1991; and Walker G.T. *et al.*, "Strand Displacement Amplification-an Isothermal *in vitro* DNA Amplification Technique", *Nucleic Acid Research* 20:1691-1696, 1992). In such procedures, the nucleic acids in the sample are contacted with the probes, the amplification reaction is performed and any resulting amplification product is detected. The amplification product may be detected by performing gel electrophoresis on the reaction products and staining the gel with an intercalator such as ethidium bromide. Alternatively, one or more of the probes may be labeled with a radioactive isotope and the presence of a radioactive amplification product may be detected by autoradiography after gel electrophoresis.

Probes derived from sequences near the ends of the sequences of the invention, may also be used in chromosome walking procedures to identify clones containing genomic sequences located adjacent to the sequences of the invention. Such methods allow the isolation of genes which encode additional proteins from the host organism.

The isolated nucleic acids of the invention, the sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the invention, or the sequences complementary thereto may be used as probes to identify and isolate related nucleic acids. In some aspects, the related nucleic acids may be cDNAs or genomic DNAs from organisms other than the one from which the nucleic acid was isolated. For example, the other organisms may be related organisms. In such procedures, a nucleic acid sample is contacted with the probe under conditions which permit the probe to specifically hybridize to related sequences. Hybridization of the probe to nucleic acids from the related organism is then detected using any of the methods described above.

By varying the stringency of the hybridization conditions used to identify nucleic acids, such as cDNAs or genomic DNAs, which hybridize to the detectable probe, nucleic acids having different levels of homology to the probe can be identified and isolated. Stringency may be varied by conducting the hybridization at varying temperatures below the melting temperatures of the probes. The melting temperature, T_m , is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly complementary probe. Very stringent conditions are selected to be equal to or about 5°C lower than the T_m for a particular probe. The melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (600/N)$ where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100µg denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100µg denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook *et al.*, *supra*.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the T_m . For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 5-10°C below the T_m . In one aspect, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Usually, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

Inhibiting Expression of Polypeptides, Enzymes, Proteins

The invention provides nucleic acids complementary to (e.g., antisense sequences to) the nucleic acids of the invention, e.g., nucleic acids comprising antisense, iRNA, ribozymes. Nucleic acids of the invention comprising antisense sequences can be capable of inhibiting the transport, splicing or transcription of polypeptide, enzyme, protein, e.g. structural or binding protein genes. The inhibition can be effected through the targeting of genomic DNA or messenger RNA. The transcription or function of targeted nucleic acid can be inhibited, for example, by hybridization and/or cleavage. In one aspect, inhibitors of the invention include oligonucleotides which are able to either bind a polypeptide, enzyme, protein, e.g. structural or binding protein, gene or message, in either case preventing or inhibiting the production or function of a polypeptide, enzyme, protein, e.g. structural or binding protein. The association can be through sequence specific hybridization. Another useful class of inhibitors includes oligonucleotides which cause inactivation or cleavage of a polypeptide, enzyme, protein, e.g. structural or binding protein, message. The oligonucleotide can have enzyme activity which causes such cleavage, such as ribozymes. The oligonucleotide can be chemically modified or conjugated to an enzyme or composition capable of cleaving the complementary nucleic acid. A pool of many different such oligonucleotides can be screened for those with the desired activity. Thus, the invention provides various compositions for the inhibition of a polypeptide, enzyme, protein, e.g. structural or binding protein, expression on a nucleic acid and/or protein level, e.g., antisense, iRNA and ribozymes comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, sequences of the invention and the

anti-polypeptide, anti-enzyme, anti-protein, e.g. anti-structural or anti-binding protein antibodies of the invention.

Inhibition of a polypeptide, enzyme, protein, e.g. structural or binding protein, expression can have a variety of industrial applications. For example, inhibition of a polypeptide, enzyme, protein, e.g. structural or binding protein, expression can slow or prevent spoilage. In one aspect, use of compositions of the invention that inhibit the expression and/or activity of a polypeptide, enzyme, protein, e.g. structural or binding protein, e.g., antibodies, antisense oligonucleotides, ribozymes and RNAi, are used to slow or prevent spoilage. Thus, in one aspect, the invention provides methods and compositions comprising application onto a plant or plant product (e.g., a cereal, a grain, a fruit, seed, root, leaf, etc.) antibodies, antisense oligonucleotides, ribozymes and RNAi of the invention to slow or prevent spoilage. These compositions also can be expressed by the plant (e.g., a transgenic plant) or another organism (e.g., a bacterium or other microorganism transformed with a polypeptide, enzyme, protein, e.g. structural or binding protein, gene of the invention).

The compositions of the invention for the inhibition of a polypeptide, enzyme, protein, e.g. structural or binding protein, expression, e.g., antisense, iRNA (e.g., siRNA, miRNA), ribozymes, antibodies, can be used as pharmaceutical compositions, e.g., as anti-pathogen agents or in other therapies, e.g., as anti-microbials for, e.g., *Salmonella*, or to neutralize a biological warfare agent, e.g., anthrax.

Antisense Oligonucleotides

The invention provides antisense oligonucleotides capable of binding a polypeptide, enzyme, protein, e.g. structural or binding protein, message which, in one aspect, can inhibit a polypeptide, enzyme, protein, e.g. structural or binding protein, activity by targeting mRNA. Strategies for designing antisense oligonucleotides are well described in the scientific and patent literature, and the skilled artisan can design such a polypeptide, enzyme, protein, e.g. structural or binding protein, oligonucleotides using the novel reagents of the invention. For example, gene walking/ RNA mapping protocols to screen for effective antisense oligonucleotides are well known in the art, see, e.g., Ho (2000) *Methods Enzymol.* 314:168-183, describing an RNA mapping assay, which is based on standard molecular techniques to provide an easy and reliable method for potent antisense sequence selection. See also Smith (2000) *Eur. J. Pharm. Sci.* 11:191-198.

Naturally occurring nucleic acids are used as antisense oligonucleotides. The antisense oligonucleotides can be of any length; for example, in alternative aspects,

the antisense oligonucleotides are between about 5 to 100, about 10 to 80, about 15 to 60, about 18 to 40. The optimal length can be determined by routine screening. The antisense oligonucleotides can be present at any concentration. The optimal concentration can be determined by routine screening. A wide variety of synthetic, non-naturally occurring nucleotide and nucleic acid analogues are known which can address this potential problem. For example, peptide nucleic acids (PNAs) containing non-ionic backbones, such as N-(2-aminoethyl) glycine units can be used. Antisense oligonucleotides having phosphorothioate linkages can also be used, as described in WO 97/03211; WO 96/39154; Mata (1997) *Toxicol Appl Pharmacol* 144:189-197; *Antisense Therapeutics*, ed. Agrawal (Humana Press, Totowa, N.J., 1996). Antisense oligonucleotides having synthetic DNA backbone analogues provided by the invention can also include phosphoro-dithioate, methylphosphonate, phosphoramidate, alkyl phosphotriester, sulfamate, 3'-thioacetal, methylene(methylimino), 3'-N-carbamate, and morpholino carbamate nucleic acids, as described above.

Combinatorial chemistry methodology can be used to create vast numbers of oligonucleotides that can be rapidly screened for specific oligonucleotides that have appropriate binding affinities and specificities toward any target, such as the sense and antisense a polypeptide, enzyme, protein, e.g. structural or binding protein, sequences of the invention (see, e.g., Gold (1995) *J. of Biol. Chem.* 270:13581-13584).

Inhibitory Ribozymes

The invention provides ribozymes capable of binding a polypeptide, enzyme, protein, e.g. structural or binding protein, message. These ribozymes can inhibit a polypeptide, enzyme, protein, e.g. structural or binding protein, activity by, e.g., targeting mRNA. Strategies for designing ribozymes and selecting the polypeptide, enzyme, protein, e.g. structural or binding protein-specific antisense sequence for targeting are well described in the scientific and patent literature, and the skilled artisan can design such ribozymes using the novel reagents of the invention. Ribozymes act by binding to a target RNA through the target RNA binding portion of a ribozyme which is held in close proximity to an enzymatic portion of the RNA that cleaves the target RNA. Thus, the ribozyme recognizes and binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cleave and inactivate the target RNA. Cleavage of a target RNA in such a manner will destroy its ability to direct synthesis of an encoded protein if the cleavage occurs in the coding sequence. After a

ribozyme has bound and cleaved its RNA target, it can be released from that RNA to bind and cleave new targets repeatedly.

In some circumstances, the enzymatic nature of a ribozyme can be advantageous over other technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its transcription, translation or association with another molecule) as the effective concentration of ribozyme necessary to effect a therapeutic treatment can be lower than that of an antisense oligonucleotide. This potential advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, a ribozyme is typically a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding, but also on the mechanism by which the molecule inhibits the expression of the RNA to which it binds. That is, the inhibition is caused by cleavage of the RNA target and so specificity is defined as the ratio of the rate of cleavage of the targeted RNA over the rate of cleavage of non-targeted RNA. This cleavage mechanism is dependent upon factors additional to those involved in base pairing. Thus, the specificity of action of a ribozyme can be greater than that of antisense oligonucleotide binding the same RNA site.

The ribozyme of the invention, e.g., an enzymatic ribozyme RNA molecule, can be formed in a hammerhead motif, a hairpin motif, as a hepatitis delta virus motif, a group I intron motif and/or an RNaseP-like RNA in association with an RNA guide sequence. Examples of hammerhead motifs are described by, e.g., Rossi (1992) *Aids Research and Human Retroviruses* 8:183; hairpin motifs by Hampel (1989) *Biochemistry* 28:4929, and Hampel (1990) *Nuc. Acids Res.* 18:299; the hepatitis delta virus motif by Perrotta (1992) *Biochemistry* 31:16; the RNaseP motif by Guerrier-Takada (1983) *Cell* 35:849; and the group I intron by Cech U.S. Pat. No. 4,987,071. The recitation of these specific motifs is not intended to be limiting. Those skilled in the art will recognize that a ribozyme of the invention, e.g., an enzymatic RNA molecule of this invention, can have a specific substrate binding site complementary to one or more of the target gene RNA regions. A ribozyme of the invention can have a nucleotide sequence within or surrounding that substrate binding site which imparts an RNA cleaving activity to the molecule.

RNA interference (RNAi)

In one aspect, the invention provides an RNA inhibitory molecule, a so-called "RNAi" molecule, comprising a polypeptide, enzyme, protein, e.g. structural or

binding protein, sequence of the invention. The RNAi molecule comprises a double-stranded RNA (dsRNA) molecule. The RNAi can inhibit expression of a polypeptide, enzyme, protein, e.g. structural or binding protein, gene. In one aspect, the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length. While the invention is not limited by any particular mechanism of action, the RNAi can enter a cell and cause the degradation of a single-stranded RNA (ssRNA) of similar or identical sequences, including endogenous mRNAs. When a cell is exposed to double-stranded RNA (dsRNA), mRNA from the homologous gene is selectively degraded by a process called RNA interference (RNAi). A possible basic mechanism behind RNAi, e.g., siRNA for inhibiting transcription and/or miRNA to inhibit translation, is the breaking of a double-stranded RNA (dsRNA) matching a specific gene sequence into short pieces called short interfering RNA, which trigger the degradation of mRNA that matches its sequence. In one aspect, the RNAi's of the invention are used in gene-silencing therapeutics, see, e.g., Shuey (2002) Drug Discov. Today 7:1040-1046. In one aspect, the invention provides methods to selectively degrade RNA using the RNAi's of the invention. The process may be practiced *in vitro*, *ex vivo* or *in vivo*. In one aspect, the RNAi molecules of the invention can be used to generate a loss-of-function mutation in a cell, an organ or an animal. Methods for making and using RNAi molecules for selectively degrade RNA are well known in the art, see, e.g., U.S. Patent No. 6,506,559; 6,511,824; 6,515,109; 6,489,127.

Modification of Nucleic Acids

The invention provides methods of generating variants of the nucleic acids of the invention, e.g., those encoding a polypeptide, enzyme, protein, e.g. structural or binding protein. These methods can be repeated or used in various combinations to generate a polypeptide, enzyme, protein, e.g. structural or binding protein, having an altered or different activity or an altered or different stability from that of a polypeptide, enzyme, protein, e.g. structural or binding protein, encoded by the template nucleic acid. These methods also can be repeated or used in various combinations, e.g., to generate variations in gene/ message expression, message translation or message stability. In another aspect, the genetic composition of a cell is altered by, e.g., modification of a homologous gene *ex vivo*, followed by its reinsertion into the cell.

A nucleic acid of the invention can be altered by any means. For example, random or stochastic methods, or, non-stochastic, or "directed evolution," methods, see, e.g., U.S. Patent No. 6,361,974. Methods for random mutation of genes are well known

in the art, see, e.g., U.S. Patent No. 5,830,696. For example, mutagens can be used to randomly mutate a gene. Mutagens include, e.g., ultraviolet light or gamma irradiation, or a chemical mutagen, e.g., mitomycin, nitrous acid, photoactivated psoralens, alone or in combination, to induce DNA breaks amenable to repair by recombination. Other chemical mutagens include, for example, sodium bisulfite, nitrous acid, hydroxylamine, hydrazine or formic acid. Other mutagens are analogues of nucleotide precursors, e.g., nitrosoguanidine, 5-bromouracil, 2-aminopurine, or acridine. These agents can be added to a PCR reaction in place of the nucleotide precursor thereby mutating the sequence. Intercalating agents such as proflavine, acriflavine, quinacrine and the like can also be used.

Any technique in molecular biology can be used, e.g., random PCR mutagenesis, see, e.g., Rice (1992) *Proc. Natl. Acad. Sci. USA* 89:5467-5471; or, combinatorial multiple cassette mutagenesis, see, e.g., Cramer (1995) *Biotechniques* 18:194-196. Alternatively, nucleic acids, e.g., genes, can be reassembled after random, or "stochastic," fragmentation, see, e.g., U.S. Patent Nos. 6,291,242; 6,287,862; 6,287,861; 5,955,358; 5,830,721; 5,824,514; 5,811,238; 5,605,793. In alternative aspects, modifications, additions or deletions are introduced by error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation, and/or a combination of these and other methods.

The following publications describe a variety of recursive recombination procedures and/or methods which can be incorporated into the methods of the invention: Stemmer (1999) "Molecular breeding of viruses for targeting and other clinical properties" *Tumor Targeting* 4:1-4; Ness (1999) *Nature Biotechnology* 17:893-896; Chang (1999) "Evolution of a cytokine using DNA family shuffling" *Nature Biotechnology* 17:793-797; Minshull (1999) "Protein evolution by molecular breeding" *Current Opinion in Chemical Biology* 3:284-290; Christians (1999) "Directed evolution

of thymidine kinase for AZT phosphorylation using DNA family shuffling" *Nature Biotechnology* 17:259-264; Cramer (1998) "DNA shuffling of a family of genes from diverse species accelerates directed evolution" *Nature* 391:288-291; Cramer (1997) "Molecular evolution of an arsenate detoxification pathway by DNA shuffling," *Nature Biotechnology* 15:436-438; Zhang (1997) "Directed evolution of an effective fucosidase from a galactosidase by DNA shuffling and screening" *Proc. Natl. Acad. Sci. USA* 94:4504-4509; Patten et al. (1997) "Applications of DNA Shuffling to Pharmaceuticals and Vaccines" *Current Opinion in Biotechnology* 8:724-733; Cramer et al. (1996) "Construction and evolution of antibody-phage libraries by DNA shuffling" *Nature Medicine* 2:100-103; Gates et al. (1996) "Affinity selective isolation of ligands from peptide libraries through display on a lac repressor 'headpiece dimer'" *Journal of Molecular Biology* 255:373-386; Stemmer (1996) "Sexual PCR and Assembly PCR" In: *The Encyclopedia of Molecular Biology*. VCH Publishers, New York. pp.447-457; Cramer and Stemmer (1995) "Combinatorial multiple cassette mutagenesis creates all the permutations of mutant and wildtype cassettes" *BioTechniques* 18:194-195; Stemmer et al. (1995) "Single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides" *Gene*, 164:49-53; Stemmer (1995) "The Evolution of Molecular Computation" *Science* 270: 1510; Stemmer (1995) "Searching Sequence Space" *Bio/Technology* 13:549-553; Stemmer (1994) "Rapid evolution of a protein in vitro by DNA shuffling" *Nature* 370:389-391; and Stemmer (1994) "DNA shuffling by random fragmentation and reassembly: In vitro recombination for molecular evolution." *Proc. Natl. Acad. Sci. USA* 91:10747-10751.

Mutational methods of generating diversity include, for example, site-directed mutagenesis (Ling et al. (1997) "Approaches to DNA mutagenesis: an overview" *Anal Biochem.* 254(2): 157-178; Dale et al. (1996) "Oligonucleotide-directed random mutagenesis using the phosphorothioate method" *Methods Mol. Biol.* 57:369-374; Smith (1985) "In vitro mutagenesis" *Ann. Rev. Genet.* 19:423-462; Botstein & Shortle (1985) "Strategies and applications of in vitro mutagenesis" *Science* 229:1193-1201; Carter (1986) "Site-directed mutagenesis" *Biochem. J.* 237:1-7; and Kunkel (1987) "The efficiency of oligonucleotide directed mutagenesis" in *Nucleic Acids & Molecular Biology* (Eckstein, F. and Lilley, D. M. J. eds., Springer Verlag, Berlin)); mutagenesis using uracil containing templates (Kunkel (1985) "Rapid and efficient site-specific mutagenesis without phenotypic selection" *Proc. Natl. Acad. Sci. USA* 82:488-492; Kunkel et al. (1987) "Rapid and efficient site-specific mutagenesis without phenotypic

selection" *Methods in Enzymol.* 154, 367-382; and Bass et al. (1988) "Mutant Trp repressors with new DNA-binding specificities" *Science* 242:240-245); oligonucleotide-directed mutagenesis (*Methods in Enzymol.* 100: 468-500 (1983); *Methods in Enzymol.* 154: 329-350 (1987); Zoller (1982) "Oligonucleotide-directed mutagenesis using M13-derived vectors: an efficient and general procedure for the production of point mutations in any DNA fragment" *Nucleic Acids Res.* 10:6487-6500; Zoller & Smith (1983) "Oligonucleotide-directed mutagenesis of DNA fragments cloned into M13 vectors" *Methods in Enzymol.* 100:468-500; and Zoller (1987) Oligonucleotide-directed mutagenesis: a simple method using two oligonucleotide primers and a single-stranded DNA template" *Methods in Enzymol.* 154:329-350); phosphorothioate-modified DNA mutagenesis (Taylor (1985) "The use of phosphorothioate-modified DNA in restriction enzyme reactions to prepare nicked DNA" *Nucl. Acids Res.* 13: 8749-8764; Taylor (1985) "The rapid generation of oligonucleotide-directed mutations at high frequency using phosphorothioate-modified DNA" *Nucl. Acids Res.* 13: 8765-8787 (1985); Nakamaye (1986) "Inhibition of restriction endonuclease Nci I cleavage by phosphorothioate groups and its application to oligonucleotide-directed mutagenesis" *Nucl. Acids Res.* 14: 9679-9698; Sayers (1988) "Y-T Exonucleases in phosphorothioate-based oligonucleotide-directed mutagenesis" *Nucl. Acids Res.* 16:791-802; and Sayers et al. (1988) "Strand specific cleavage of phosphorothioate-containing DNA by reaction with restriction endonucleases in the presence of ethidium bromide" *Nucl. Acids Res.* 16: 803-814); mutagenesis using gapped duplex DNA (Kramer et al. (1984) "The gapped duplex DNA approach to oligonucleotide-directed mutation construction" *Nucl. Acids Res.* 12: 9441-9456; Kramer & Fritz (1987) *Methods in Enzymol.* "Oligonucleotide-directed construction of mutations via gapped duplex DNA" 154:350-367; Kramer (1988) "Improved enzymatic *in vitro* reactions in the gapped duplex DNA approach to oligonucleotide-directed construction of mutations" *Nucl. Acids Res.* 16: 7207; and Fritz (1988) "Oligonucleotide-directed construction of mutations: a gapped duplex DNA procedure without enzymatic reactions *in vitro*" *Nucl. Acids Res.* 16: 6987-6999).

Additional protocols that can be used to practice the invention include point mismatch repair (Kramer (1984) "Point Mismatch Repair" *Cell* 38:879-887), mutagenesis using repair-deficient host strains (Carter et al. (1985) "Improved oligonucleotide site-directed mutagenesis using M13 vectors" *Nucl. Acids Res.* 13: 4431-4443; and Carter (1987) "Improved oligonucleotide-directed mutagenesis using M13 vectors" *Methods in Enzymol.* 154: 382-403), deletion mutagenesis (Eghtedarzadeh

(1986) "Use of oligonucleotides to generate large deletions" Nucl. Acids Res. 14: 5115), restriction-selection and restriction-selection and restriction-purification (Wells et al. (1986) "Importance of hydrogen-bond formation in stabilizing the transition state of subtilisin" Phil. Trans. R. Soc. Lond. A 317: 415-423), mutagenesis by total gene synthesis (Nambiar et al. (1984) "Total synthesis and cloning of a gene coding for the ribonuclease S protein" Science 223: 1299-1301; Sakamar and Khorana (1988) "Total synthesis and expression of a gene for the α -subunit of bovine rod outer segment guanine nucleotide-binding protein (transducin)" Nucl. Acids Res. 14: 6361-6372; Wells et al. (1985) "Cassette mutagenesis: an efficient method for generation of multiple mutations at defined sites" Gene 34:315-323; and Grundstrom et al. (1985) "Oligonucleotide-directed mutagenesis by microscale 'shot-gun' gene synthesis" Nucl. Acids Res. 13: 3305-3316), double-strand break repair (Mandecki (1986); Arnold (1993) "Protein engineering for unusual environments" Current Opinion in Biotechnology 4:450-455. "Oligonucleotide-directed double-strand break repair in plasmids of Escherichia coli: a method for site-specific mutagenesis" Proc. Natl. Acad. Sci. USA, 83:7177-7181). Additional details on many of the above methods can be found in Methods in Enzymology Volume 154, which also describes useful controls for trouble-shooting problems with various mutagenesis methods.

Protocols that can be used to practice the invention are described, e.g., in U.S. Patent Nos. 5,605,793 to Stemmer (Feb. 25, 1997), "Methods for In Vitro Recombination;" U.S. Pat. No. 5,811,238 to Stemmer et al. (Sep. 22, 1998) "Methods for Generating Polynucleotides having Desired Characteristics by Iterative Selection and Recombination;" U.S. Pat. No. 5,830,721 to Stemmer et al. (Nov. 3, 1998), "DNA Mutagenesis by Random Fragmentation and Reassembly;" U.S. Pat. No. 5,834,252 to Stemmer, et al. (Nov. 10, 1998) "End-Complementary Polymerase Reaction;" U.S. Pat. No. 5,837,458 to Minshull, et al. (Nov. 17, 1998), "Methods and Compositions for Cellular and Metabolic Engineering;" WO 95/22625, Stemmer and Cramer, "Mutagenesis by Random Fragmentation and Reassembly;" WO 96/33207 by Stemmer and Lipschutz "End Complementary Polymerase Chain Reaction;" WO 97/20078 by Stemmer and Cramer "Methods for Generating Polynucleotides having Desired Characteristics by Iterative Selection and Recombination;" WO 97/35966 by Minshull and Stemmer, "Methods and Compositions for Cellular and Metabolic Engineering;" WO 99/41402 by Punnonen et al. "Targeting of Genetic Vaccine Vectors;" WO 99/41383 by Punnonen et al. "Antigen Library Immunization;" WO 99/41369 by Punnonen et al.

"Genetic Vaccine Vector Engineering;" WO 99/41368 by Punnonen et al. "Optimization of Immunomodulatory Properties of Genetic Vaccines;" EP 752008 by Stemmer and Crameri, "DNA Mutagenesis by Random Fragmentation and Reassembly;" EP 0932670 by Stemmer "Evolving Cellular DNA Uptake by Recursive Sequence Recombination;" WO 99/23107 by Stemmer et al., "Modification of Virus Tropism and Host Range by Viral Genome Shuffling;" WO 99/21979 by Apt et al., "Human Papillomavirus Vectors;" WO 98/31837 by del Cardayre et al. "Evolution of Whole Cells and Organisms by Recursive Sequence Recombination;" WO 98/27230 by Patten and Stemmer, "Methods and Compositions for Polypeptide Engineering;" WO 98/27230 by Stemmer et al., "Methods for Optimization of Gene Therapy by Recursive Sequence Shuffling and Selection," WO 00/00632, "Methods for Generating Highly Diverse Libraries," WO 00/09679, "Methods for Obtaining in Vitro Recombined Polynucleotide Sequence Banks and Resulting Sequences," WO 98/42832 by Arnold et al., "Recombination of Polynucleotide Sequences Using Random or Defined Primers," WO 99/29902 by Arnold et al., "Method for Creating Polynucleotide and Polypeptide Sequences," WO 98/41653 by Vind, "An in Vitro Method for Construction of a DNA Library," WO 98/41622 by Borchert et al., "Method for Constructing a Library Using DNA Shuffling," and WO 98/42727 by Pati and Zarling, "Sequence Alterations using Homologous Recombination."

Protocols that can be used to practice the invention (providing details regarding various diversity generating methods) are described, e.g., in U.S. Patent application serial no. (USSN) 09/407,800, "SHUFFLING OF CODON ALTERED GENES" by Patten et al. filed Sep. 28, 1999; "EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE SEQUENCE RECOMBINATION" by del Cardayre et al., United States Patent No. 6,379,964; "OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION" by Crameri et al., United States Patent Nos. 6,319,714; 6,368,861; 6,376,246; 6,423,542; 6,426,224 and PCT/US00/01203; "USE OF CODON-VARIED OLIGONUCLEOTIDE SYNTHESIS FOR SYNTHETIC SHUFFLING" by Welch et al., United States Patent No. 6,436,675; "METHODS FOR MAKING CHARACTER STRINGS, POLYNUCLEOTIDES & POLYPEPTIDES HAVING DESIRED CHARACTERISTICS" by Selifonov et al., filed Jan. 18, 2000, (PCT/US00/01202) and, e.g. "METHODS FOR MAKING CHARACTER STRINGS, POLYNUCLEOTIDES & POLYPEPTIDES HAVING DESIRED CHARACTERISTICS" by Selifonov et al., filed Jul. 18, 2000 (U.S. Ser. No. 09/618,579); "METHODS OF POPULATING DATA STRUCTURES FOR USE IN

EVOLUTIONARY SIMULATIONS" by Selifonov and Stemmer, filed Jan. 18, 2000 (PCT/US00/01138); and "SINGLE-STRANDED NUCLEIC ACID TEMPLATE-MEDIATED RECOMBINATION AND NUCLEIC ACID FRAGMENT ISOLATION" by Affholter, filed Sep. 6, 2000 (U.S. Ser. No. 09/656,549); and United States Patent Nos. 6,177,263; 6,153,410.

Non-stochastic, or "directed evolution," methods include, e.g., saturation mutagenesis, such as Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), or a combination thereof are used to modify the nucleic acids of the invention to generate a polypeptide, enzyme, protein, e.g. structural or binding protein, with new or altered properties (e.g., activity under highly acidic or alkaline conditions, high or low temperatures, and the like). Polypeptides encoded by the modified nucleic acids can be screened for an activity before testing for glucan hydrolysis or other activity. Any testing modality or protocol can be used, e.g., using a capillary array platform. See, e.g., U.S. Patent Nos. 6,361,974; 6,280,926; 5,939,250.

Gene Site Saturation mutagenesis, or, GSSM

The invention also provides methods for making enzyme using Gene Site Saturation mutagenesis, or, GSSM, as described herein, and also in U.S. Patent Nos. 6,171,820 and 6,579,258.

In one aspect, codon primers containing a degenerate N,N,G/T sequence are used to introduce point mutations into a polynucleotide, e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, or an antibody of the invention, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position, e.g., an amino acid residue in an enzyme active site or ligand binding site targeted to be modified. These oligonucleotides can comprise a contiguous first homologous sequence, a degenerate N,N,G/T sequence, and, optionally, a second homologous sequence. The downstream progeny translational products from the use of such oligonucleotides include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,G/T sequence includes codons for all 20 amino acids. In one aspect, one such degenerate oligonucleotide (comprised of, e.g., one degenerate N,N,G/T cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate cassettes are used – either in the same oligonucleotide or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. For example, more than

one N,N,G/T sequence can be contained in one oligonucleotide to introduce amino acid mutations at more than one site. This plurality of N,N,G/T sequences can be directly contiguous, or separated by one or more additional nucleotide sequence(s). In another aspect, oligonucleotides serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,G/T sequence, to introduce any combination or permutation of amino acid additions, deletions, and/or substitutions.

In one aspect, simultaneous mutagenesis of two or more contiguous amino acid positions is done using an oligonucleotide that contains contiguous N,N,G/T triplets, i.e. a degenerate (N,N,G/T)_n sequence. In another aspect, degenerate cassettes having less degeneracy than the N,N,G/T sequence are used. For example, it may be desirable in some instances to use (e.g. in an oligonucleotide) a degenerate triplet sequence comprised of only one N, where said N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use (e.g. in an oligo) a degenerate N,N,N triplet sequence.

In one aspect, use of degenerate triplets (e.g., N,N,G/T triplets) allows for systematic and easy generation of a full range of possible natural amino acids (for a total of 20 amino acids) into each and every amino acid position in a polypeptide (in alternative aspects, the methods also include generation of less than all possible substitutions per amino acid residue, or codon, position). For example, for a 100 amino acid polypeptide, 2000 distinct species (i.e. 20 possible amino acids per position X 100 amino acid positions) can be generated. Through the use of an oligonucleotide or set of oligonucleotides containing a degenerate N,N,G/T triplet, 32 individual sequences can code for all 20 possible natural amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using at least one such oligonucleotide, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligonucleotide in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel. Nondegenerate oligonucleotides can optionally be used in combination with degenerate primers disclosed; for example, nondegenerate oligonucleotides can be used to generate specific point mutations in a working polynucleotide. This provides one means to generate specific silent point mutations, point mutations leading to corresponding amino

acid changes, and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

In one aspect, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,) molecules such that all 20 natural amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide (other aspects use less than all 20 natural combinations). The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (e.g. cloned into a suitable host, e.g., *E. coli* host, using, e.g., an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the parental polypeptide, such as increased glucan hydrolysis activity under alkaline or acidic conditions), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

In one aspect, upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid, and each of two favorable changes) and 3 positions. Thus, there are $3 \times 3 \times 3$ or 27 total possibilities, including 7 that were previously examined - 6 single point mutations (i.e. 2 at each of three positions) and no change at any position.

In yet another aspect, site-saturation mutagenesis can be used together with shuffling, chimerization, recombination and other mutagenizing processes, along with screening. This invention provides for the use of any mutagenizing process(es), including saturation mutagenesis, in an iterative manner. In one exemplification, the iterative use of any mutagenizing process(es) is used in combination with screening.

The invention also provides for the use of proprietary codon primers (containing a degenerate N,N,N sequence) to introduce point mutations into a polynucleotide, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position; e.g., with Gene

Site Saturation Mutagenesis (GSSM). The oligos used are comprised contiguously of a first homologous sequence, a degenerate N,N,N sequence and in one aspect but not necessarily a second homologous sequence. The downstream progeny translational products from the use of such oligos include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,N sequence includes codons for all 20 amino acids.

In one aspect, one such degenerate oligo (comprised of one degenerate N,N,N cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate N,N,N cassettes are used – either in the same oligo or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. Thus, more than one N,N,N sequence can be contained in one oligo to introduce amino acid mutations at more than one site. This plurality of N,N,N sequences can be directly contiguous, or separated by one or more additional nucleotide sequence(s). In another aspect, oligos serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,N sequence, to introduce any combination or permutation of amino acid additions, deletions and/or substitutions.

In a particular exemplification, it is possible to simultaneously mutagenize two or more contiguous amino acid positions using an oligo that contains contiguous N,N,N triplets, *i.e.* a degenerate (N,N,N)_n sequence.

In another aspect, the present invention provides for the use of degenerate cassettes having less degeneracy than the N,N,N sequence. For example, it may be desirable in some instances to use (*e.g.* in an oligo) a degenerate triplet sequence comprised of only one N, where the N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use (*e.g.*, in an oligo) a degenerate N,N,N triplet sequence, N,N,G/T, or an N,N, G/C triplet sequence.

It is appreciated, however, that the use of a degenerate triplet (such as N,N,G/T or an N,N, G/C triplet sequence) as disclosed in the instant invention is advantageous for several reasons. In one aspect, this invention provides a means to systematically and fairly easily generate the substitution of the full range of possible amino acids (for a total of 20 amino acids) into each and every amino acid position in a

polypeptide. Thus, for a 100 amino acid polypeptide, the invention provides a way to systematically and fairly easily generate 2000 distinct species (*i.e.*, 20 possible amino acids per position times 100 amino acid positions). It is appreciated that there is provided, through the use of an oligo containing a degenerate N,N,G/T or an N,N, G/C triplet sequence, 32 individual sequences that code for 20 possible amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using one such oligo, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligo in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel.

This invention also provides for the use of nondegenerate oligos, which can optionally be used in combination with degenerate primers disclosed. It is appreciated that in some situations, it is advantageous to use nondegenerate oligos to generate specific point mutations in a working polynucleotide. This provides a means to generate specific silent point mutations, point mutations leading to corresponding amino acid changes and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

Thus, in one aspect of this invention, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide molecules such that all 20 amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide. The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (*e.g.*, cloned into a suitable *E. coli* host using an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the parental polypeptide), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

It is appreciated that upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid and each of two favorable changes) and 3 positions. Thus, there are $3 \times 3 \times 3$ or 27

total possibilities, including 7 that were previously examined - 6 single point mutations (*i.e.*, 2 at each of three positions) and no change at any position.

Thus, in a non-limiting exemplification, this invention provides for the use of saturation mutagenesis in combination with additional mutagenization processes, such as process where two or more related polynucleotides are introduced into a suitable host cell such that a hybrid polynucleotide is generated by recombination and reductive reassortment.

In addition to performing mutagenesis along the entire sequence of a gene, the instant invention provides that mutagenesis can be used to replace each of any number of bases in a polynucleotide sequence, wherein the number of bases to be mutagenized is in one aspect every integer from 15 to 100,000. Thus, instead of mutagenizing every position along a molecule, one can subject every or a discrete number of bases (in one aspect a subset totaling from 15 to 100,000) to mutagenesis. In one aspect, a separate nucleotide is used for mutagenizing each position or group of positions along a polynucleotide sequence. A group of 3 positions to be mutagenized may be a codon. The mutations can be introduced using a mutagenic primer, containing a heterologous cassette, also referred to as a mutagenic cassette. Exemplary cassettes can have from 1 to 500 bases. Each nucleotide position in such heterologous cassettes be N, A, C, G, T, A/C, A/G, A/T, C/G, C/T, G/T, C/G/T, A/G/T, A/C/T, A/C/G, or E, where E is any base that is not A, C, G, or T (E can be referred to as a designer oligo).

In a general sense, saturation mutagenesis is comprised of mutagenizing a complete set of mutagenic cassettes (wherein each cassette is in one aspect about 1-500 bases in length) in defined polynucleotide sequence to be mutagenized (wherein the sequence to be mutagenized is in one aspect from about 15 to 100,000 bases in length). Thus, a group of mutations (ranging from 1 to 100 mutations) is introduced into each cassette to be mutagenized. A grouping of mutations to be introduced into one cassette can be different or the same from a second grouping of mutations to be introduced into a second cassette during the application of one round of saturation mutagenesis. Such groupings are exemplified by deletions, additions, groupings of particular codons and groupings of particular nucleotide cassettes.

Defined sequences to be mutagenized include a whole gene, pathway, cDNA, an entire open reading frame (ORF) and entire promoter, enhancer, repressor/transactivator, origin of replication, intron, operator, or any polynucleotide functional group. Generally, a "defined sequences" for this purpose may be any

polynucleotide that a 15 base-polynucleotide sequence and polynucleotide sequences of lengths between 15 bases and 15,000 bases (this invention specifically names every integer in between). Considerations in choosing groupings of codons include types of amino acids encoded by a degenerate mutagenic cassette.

In one exemplification a grouping of mutations that can be introduced into a mutagenic cassette, this invention specifically provides for degenerate codon substitutions (using degenerate oligos) that code for 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 and 20 amino acids at each position and a library of polypeptides encoded thereby.

Synthetic Ligation Reassembly (SLR)

The invention provides a non-stochastic gene modification system termed "synthetic ligation reassembly," or simply "SLR," a "directed evolution process," to generate polypeptides, e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, or antibodies of the invention, with new or altered properties. SLR is a method of ligating oligonucleotide fragments together non-stochastically. This method differs from stochastic oligonucleotide shuffling in that the nucleic acid building blocks are not shuffled, concatenated or chimerized randomly, but rather are assembled non-stochastically. See, e.g., U.S. Patent Nos. 6,773,900; 6,740,506; 6,713,282; 6,635,449; 6,605,449; 6,537,776.

In one aspect, SLR comprises the following steps: (a) providing a template polynucleotide, wherein the template polynucleotide comprises sequence encoding a homologous gene; (b) providing a plurality of building block polynucleotides, wherein the building block polynucleotides are designed to cross-over reassemble with the template polynucleotide at a predetermined sequence, and a building block polynucleotide comprises a sequence that is a variant of the homologous gene and a sequence homologous to the template polynucleotide flanking the variant sequence; (c) combining a building block polynucleotide with a template polynucleotide such that the building block polynucleotide cross-over reassembles with the template polynucleotide to generate polynucleotides comprising homologous gene sequence variations.

SLR does not depend on the presence of high levels of homology between polynucleotides to be rearranged. Thus, this method can be used to non-stochastically generate libraries (or sets) of progeny molecules comprised of over 10^{100} different chimeras. SLR can be used to generate libraries comprised of over 10^{1000} different progeny chimeras. Thus, aspects of the present invention include non-stochastic methods

of producing a set of finalized chimeric nucleic acid molecule having an overall assembly order that is chosen by design. This method includes the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends, and assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends. If more than one assembly step is to be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In one aspect, the annealed building pieces are treated with an enzyme, such as a ligase (e.g. T4 DNA ligase), to achieve covalent bonding of the building pieces.

In one aspect, the design of the oligonucleotide building blocks is obtained by analyzing a set of progenitor nucleic acid sequence templates that serve as a basis for producing a progeny set of finalized chimeric polynucleotides. These parental oligonucleotide templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, e.g., chimerized or shuffled. In one aspect of this method, the sequences of a plurality of parental nucleic acid templates are aligned in order to select one or more demarcation points. The demarcation points can be located at an area of homology, and are comprised of one or more nucleotides. These demarcation points are in one aspect shared by at least two of the progenitor templates. The demarcation points can thereby be used to delineate the boundaries of oligonucleotide building blocks to be generated in order to rearrange the parental polynucleotides. The demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the final chimeric progeny molecules. A demarcation point can be an area of homology (comprised of at least one homologous nucleotide base) shared by at least two parental polynucleotide sequences. Alternatively, a demarcation point can be an area of homology that is shared by at least half of the parental polynucleotide sequences, or, it can be an area of homology that is shared by at least two thirds of the parental polynucleotide sequences. Even more in one aspect a serviceable demarcation points is an area of homology that is shared by at least three fourths of the parental polynucleotide sequences,

or, it can be shared by at almost all of the parental polynucleotide sequences. In one aspect, a demarcation point is an area of homology that is shared by all of the parental polynucleotide sequences.

In one aspect, a ligation reassembly process is performed exhaustively in order to generate an exhaustive library of progeny chimeric polynucleotides. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, in another aspect, the assembly order (i.e. the order of assembly of each building block in the 5' to 3' sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic) as described above. Because of the non-stochastic nature of this invention, the possibility of unwanted side products is greatly reduced.

In another aspect, the ligation reassembly method is performed systematically. For example, the method is performed in order to generate a systematically compartmentalized library of progeny molecules, with compartments that can be screened systematically, e.g. one by one. In other words this invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, a design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, these methods allow a potentially very large number of progeny molecules to be examined systematically in smaller groups. Because of its ability to perform chimerizations in a manner that is highly flexible yet exhaustive and systematic as well, particularly when there is a low level of homology among the progenitor molecules, these methods provide for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the instant ligation reassembly invention, the progeny molecules generated in one aspect comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. The saturation mutagenesis and optimized directed evolution methods also can be used to generate different progeny molecular species. It is appreciated that the invention provides freedom of choice and control regarding the selection of demarcation points, the size and number of the nucleic acid building blocks, and the size and design of the couplings. It is appreciated, furthermore, that the requirement for intermolecular homology is highly relaxed for the operability of this invention. In fact, demarcation points can even be chosen in areas of little or no

intermolecular homology. For example, because of codon wobble, i.e. the degeneracy of codons, nucleotide substitutions can be introduced into nucleic acid building blocks without altering the amino acid originally encoded in the corresponding progenitor template. Alternatively, a codon can be altered such that the coding for an originally amino acid is altered. This invention provides that such substitutions can be introduced into the nucleic acid building block in order to increase the incidence of intermolecular homologous demarcation points and thus to allow an increased number of couplings to be achieved among the building blocks, which in turn allows a greater number of progeny chimeric molecules to be generated.

In one aspect, the present invention provides a non-stochastic method termed synthetic gene reassembly, that is somewhat related to stochastic shuffling, save that the nucleic acid building blocks are not shuffled or concatenated or chimerized randomly, but rather are assembled non-stochastically.

The synthetic gene reassembly method does not depend on the presence of a high level of homology between polynucleotides to be shuffled. The invention can be used to non-stochastically generate libraries (or sets) of progeny molecules comprised of over 10^{100} different chimeras. Conceivably, synthetic gene reassembly can even be used to generate libraries comprised of over 10^{1000} different progeny chimeras.

Thus, in one aspect, the invention provides a non-stochastic method of producing a set of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design, which method is comprised of the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends and assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, in one aspect, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends and, if more than one assembly step is to be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In one aspect of the invention, the annealed building pieces are treated with an enzyme, such as a ligase (e.g., T4 DNA ligase) to achieve covalent bonding of the building pieces.

In another aspect, the design of nucleic acid building blocks is obtained upon analysis of the sequences of a set of progenitor nucleic acid templates that serve as a basis for producing a progeny set of finalized chimeric nucleic acid molecules. These progenitor nucleic acid templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, *i.e.* chimerized or shuffled.

In one exemplification, the invention provides for the chimerization of a family of related genes and their encoded family of related products. In a particular exemplification, the encoded products are enzymes. The polypeptide, enzyme, protein, *e.g.* structural or binding proteins of the present invention can be mutagenized in accordance with the methods described herein.

Thus according to one aspect of the invention, the sequences of a plurality of progenitor nucleic acid templates (*e.g.*, polynucleotides of the invention) are aligned in order to select one or more demarcation points, which demarcation points can be located at an area of homology. The demarcation points can be used to delineate the boundaries of nucleic acid building blocks to be generated. Thus, the demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the progeny molecules.

Typically a serviceable demarcation point is an area of homology (comprised of at least one homologous nucleotide base) shared by at least two progenitor templates, but the demarcation point can be an area of homology that is shared by at least half of the progenitor templates, at least two thirds of the progenitor templates, at least three fourths of the progenitor templates and in one aspect at almost all of the progenitor templates. Even more in one aspect still a serviceable demarcation point is an area of homology that is shared by all of the progenitor templates.

In one aspect, the gene reassembly process is performed exhaustively in order to generate an exhaustive library. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, the assembly order (*i.e.* the order of assembly of each building block in the 5' to 3' sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic). Because of the non-stochastic nature of the method, the possibility of unwanted side products is greatly reduced.

In another aspect, the method provides that the gene reassembly process is performed systematically, for example to generate a systematically compartmentalized

library, with compartments that can be screened systematically, *e.g.*, one by one. In other words the invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, an experimental design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, it allows a potentially very large number of progeny molecules to be examined systematically in smaller groups.

Because of its ability to perform chimerizations in a manner that is highly flexible yet exhaustive and systematic as well, particularly when there is a low level of homology among the progenitor molecules, the instant invention provides for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the instant gene reassembly invention, the progeny molecules generated in one aspect comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. In a particularly aspect, such a generated library is comprised of greater than 10^3 to greater than 10^{1000} different progeny molecular species.

In one aspect, a set of finalized chimeric nucleic acid molecules, produced as described is comprised of a polynucleotide encoding a polypeptide. According to one aspect, this polynucleotide is a gene, which may be a man-made gene. According to another aspect, this polynucleotide is a gene pathway, which may be a man-made gene pathway. The invention provides that one or more man-made genes generated by the invention may be incorporated into a man-made gene pathway, such as pathway operable in a eukaryotic organism (including a plant).

In another exemplification, the synthetic nature of the step in which the building blocks are generated allows the design and introduction of nucleotides (*e.g.*, one or more nucleotides, which may be, for example, codons or introns or regulatory sequences) that can later be optionally removed in an *in vitro* process (*e.g.*, by mutagenesis) or in an *in vivo* process (*e.g.*, by utilizing the gene splicing ability of a host organism). It is appreciated that in many instances the introduction of these nucleotides may also be desirable for many other reasons in addition to the potential benefit of creating a serviceable demarcation point.

Thus, according to another aspect, the invention provides that a nucleic acid building block can be used to introduce an intron. Thus, the invention provides that

functional introns may be introduced into a man-made gene of the invention. The invention also provides that functional introns may be introduced into a man-made gene pathway of the invention. Accordingly, the invention provides for the generation of a chimeric polynucleotide that is a man-made gene containing one (or more) artificially introduced intron(s).

Accordingly, the invention also provides for the generation of a chimeric polynucleotide that is a man-made gene pathway containing one (or more) artificially introduced intron(s). In one aspect, the artificially introduced intron(s) are functional in one or more host cells for gene splicing much in the way that naturally-occurring introns serve functionally in gene splicing. The invention provides a process of producing man-made intron-containing polynucleotides to be introduced into host organisms for recombination and/or splicing.

A man-made gene produced using the invention can also serve as a substrate for recombination with another nucleic acid. Likewise, a man-made gene pathway produced using the invention can also serve as a substrate for recombination with another nucleic acid. In one aspect, the recombination is facilitated by, or occurs at, areas of homology between the man-made, intron-containing gene and a nucleic acid, which serves as a recombination partner. In one aspect, the recombination partner may also be a nucleic acid generated by the invention, including a man-made gene or a man-made gene pathway. Recombination may be facilitated by or may occur at areas of homology that exist at the one (or more) artificially introduced intron(s) in the man-made gene.

The synthetic gene reassembly method of the invention utilizes a plurality of nucleic acid building blocks, each of which in one aspect has two ligatable ends. The two ligatable ends on each nucleic acid building block may be two blunt ends (*i.e.* each having an overhang of zero nucleotides), or in one aspect one blunt end and one overhang, or more in one aspect still two overhangs.

A useful overhang for this purpose may be a 3' overhang or a 5' overhang. Thus, a nucleic acid building block may have a 3' overhang or alternatively a 5' overhang or alternatively two 3' overhangs or alternatively two 5' overhangs. The overall order in which the nucleic acid building blocks are assembled to form a finalized chimeric nucleic acid molecule is determined by purposeful experimental design and is not random.

In one aspect, a nucleic acid building block is generated by chemical synthesis of two single-stranded nucleic acids (also referred to as single-stranded oligos)

and contacting them so as to allow them to anneal to form a double-stranded nucleic acid building block.

A double-stranded nucleic acid building block can be of variable size. The sizes of these building blocks can be small or large. Exemplary sizes for building block range from 1 base pair (not including any overhangs) to 100,000 base pairs (not including any overhangs). Other exemplary size ranges are also provided, which have lower limits of from 1 bp to 10,000 bp (including every integer value in between) and upper limits of from 2 bp to 100, 000 bp (including every integer value in between).

Many methods exist by which a double-stranded nucleic acid building block can be generated that is serviceable for the invention; and these are known in the art and can be readily performed by the skilled artisan.

According to one aspect, a double-stranded nucleic acid building block is generated by first generating two single stranded nucleic acids and allowing them to anneal to form a double-stranded nucleic acid building block. The two strands of a double-stranded nucleic acid building block may be complementary at every nucleotide apart from any that form an overhang; thus containing no mismatches, apart from any overhang(s). According to another aspect, the two strands of a double-stranded nucleic acid building block are complementary at fewer than every nucleotide apart from any that form an overhang. Thus, according to this aspect, a double-stranded nucleic acid building block can be used to introduce codon degeneracy. In one aspect the codon degeneracy is introduced using the site-saturation mutagenesis described herein, using one or more N,N,G/T cassettes or alternatively using one or more N,N,N cassettes.

The *in vivo* recombination method of the invention can be performed blindly on a pool of unknown hybrids or alleles of a specific polynucleotide or sequence. However, it is not necessary to know the actual DNA or RNA sequence of the specific polynucleotide.

The approach of using recombination within a mixed population of genes can be useful for the generation of any useful proteins, for example, interleukin I, antibodies, tPA and growth hormone. This approach may be used to generate proteins having altered specificity or activity. The approach may also be useful for the generation of hybrid nucleic acid sequences, for example, promoter regions, introns, exons, enhancer sequences, 3' untranslated regions or 5' untranslated regions of genes. Thus this approach may be used to generate genes having increased rates of expression. This

approach may also be useful in the study of repetitive DNA sequences. Finally, this approach may be useful to mutate ribozymes or aptamers.

In one aspect the invention described herein is directed to the use of repeated cycles of reductive reassortment, recombination and selection which allow for the directed molecular evolution of highly complex linear sequences, such as DNA, RNA or proteins thorough recombination.

Optimized Directed Evolution System

The invention provides a non-stochastic gene modification system termed "optimized directed evolution system" to generate polypeptides, e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, or antibodies of the invention, with new or altered properties. Optimized directed evolution is directed to the use of repeated cycles of reductive reassortment, recombination and selection that allow for the directed molecular evolution of nucleic acids through recombination. Optimized directed evolution allows generation of a large population of evolved chimeric sequences, wherein the generated population is significantly enriched for sequences that have a predetermined number of crossover events.

A crossover event is a point in a chimeric sequence where a shift in sequence occurs from one parental variant to another parental variant. Such a point is normally at the juncture of where oligonucleotides from two parents are ligated together to form a single sequence. This method allows calculation of the correct concentrations of oligonucleotide sequences so that the final chimeric population of sequences is enriched for the chosen number of crossover events. This provides more control over choosing chimeric variants having a predetermined number of crossover events.

In addition, this method provides a convenient means for exploring a tremendous amount of the possible protein variant space in comparison to other systems. Previously, if one generated, for example, 10^{13} chimeric molecules during a reaction, it would be extremely difficult to test such a high number of chimeric variants for a particular activity. Moreover, a significant portion of the progeny population would have a very high number of crossover events which resulted in proteins that were less likely to have increased levels of a particular activity. By using these methods, the population of chimerics molecules can be enriched for those variants that have a particular number of crossover events. Thus, although one can still generate 10^{13} chimeric molecules during a reaction, each of the molecules chosen for further analysis most likely has, for example, only three crossover events. Because the resulting progeny population can be skewed to

have a predetermined number of crossover events, the boundaries on the functional variety between the chimeric molecules is reduced. This provides a more manageable number of variables when calculating which oligonucleotide from the original parental polynucleotides might be responsible for affecting a particular trait.

One method for creating a chimeric progeny polynucleotide sequence is to create oligonucleotides corresponding to fragments or portions of each parental sequence. Each oligonucleotide in one aspect includes a unique region of overlap so that mixing the oligonucleotides together results in a new variant that has each oligonucleotide fragment assembled in the correct order. Alternatively protocols for practicing these methods of the invention can be found in U.S. Patent Nos. 6,773,900; 6,740,506; 6,713,282; 6,635,449; 6,605,449; 6,537,776; 6,361,974.

The number of oligonucleotides generated for each parental variant bears a relationship to the total number of resulting crossovers in the chimeric molecule that is ultimately created. For example, three parental nucleotide sequence variants might be provided to undergo a ligation reaction in order to find a chimeric variant having, for example, greater activity at high temperature. As one example, a set of 50 oligonucleotide sequences can be generated corresponding to each portions of each parental variant. Accordingly, during the ligation reassembly process there could be up to 50 crossover events within each of the chimeric sequences. The probability that each of the generated chimeric polynucleotides will contain oligonucleotides from each parental variant in alternating order is very low. If each oligonucleotide fragment is present in the ligation reaction in the same molar quantity it is likely that in some positions oligonucleotides from the same parental polynucleotide will ligate next to one another and thus not result in a crossover event. If the concentration of each oligonucleotide from each parent is kept constant during any ligation step in this example, there is a 1/3 chance (assuming 3 parents) that an oligonucleotide from the same parental variant will ligate within the chimeric sequence and produce no crossover.

Accordingly, a probability density function (PDF) can be determined to predict the population of crossover events that are likely to occur during each step in a ligation reaction given a set number of parental variants, a number of oligonucleotides corresponding to each variant, and the concentrations of each variant during each step in the ligation reaction. The statistics and mathematics behind determining the PDF is described below. By utilizing these methods, one can calculate such a probability density function, and thus enrich the chimeric progeny population for a predetermined number of

crossover events resulting from a particular ligation reaction. Moreover, a target number of crossover events can be predetermined, and the system then programmed to calculate the starting quantities of each parental oligonucleotide during each step in the ligation reaction to result in a probability density function that centers on the predetermined number of crossover events. These methods are directed to the use of repeated cycles of reductive reassortment, recombination and selection that allow for the directed molecular evolution of a nucleic acid encoding a polypeptide through recombination. This system allows generation of a large population of evolved chimeric sequences, wherein the generated population is significantly enriched for sequences that have a predetermined number of crossover events. A crossover event is a point in a chimeric sequence where a shift in sequence occurs from one parental variant to another parental variant. Such a point is normally at the juncture of where oligonucleotides from two parents are ligated together to form a single sequence. The method allows calculation of the correct concentrations of oligonucleotide sequences so that the final chimeric population of sequences is enriched for the chosen number of crossover events. This provides more control over choosing chimeric variants having a predetermined number of crossover events.

In addition, these methods provide a convenient means for exploring a tremendous amount of the possible protein variant space in comparison to other systems. By using the methods described herein, the population of chimeric molecules can be enriched for those variants that have a particular number of crossover events. Thus, although one can still generate 10^{13} chimeric molecules during a reaction, each of the molecules chosen for further analysis most likely has, for example, only three crossover events. Because the resulting progeny population can be skewed to have a predetermined number of crossover events, the boundaries on the functional variety between the chimeric molecules is reduced. This provides a more manageable number of variables when calculating which oligonucleotide from the original parental polynucleotides might be responsible for affecting a particular trait.

In one aspect, the method creates a chimeric progeny polynucleotide sequence by creating oligonucleotides corresponding to fragments or portions of each parental sequence. Each oligonucleotide in one aspect includes a unique region of overlap so that mixing the oligonucleotides together results in a new variant that has each oligonucleotide fragment assembled in the correct order. See also USSN 09/332,835.

Determining Crossover Events

Aspects of the invention include a system and software that receive a desired crossover probability density function (PDF), the number of parent genes to be reassembled, and the number of fragments in the reassembly as inputs. The output of this program is a "fragment PDF" that can be used to determine a recipe for producing reassembled genes, and the estimated crossover PDF of those genes. The processing described herein is in one aspect performed in MATLAB™ (The Mathworks, Natick, Massachusetts) a programming language and development environment for technical computing.

Iterative Processes

In practicing the invention, these processes can be iteratively repeated. For example, a nucleic acid (or, the nucleic acid) responsible for an altered or new a polypeptide, enzyme, protein, e.g. structural or binding protein, phenotype is identified, re-isolated, again modified, re-tested for activity. This process can be iteratively repeated until a desired phenotype is engineered. For example, an entire biochemical anabolic or catabolic pathway can be engineered into a cell, including, e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, activity.

Similarly, if it is determined that a particular oligonucleotide has no affect at all on the desired trait (e.g., a new a polypeptide, enzyme, protein, e.g. structural or binding protein, phenotype), it can be removed as a variable by synthesizing larger parental oligonucleotides that include the sequence to be removed. Since incorporating the sequence within a larger sequence prevents any crossover events, there will no longer be any variation of this sequence in the progeny polynucleotides. This iterative practice of determining which oligonucleotides are most related to the desired trait, and which are unrelated, allows more efficient exploration all of the possible protein variants that might be provide a particular trait or activity.

In vivo shuffling

In vivo shuffling of molecules is use in methods of the invention that provide variants of polypeptides of the invention, e.g., antibodies, a polypeptide, enzyme, protein, e.g. structural or binding protein, and the like. *In vivo* shuffling can be performed utilizing the natural property of cells to recombine multimers. While recombination *in vivo* has provided the major natural route to molecular diversity, genetic recombination remains a relatively complex process that involves 1) the recognition of homologies; 2)

strand cleavage, strand invasion, and metabolic steps leading to the production of recombinant chiasma; and finally 3) the resolution of chiasma into discrete recombined molecules. The formation of the chiasma requires the recognition of homologous sequences.

In another aspect, the invention includes a method for producing a hybrid polynucleotide from at least a first polynucleotide and a second polynucleotide. The invention can be used to produce a hybrid polynucleotide by introducing at least a first polynucleotide and a second polynucleotide (e.g., one, or both, being an exemplary polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding sequence of the invention) which share at least one region of partial sequence homology into a suitable host cell. The regions of partial sequence homology promote processes which result in sequence reorganization producing a hybrid polynucleotide. The term "hybrid polynucleotide", as used herein, is any nucleotide sequence which results from the method of the present invention and contains sequence from at least two original polynucleotide sequences. Such hybrid polynucleotides can result from intermolecular recombination events which promote sequence integration between DNA molecules. In addition, such hybrid polynucleotides can result from intramolecular reductive reassortment processes which utilize repeated sequences to alter a nucleotide sequence within a DNA molecule.

In vivo reassortment is focused on "inter-molecular" processes collectively referred to as "recombination" which in bacteria, is generally viewed as a "RecA-dependent" phenomenon. The invention can rely on recombination processes of a host cell to recombine and re-assort sequences, or the cells' ability to mediate reductive processes to decrease the complexity of quasi-repeated sequences in the cell by deletion. This process of "reductive reassortment" occurs by an "intra-molecular", RecA-independent process.

Therefore, in another aspect of the invention, novel polynucleotides can be generated by the process of reductive reassortment. The method involves the generation of constructs containing consecutive sequences (original encoding sequences), their insertion into an appropriate vector and their subsequent introduction into an appropriate host cell. The reassortment of the individual molecular identities occurs by combinatorial processes between the consecutive sequences in the construct possessing regions of homology, or between quasi-repeated units. The reassortment process recombines and/or reduces the complexity and extent of the repeated sequences and results in the production

of novel molecular species. Various treatments may be applied to enhance the rate of reassortment. These could include treatment with ultra-violet light, or DNA damaging chemicals and/or the use of host cell lines displaying enhanced levels of "genetic instability". Thus the reassortment process may involve homologous recombination or the natural property of quasi-repeated sequences to direct their own evolution.

Repeated or "quasi-repeated" sequences play a role in genetic instability. In the present invention, "quasi-repeats" are repeats that are not restricted to their original unit structure. Quasi-repeated units can be presented as an array of sequences in a construct; consecutive units of similar sequences. Once ligated, the junctions between the consecutive sequences become essentially invisible and the quasi-repetitive nature of the resulting construct is now continuous at the molecular level. The deletion process the cell performs to reduce the complexity of the resulting construct operates between the quasi-repeated sequences. The quasi-repeated units provide a practically limitless repertoire of templates upon which slippage events can occur. The constructs containing the quasi-repeats thus effectively provide sufficient molecular elasticity that deletion (and potentially insertion) events can occur virtually anywhere within the quasi-repetitive units.

When the quasi-repeated sequences are all ligated in the same orientation, for instance head to tail or vice versa, the cell cannot distinguish individual units. Consequently, the reductive process can occur throughout the sequences. In contrast, when for example, the units are presented head to head, rather than head to tail, the inversion delineates the endpoints of the adjacent unit so that deletion formation will favor the loss of discrete units. Thus, it is preferable with the present method that the sequences are in the same orientation. Random orientation of quasi-repeated sequences will result in the loss of reassortment efficiency, while consistent orientation of the sequences will offer the highest efficiency. However, while having fewer of the contiguous sequences in the same orientation decreases the efficiency, it may still provide sufficient elasticity for the effective recovery of novel molecules. Constructs can be made with the quasi-repeated sequences in the same orientation to allow higher efficiency.

Sequences can be assembled in a head to tail orientation using any of a variety of methods, including the following:

- a) Primers that include a poly-A head and poly-T tail which when made single-stranded would provide orientation can be utilized. This is accomplished by

having the first few bases of the primers made from RNA and hence easily removed RNaseH.

- b) Primers that include unique restriction cleavage sites can be utilized. Multiple sites, a battery of unique sequences and repeated synthesis and ligation steps would be required.
- c) The inner few bases of the primer could be thiolated and an exonuclease used to produce properly tailed molecules.

The recovery of the re-assorted sequences relies on the identification of cloning vectors with a reduced repetitive index (RI). The re-assorted encoding sequences can then be recovered by amplification. The products are re-cloned and expressed. The recovery of cloning vectors with reduced RI can be affected by:

- 1) The use of vectors only stably maintained when the construct is reduced in complexity.
- 2) The physical recovery of shortened vectors by physical procedures. In this case, the cloning vector would be recovered using standard plasmid isolation procedures and size fractionated on either an agarose gel, or column with a low molecular weight cut off utilizing standard procedures.
- 3) The recovery of vectors containing interrupted genes which can be selected when insert size decreases.
- 4) The use of direct selection techniques with an expression vector and the appropriate selection.

Encoding sequences (for example, genes) from related organisms may demonstrate a high degree of homology and encode quite diverse protein products. These types of sequences are particularly useful in the present invention as quasi-repeats. However, while the examples illustrated below demonstrate the reassortment of nearly identical original encoding sequences (quasi-repeats), this process is not limited to such nearly identical repeats.

The following example demonstrates a method of the invention. Encoding nucleic acid sequences (quasi-repeats) derived from three (3) unique species are described. Each sequence encodes a protein with a distinct set of properties. Each of the sequences differs by a single or a few base pairs at a unique position in the sequence. The quasi-repeated sequences are separately or collectively amplified and ligated into random assemblies such that all possible permutations and combinations are available in the population of ligated molecules. The number of quasi-repeat units can be controlled by

the assembly conditions. The average number of quasi-repeated units in a construct is defined as the repetitive index (RI).

Once formed, the constructs may, or may not be size fractionated on an agarose gel according to published protocols, inserted into a cloning vector and transfected into an appropriate host cell. The cells are then propagated and "reductive reassortment" is effected. The rate of the reductive reassortment process may be stimulated by the introduction of DNA damage if desired. Whether the reduction in RI is mediated by deletion formation between repeated sequences by an "intra-molecular" mechanism, or mediated by recombination-like events through "inter-molecular" mechanisms is immaterial. The end result is a reassortment of the molecules into all possible combinations.

Optionally, the method comprises the additional step of screening the library members of the shuffled pool to identify individual shuffled library members having the ability to bind or otherwise interact, or catalyze a particular reaction (*e.g.*, such as catalytic domain of an enzyme) with a predetermined macromolecule, such as for example a proteinaceous receptor, an oligosaccharide, virion, or other predetermined compound or structure.

The polypeptides that are identified from such libraries can be used for therapeutic, diagnostic, research and related purposes (*e.g.*, catalysts, solutes for increasing osmolarity of an aqueous solution and the like) and/or can be subjected to one or more additional cycles of shuffling and/or selection.

In another aspect, it is envisioned that prior to or during recombination or reassortment, polynucleotides generated by the method of the invention can be subjected to agents or processes which promote the introduction of mutations into the original polynucleotides. The introduction of such mutations would increase the diversity of resulting hybrid polynucleotides and polypeptides encoded therefrom. The agents or processes which promote mutagenesis can include, but are not limited to: (+)-CC-1065, or a synthetic analog such as (+)-CC-1065-(N3-Adenine (*See* Sun and Hurley, (1992); an N-acetylated or deacetylated 4'-fluoro-4-aminobiphenyl adduct capable of inhibiting DNA synthesis (*See*, for example, van de Poll *et al.* (1992))); or a N-acetylated or deacetylated 4-aminobiphenyl adduct capable of inhibiting DNA synthesis (*See* also, van de Poll *et al.* (1992), pp. 751-758); trivalent chromium, a trivalent chromium salt, a polycyclic aromatic hydrocarbon (PAH) DNA adduct capable of inhibiting DNA replication, such as 7-bromomethyl-benz[*a*]anthracene ("BMA"), tris(2,3-dibromopropyl)phosphate ("Tris-

BP”), 1,2-dibromo-3-chloropropane (“DBCP”), 2-bromoacrolein (2BA), benzo[*a*]pyrene-7,8-dihydrodiol-9-10-epoxide (“BPDE”), a platinum(II) halogen salt, N-hydroxy-2-amino-3-methylimidazo[4,5-*f*]-quinoline (“N-hydroxy-IQ”) and N-hydroxy-2-amino-1-methyl-6-phenylimidazo[4,5-*f*]-pyridine (“N-hydroxy-PhIP”). Exemplary means for slowing or halting PCR amplification consist of UV light (+)-CC-1065 and (+)-CC-1065-(N3-Adenine). Particularly encompassed means are DNA adducts or polynucleotides comprising the DNA adducts from the polynucleotides or polynucleotides pool, which can be released or removed by a process including heating the solution comprising the polynucleotides prior to further processing.

In another aspect the invention is directed to a method of producing recombinant proteins having biological activity by treating a sample comprising double-stranded template polynucleotides encoding a wild-type protein under conditions according to the invention which provide for the production of hybrid or re-assorted polynucleotides.

Producing sequence variants

The invention also provides additional methods for making sequence variants of the nucleic acid (e.g., polypeptide, enzyme, protein, e.g. structural or binding protein) sequences of the invention. The invention also provides additional methods for isolating a polypeptide, enzyme, protein, e.g. structural or binding protein, using the nucleic acids and polypeptides of the invention. In one aspect, the invention provides for variants of a polypeptide, enzyme, protein, e.g. structural or binding protein, coding sequence (e.g., a gene, cDNA or message) of the invention, which can be altered by any means, including, e.g., random or stochastic methods, or, non-stochastic, or “directed evolution,” methods, as described above.

The isolated variants may be naturally occurring. Variant can also be created *in vitro*. Variants may be created using genetic engineering techniques such as site directed mutagenesis, random chemical mutagenesis, Exonuclease III deletion procedures, and standard cloning techniques. Alternatively, such variants, fragments, analogs, or derivatives may be created using chemical synthesis or modification procedures. Other methods of making variants are also familiar to those skilled in the art. These include procedures in which nucleic acid sequences obtained from natural isolates are modified to generate nucleic acids which encode polypeptides having characteristics which enhance their value in industrial or laboratory applications. In such procedures, a large number of variant sequences having one or more nucleotide differences with respect

to the sequence obtained from the natural isolate are generated and characterized. These nucleotide differences can result in amino acid changes with respect to the polypeptides encoded by the nucleic acids from the natural isolates.

For example, variants may be created using error prone PCR. In error prone PCR, PCR is performed under conditions where the copying fidelity of the DNA polymerase is low, such that a high rate of point mutations is obtained along the entire length of the PCR product. Error prone PCR is described, e.g., in Leung (1989) Technique 1:11-15) and Caldwell (1992) PCR Methods Applic. 2:28-33. Briefly, in such procedures, nucleic acids to be mutagenized are mixed with PCR primers, reaction buffer, MgCl₂, MnCl₂, Taq polymerase and an appropriate concentration of dNTPs for achieving a high rate of point mutation along the entire length of the PCR product. For example, the reaction may be performed using 20 fmoles of nucleic acid to be mutagenized, 30 pmole of each PCR primer, a reaction buffer comprising 50mM KCl, 10mM Tris HCl (pH 8.3) and 0.01% gelatin, 7mM MgCl₂, 0.5mM MnCl₂, 5 units of Taq polymerase, 0.2mM dGTP, 0.2mM dATP, 1mM dCTP, and 1mM dTTP. PCR may be performed for 30 cycles of 94°C for 1 min, 45°C for 1 min, and 72°C for 1 min. However, it will be appreciated that these parameters may be varied as appropriate. The mutagenized nucleic acids are cloned into an appropriate vector and the activities of the polypeptides encoded by the mutagenized nucleic acids are evaluated.

Variants may also be created using oligonucleotide directed mutagenesis to generate site-specific mutations in any cloned DNA of interest. Oligonucleotide mutagenesis is described, e.g., in Reidhaar-Olson (1988) Science 241:53-57. Briefly, in such procedures a plurality of double stranded oligonucleotides bearing one or more mutations to be introduced into the cloned DNA are synthesized and inserted into the cloned DNA to be mutagenized. Clones containing the mutagenized DNA are recovered and the activities of the polypeptides they encode are assessed.

Another method for generating variants is assembly PCR. Assembly PCR involves the assembly of a PCR product from a mixture of small DNA fragments. A large number of different PCR reactions occur in parallel in the same vial, with the products of one reaction priming the products of another reaction. Assembly PCR is described in, e.g., U.S. Patent No. 5,965,408.

Still another method of generating variants is sexual PCR mutagenesis. In sexual PCR mutagenesis, forced homologous recombination occurs between DNA molecules of different but highly related DNA sequence *in vitro*, as a result of random

fragmentation of the DNA molecule based on sequence homology, followed by fixation of the crossover by primer extension in a PCR reaction. Sexual PCR mutagenesis is described, e.g., in Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751. Briefly, in such procedures a plurality of nucleic acids to be recombined are digested with DNase to generate fragments having an average size of 50-200 nucleotides. Fragments of the desired average size are purified and resuspended in a PCR mixture. PCR is conducted under conditions which facilitate recombination between the nucleic acid fragments. For example, PCR may be performed by resuspending the purified fragments at a concentration of 10-30ng/ μ l in a solution of 0.2mM of each dNTP, 2.2mM $MgCl_2$, 50mM KCL, 10mM Tris HCl, pH 9.0, and 0.1% Triton X-100. 2.5 units of Taq polymerase per 100:1 of reaction mixture is added and PCR is performed using the following regime: 94°C for 60 seconds, 94°C for 30 seconds, 50-55°C for 30 seconds, 72°C for 30 seconds (30-45 times) and 72°C for 5 minutes. However, it will be appreciated that these parameters may be varied as appropriate. In some aspects, oligonucleotides may be included in the PCR reactions. In other aspects, the Klenow fragment of DNA polymerase I may be used in a first set of PCR reactions and Taq polymerase may be used in a subsequent set of PCR reactions. Recombinant sequences are isolated and the activities of the polypeptides they encode are assessed.

Variants may also be created by *in vivo* mutagenesis. In some aspects, random mutations in a sequence of interest are generated by propagating the sequence of interest in a bacterial strain, such as an E. coli strain, which carries mutations in one or more of the DNA repair pathways. Such "mutator" strains have a higher random mutation rate than that of a wild-type parent. Propagating the DNA in one of these strains will eventually generate random mutations within the DNA. Mutator strains suitable for use for *in vivo* mutagenesis are described in PCT Publication No. WO 91/16427, published October 31, 1991, entitled "Methods for Phenotype Creation from Multiple Gene Populations".

Variants may also be generated using cassette mutagenesis. In cassette mutagenesis a small region of a double stranded DNA molecule is replaced with a synthetic oligonucleotide "cassette" that differs from the native sequence. The oligonucleotide often contains completely and/or partially randomized native sequence.

Recursive ensemble mutagenesis may also be used to generate variants. Recursive ensemble mutagenesis is an algorithm for protein engineering (protein mutagenesis) developed to produce diverse populations of phenotypically related mutants

whose members differ in amino acid sequence. This method uses a feedback mechanism to control successive rounds of combinatorial cassette mutagenesis. Recursive ensemble mutagenesis is described, e.g., in Arkin (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815.

In some aspects, variants are created using exponential ensemble mutagenesis. Exponential ensemble mutagenesis is a process for generating combinatorial libraries with a high percentage of unique and functional mutants, wherein small groups of residues are randomized in parallel to identify, at each altered position, amino acids which lead to functional proteins. Exponential ensemble mutagenesis is described, e.g., in Delegrave (1993) *Biotechnology Res.* 11:1548-1552. Random and site-directed mutagenesis are described, e.g., in Arnold (1993) *Current Opinion in Biotechnology* 4:450-455.

In some aspects, the variants are created using shuffling procedures wherein portions of a plurality of nucleic acids which encode distinct polypeptides are fused together to create chimeric nucleic acid sequences which encode chimeric polypeptides as described in U.S. Patent No. 5,965,408, filed July 9, 1996, entitled, "Method of DNA Reassembly by Interrupting Synthesis" and U.S. Patent No. 5,939,250, filed May 22, 1996, entitled, "Production of Enzymes Having Desired Activities by Mutagenesis.

The variants of the polypeptides of the invention may be variants in which one or more of the amino acid residues of the polypeptides of the sequences of the invention are substituted with a conserved or non-conserved amino acid residue (in one aspect a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code.

Conservative substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the following replacements: replacements of an aliphatic amino acid such as Alanine, Valine, Leucine and Isoleucine with another aliphatic amino acid; replacement of a Serine with a Threonine or vice versa; replacement of an acidic residue such as Aspartic acid and Glutamic acid with another acidic residue; replacement of a residue bearing an amide group, such as Asparagine and Glutamine, with another residue bearing an amide group; exchange of a basic residue such as Lysine and Arginine with another basic residue; and replacement of an aromatic residue such as Phenylalanine, Tyrosine with another aromatic residue.

Other variants are those in which one or more of the amino acid residues of a polypeptide of the invention includes a substituent group.

Still other variants are those in which the polypeptide is associated with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol).

Additional variants are those in which additional amino acids are fused to the polypeptide, such as a leader sequence, a secretory sequence, a proprotein sequence or a sequence which facilitates purification, enrichment, or stabilization of the polypeptide.

In some aspects, the fragments, derivatives and analogs retain the same biological function or activity as the polypeptides of the invention. In other aspects, the fragment, derivative, or analog includes a proprotein, such that the fragment, derivative, or analog can be activated by cleavage of the proprotein portion to produce an active polypeptide.

Optimizing codons to achieve high levels of protein expression in host cells

The invention provides methods for modifying polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding nucleic acids to modify codon usage. In one aspect, the invention provides methods for modifying codons in a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, to increase or decrease its expression in a host cell. The invention also provides nucleic acids encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, modified to increase its expression in a host cell, a polypeptide, enzyme, protein, e.g. structural or binding protein, so modified, and methods of making the modified a polypeptide, enzyme, protein, e.g. structural or binding protein. The method comprises identifying a "non-preferred" or a "less preferred" codon in a polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding nucleic acid and replacing one or more of these non-preferred or less preferred codons with a "preferred codon" encoding the same amino acid as the replaced codon and at least one non-preferred or less preferred codon in the nucleic acid has been replaced by a preferred codon encoding the same amino acid. A preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell.

Host cells for expressing the nucleic acids, expression cassettes and vectors of the invention include bacteria, yeast, fungi, plant cells, insect cells and mammalian cells. Thus, the invention provides methods for optimizing codon usage in

all of these cells, codon-altered nucleic acids and polypeptides made by the codon-altered nucleic acids. Exemplary host cells include gram negative bacteria, such as *Escherichia coli*; gram positive bacteria, such as *Streptomyces* sp., *Lactobacillus gasseri*, *Lactococcus lactis*, *Lactococcus cremoris*, *Bacillus subtilis*, *Bacillus cereus*. Exemplary host cells also include eukaryotic organisms, e.g., various yeast, such as *Saccharomyces* sp., including *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, and *Kluyveromyces lactis*, *Hansenula polymorpha*, *Aspergillus niger*, and mammalian cells and cell lines and insect cells and cell lines. Thus, the invention also includes nucleic acids and polypeptides optimized for expression in these organisms and species.

For example, the codons of a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, isolated from a bacterial cell are modified such that the nucleic acid is optimally expressed in a bacterial cell different from the bacteria from which the polypeptide, enzyme, protein, e.g. structural or binding protein was derived, a yeast, a fungi, a plant cell, an insect cell or a mammalian cell. Methods for optimizing codons are well known in the art, see, e.g., U.S. Patent No. 5,795,737; Baca (2000) Int. J. Parasitol. 30:113-118; Hale (1998) Protein Expr. Purif. 12:185-188; Narum (2001) Infect. Immun. 69:7250-7253. See also Narum (2001) Infect. Immun. 69:7250-7253, describing optimizing codons in mouse systems; Outchkourov (2002) Protein Expr. Purif. 24:18-24, describing optimizing codons in yeast; Feng (2000) Biochemistry 39:15399-15409, describing optimizing codons in *E. coli*; Humphreys (2000) Protein Expr. Purif. 20:252-264, describing optimizing codon usage that affects secretion in *E. coli*.

Transgenic non-human animals

The invention provides transgenic non-human animals comprising a nucleic acid, a polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein), an expression cassette or vector or a transfected or transformed cell of the invention. The invention also provides methods of making and using these transgenic non-human animals.

The transgenic non-human animals can be, e.g., goats, rabbits, sheep, pigs (including all swine, hogs and related animals), cows, rats and mice, comprising the nucleic acids of the invention. These animals can be used, e.g., as *in vivo* models to study a polypeptide, enzyme, protein, e.g. structural or binding protein, activity, or, as models to screen for agents that change the polypeptide, enzyme, protein, e.g. structural or binding protein activity *in vivo*. The coding sequences for the polypeptides to be

expressed in the transgenic non-human animals can be designed to be constitutive, or, under the control of tissue-specific, developmental-specific or inducible transcriptional regulatory factors. Transgenic non-human animals can be designed and generated using any method known in the art; see, e.g., U.S. Patent Nos. 6,211,428; 6,187,992; 6,156,952; 6,118,044; 6,111,166; 6,107,541; 5,959,171; 5,922,854; 5,892,070; 5,880,327; 5,891,698; 5,639,940; 5,573,933; 5,387,742; 5,087,571, describing making and using transformed cells and eggs and transgenic mice, rats, rabbits, sheep, pigs and cows. See also, e.g., Pollock (1999) *J. Immunol. Methods* 231:147-157, describing the production of recombinant proteins in the milk of transgenic dairy animals; Baguisi (1999) *Nat. Biotechnol.* 17:456-461, demonstrating the production of transgenic goats. U.S. Patent No. 6,211,428, describes making and using transgenic non-human mammals which express in their brains a nucleic acid construct comprising a DNA sequence. U.S. Patent No. 5,387,742, describes injecting cloned recombinant or synthetic DNA sequences into fertilized mouse eggs, implanting the injected eggs in pseudo-pregnant females, and growing to term transgenic mice. U.S. Patent No. 6,187,992, describes making and using a transgenic mouse.

"Knockout animals" can also be used to practice the methods of the invention. For example, in one aspect, the transgenic or modified animals of the invention comprise a "knockout animal," e.g., a "knockout mouse," engineered not to express an endogenous gene, which is replaced with a gene expressing a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, or, a fusion protein comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention.

Transgenic Plants and Seeds

The invention provides transgenic plants and seeds comprising a nucleic acid, a polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,), an expression cassette or vector or a transfected or transformed cell of the invention. The invention also provides plant products, e.g., oils, seeds, leaves, extracts and the like, comprising a nucleic acid and/or a polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,) of the invention. The transgenic plant can be dicotyledonous (a dicot) or monocotyledonous (a monocot). The invention also provides methods of making and using these transgenic plants and seeds. The transgenic plant or plant cell expressing a polypeptide of the present invention may be constructed in

accordance with any method known in the art. See, for example, U.S. Patent No. 6,309,872.

Nucleic acids and expression constructs of the invention can be introduced into a plant cell by any means. For example, nucleic acids or expression constructs can be introduced into the genome of a desired plant host, or, the nucleic acids or expression constructs can be episomes. Introduction into the genome of a desired plant can be such that the host's a polypeptide, enzyme, protein, e.g. structural or binding protein, production is regulated by endogenous transcriptional or translational control elements. The invention also provides "knockout plants" where insertion of gene sequence by, e.g., homologous recombination, has disrupted the expression of the endogenous gene. Means to generate "knockout" plants are well-known in the art, see, e.g., Strepp (1998) Proc Natl. Acad. Sci. USA 95:4368-4373; Miao (1995) Plant J 7:359-365. See discussion on transgenic plants, below.

The nucleic acids of the invention can be used to confer desired traits on essentially any plant, e.g., on starch-producing plants, such as potato, wheat, rice, barley, and the like. Nucleic acids of the invention can be used to manipulate metabolic pathways of a plant in order to optimize or alter host's expression of polypeptide, enzyme, protein, e.g. structural or binding protein. The can change a polypeptide, enzyme, protein, e.g. structural or binding protein, activity in a plant. Alternatively, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can be used in production of a transgenic plant to produce a compound not naturally produced by that plant. This can lower production costs or create a novel product.

In one aspect, the first step in production of a transgenic plant involves making an expression construct for expression in a plant cell. These techniques are well known in the art. They can include selecting and cloning a promoter, a coding sequence for facilitating efficient binding of ribosomes to mRNA and selecting the appropriate gene terminator sequences. One exemplary constitutive promoter is CaMV35S, from the cauliflower mosaic virus, which generally results in a high degree of expression in plants. Other promoters are more specific and respond to cues in the plant's internal or external environment. An exemplary light-inducible promoter is the promoter from the cab gene, encoding the major chlorophyll a/b binding protein.

In one aspect, the nucleic acid is modified to achieve greater expression in a plant cell. For example, a sequence of the invention is likely to have a higher percentage of A-T nucleotide pairs compared to that seen in a plant, some of which prefer

G-C nucleotide pairs. Therefore, A-T nucleotides in the coding sequence can be substituted with G-C nucleotides without significantly changing the amino acid sequence to enhance production of the gene product in plant cells.

Selectable marker gene can be added to the gene construct in order to identify plant cells or tissues that have successfully integrated the transgene. This may be necessary because achieving incorporation and expression of genes in plant cells is a rare event, occurring in just a few percent of the targeted tissues or cells. Selectable marker genes encode proteins that provide resistance to agents that are normally toxic to plants, such as antibiotics or herbicides. Only plant cells that have integrated the selectable marker gene will survive when grown on a medium containing the appropriate antibiotic or herbicide. As for other inserted genes, marker genes also require promoter and termination sequences for proper function.

In one aspect, making transgenic plants or seeds comprises incorporating sequences of the invention and, optionally, marker genes into a target expression construct (e.g., a plasmid), along with positioning of the promoter and the terminator sequences. This can involve transferring the modified gene into the plant through a suitable method. For example, a construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the constructs can be introduced directly to plant tissue using ballistic methods, such as DNA particle bombardment. For example, see, e.g., Christou (1997) *Plant Mol. Biol.* 35:197-203; Pawlowski (1996) *Mol. Biotechnol.* 6:17-30; Klein (1987) *Nature* 327:70-73; Takumi (1997) *Genes Genet. Syst.* 72:63-69, discussing use of particle bombardment to introduce transgenes into wheat; and Adam (1997) *supra*, for use of particle bombardment to introduce YACs into plant cells. For example, Rinehart (1997) *supra*, used particle bombardment to generate transgenic cotton plants. Apparatus for accelerating particles is described U.S. Pat. No. 5,015,580; and, the commercially available BioRad (Biolistics) PDS-2000 particle acceleration instrument; see also, John, U.S. Patent No. 5,608,148; and Ellis, U.S. Patent No. 5,681,730, describing particle-mediated transformation of gymnosperms.

In one aspect, protoplasts can be immobilized and injected with a nucleic acids, e.g., an expression construct. Although plant regeneration from protoplasts is not easy with cereals, plant regeneration is possible in legumes using somatic embryogenesis from protoplast derived callus. Organized tissues can be transformed with naked DNA using gene gun technique, where DNA is coated on tungsten microprojectiles, shot

1/100th the size of cells, which carry the DNA deep into cells and organelles.

Transformed tissue is then induced to regenerate, usually by somatic embryogenesis. This technique has been successful in several cereal species including maize and rice.

Nucleic acids, e.g., expression constructs, can also be introduced in to plant cells using recombinant viruses. Plant cells can be transformed using viral vectors, such as, e.g., tobacco mosaic virus derived vectors (Rouwendal (1997) *Plant Mol. Biol.* 33:989-999), see Porta (1996) "Use of viral replicons for the expression of genes in plants," *Mol. Biotechnol.* 5:209-221.

Alternatively, nucleic acids, e.g., an expression construct, can be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, e.g., Horsch (1984) *Science* 233:496-498; Fraley (1983) *Proc. Natl. Acad. Sci. USA* 80:4803 (1983); *Gene Transfer to Plants*, Potrykus, ed. (Springer-Verlag, Berlin 1995). The DNA in an *A. tumefaciens* cell is contained in the bacterial chromosome as well as in another structure known as a Ti (tumor-inducing) plasmid. The Ti plasmid contains a stretch of DNA termed T-DNA (~20 kb long) that is transferred to the plant cell in the infection process and a series of vir (virulence) genes that direct the infection process. *A. tumefaciens* can only infect a plant through wounds: when a plant root or stem is wounded it gives off certain chemical signals, in response to which, the vir genes of *A. tumefaciens* become activated and direct a series of events necessary for the transfer of the T-DNA from the Ti plasmid to the plant's chromosome. The T-DNA enters the plant cell through the wound. One speculation is that the T-DNA waits until the plant DNA is being replicated or transcribed, then inserts itself into the exposed plant DNA. In order to use *A. tumefaciens* as a transgene vector, the tumor-inducing section of T-DNA have to be removed, while retaining the T-DNA border regions and the vir genes. The transgene is then inserted between the T-DNA border regions, where it is transferred to the plant cell and becomes integrated into the plant's chromosomes.

The invention provides for the transformation of monocotyledonous plants using the nucleic acids of the invention, including important cereals, see Hiei (1997) *Plant Mol. Biol.* 35:205-218. See also, e.g., Horsch, *Science* (1984) 233:496; Fraley (1983)

Proc. Natl. Acad. Sci USA 80:4803; Thykjaer (1997) *supra*; Park (1996) Plant Mol. Biol. 32:1135-1148, discussing T-DNA integration into genomic DNA. See also D'Halluin, U.S. Patent No. 5,712,135, describing a process for the stable integration of a DNA comprising a gene that is functional in a cell of a cereal, or other monocotyledonous plant.

In one aspect, the third step can involve selection and regeneration of whole plants capable of transmitting the incorporated target gene to the next generation. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker that has been introduced together with the desired nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture, Handbook of Plant Cell Culture*, pp. 124-176, MacMillan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee (1987) Ann. Rev. of Plant Phys. 38:467-486. To obtain whole plants from transgenic tissues such as immature embryos, they can be grown under controlled environmental conditions in a series of media containing nutrients and hormones, a process known as tissue culture. Once whole plants are generated and produce seed, evaluation of the progeny begins.

After the expression cassette is stably incorporated in transgenic plants, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. Since transgenic expression of the nucleic acids of the invention leads to phenotypic changes, plants comprising the recombinant nucleic acids of the invention can be sexually crossed with a second plant to obtain a final product. Thus, the seed of the invention can be derived from a cross between two transgenic plants of the invention, or a cross between a plant of the invention and another plant. The desired effects (e.g., expression of the polypeptides of the invention to produce a plant in which flowering behavior is altered) can be enhanced when both parental plants express the polypeptides (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,) of the invention. The desired effects can be passed to future plant generations by standard propagation means.

The nucleic acids and polypeptides of the invention are expressed in or inserted in any plant or seed. Transgenic plants of the invention can be dicotyledonous or

monocotyledonous. Examples of monocot transgenic plants of the invention are grasses, such as meadow grass (blue grass, *Poa*), forage grass such as *festuca*, *lolium*, temperate grass, such as *Agrostis*, and cereals, e.g., wheat, oats, rye, barley, rice, sorghum, and maize (corn). Examples of dicot transgenic plants of the invention are tobacco, legumes, such as lupins, potato, sugar beet, pea, bean and soybean, and cruciferous plants (family *Brassicaceae*), such as cauliflower, rape seed, and the closely related model organism *Arabidopsis thaliana*. Thus, the transgenic plants and seeds of the invention include a broad range of plants, including, but not limited to, species from the genera *Anacardium*, *Arachis*, *Asparagus*, *Atropa*, *Avena*, *Brassica*, *Citrus*, *Citrullus*, *Capsicum*, *Carthamus*, *Cocos*, *Coffea*, *Cucumis*, *Cucurbita*, *Daucus*, *Elaeis*, *Fragaria*, *Glycine*, *Gossypium*, *Helianthus*, *Heterocallis*, *Hordeum*, *Hyoscyamus*, *Lactuca*, *Linum*, *Lolium*, *Lupinus*, *Lycopersicon*, *Malus*, *Manihot*, *Majorana*, *Medicago*, *Nicotiana*, *Olea*, *Oryza*, *Panicum*, *Pennisetum*, *Persea*, *Phaseolus*, *Pistachia*, *Pisum*, *Pyrus*, *Prunus*, *Raphanus*, *Ricinus*, *Secale*, *Senecio*, *Sinapis*, *Solanum*, *Sorghum*, *Theobromus*, *Trigonella*, *Triticum*, *Vicia*, *Vitis*, *Vigna*, and *Zea*.

In alternative embodiments, the nucleic acids of the invention are expressed in plants which contain fiber cells, including, e.g., cotton, silk cotton tree (Kapok, *Ceiba pentandra*), desert willow, creosote bush, winterfat, balsa, ramie, kenaf, hemp, roselle, jute, sisal abaca and flax. In alternative embodiments, the transgenic plants of the invention can be members of the genus *Gossypium*, including members of any *Gossypium* species, such as *G. arboreum*, *G. herbaceum*, *G. barbadense*, and *G. hirsutum*.

The invention also provides for transgenic plants to be used for producing large amounts of the polypeptides (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, or antibody) of the invention. For example, see Palmgren (1997) Trends Genet. 13:348; Chong (1997) Transgenic Res. 6:289-296 (producing human milk protein beta-casein in transgenic potato plants using an auxin-inducible, bidirectional mannopine synthase (*mas1'*,*2'*) promoter with *Agrobacterium tumefaciens*-mediated leaf disc transformation methods).

Using known procedures, one of skill can screen for plants of the invention by detecting the increase or decrease of transgene mRNA or protein in transgenic plants. Means for detecting and quantitation of mRNAs or proteins are well known in the art.

Polypeptides and peptides

In one aspect, the invention provides isolated or recombinant polypeptides having a sequence identity (e.g., at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity, or homology) to an exemplary sequence of the invention, e.g., proteins having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898). The percent sequence identity can be over the full length of the polypeptide, or, the identity can be over a region of at least about 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700 or more residues.

“Amino acid” or “amino acid sequence” as used herein refer to an oligopeptide, peptide, polypeptide, or protein sequence, or to a fragment, portion, or subunit of any of these and to naturally occurring or synthetic molecules. “Amino acid” or “amino acid sequence” include an oligopeptide, peptide, polypeptide, or protein sequence, or to a fragment, portion, or subunit of any of these, and to naturally occurring or synthetic molecules. The term “polypeptide” as used herein, refers to amino acids joined to each other by peptide bonds or modified peptide bonds, *i.e.*, peptide isosteres and may contain modified amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide may have many types of modifications. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, cross-linking cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation,

pegylation, glucan hydrolase processing, phosphorylation, prenylation, racemization, selenoylation, sulfation and transfer-RNA mediated addition of amino acids to protein such as arginylation. (See Creighton, T.E., *Proteins – Structure and Molecular Properties* 2nd Ed., W.H. Freeman and Company, New York (1993); *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983)). The peptides and polypeptides of the invention also include all “mimetic” and “peptidomimetic” forms, as described in further detail, below.

As used herein, the term “isolated” means that the material is removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition and still be isolated in that such vector or composition is not part of its natural environment. As used herein, the term “purified” does not require absolute purity; rather, it is intended as a relative definition. Individual nucleic acids obtained from a library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The purified nucleic acids of the invention have been purified from the remainder of the genomic DNA in the organism by at least 10^4 - 10^6 fold. However, the term “purified” also includes nucleic acids which have been purified from the remainder of the genomic DNA or from other sequences in a library or other environment by at least one order of magnitude, typically two or three orders and more typically four or five orders of magnitude.

“Recombinant” polypeptides or proteins refer to polypeptides or proteins produced by recombinant DNA techniques; *i.e.*, produced from cells transformed by an exogenous DNA construct encoding the desired polypeptide or protein. “Synthetic” polypeptides or protein are those prepared by chemical synthesis. Solid-phase chemical peptide synthesis methods can also be used to synthesize the polypeptide or fragments of the invention. Such method have been known in the art since the early 1960's (Merrifield, R. B., *J. Am. Chem. Soc.*, 85:2149-2154, 1963) (See also Stewart, J. M. and Young, J. D., *Solid Phase Peptide Synthesis*, 2nd Ed., Pierce Chemical Co., Rockford, Ill., pp. 11-12)) and have recently been employed in commercially available laboratory peptide design and synthesis kits (Cambridge Research Biochemicals). Such commercially available laboratory kits have generally utilized the teachings of H. M. Geysen *et al*, *Proc. Natl. Acad. Sci., USA*, 81:3998

(1984) and provide for synthesizing peptides upon the tips of a multitude of "rods" or "pins" all of which are connected to a single plate.

Polypeptides of the invention can also be shorter than the full length of exemplary polypeptides. In alternative aspects, the invention provides polypeptides (peptides, fragments) ranging in size between about 5 and the full length of a polypeptide, e.g., an enzyme, such as a polypeptide, enzyme, protein, e.g. structural or binding protein,; exemplary sizes being of about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, or more residues, e.g., contiguous residues of an exemplary a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention. Peptides of the invention (e.g., a subsequence of an exemplary polypeptide of the invention) can be useful as, e.g., labeling probes, antigens, toleragens, motifs, a polypeptide, enzyme, protein, e.g. structural or binding protein, active sites (e.g., "catalytic domains"), signal sequences and/or prepro domains.

In alternative aspects, polypeptides of the invention having enzyme, structural or binding activity are members of a genus of polypeptides sharing specific structural elements, e.g., amino acid residues, that correlate with enzyme, structural or binding activity. These shared structural elements can be used for the routine generation of polypeptide, enzyme, protein, e.g. structural or binding protein, variants. These shared structural elements of a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can be used as guidance for the routine generation of a polypeptide, enzyme, protein, e.g. structural or binding protein, variants within the scope of the genus of polypeptides of the invention.

Polypeptides and peptides of the invention can be isolated from natural sources, be synthetic, or be recombinantly generated polypeptides. Peptides and proteins can be recombinantly expressed *in vitro* or *in vivo*. The peptides and polypeptides of the invention can be made and isolated using any method known in the art. Polypeptide and peptides of the invention can also be synthesized, whole or in part, using chemical methods well known in the art. See e.g., Caruthers (1980) Nucleic Acids Res. Symp. Ser. 215-223; Horn (1980) Nucleic Acids Res. Symp. Ser. 225-232; Banga, A.K., Therapeutic Peptides and Proteins, Formulation, Processing and Delivery Systems (1995) Technomic Publishing Co., Lancaster, PA. For example, peptide synthesis can be performed using various solid-phase techniques (see e.g., Roberge (1995) Science 269:202; Merrifield (1997) Methods Enzymol. 289:3-13) and automated synthesis may be achieved, e.g.,

using the ABI 431A Peptide Synthesizer (Perkin Elmer) in accordance with the instructions provided by the manufacturer.

The peptides and polypeptides of the invention can also be glycosylated. The glycosylation can be added post-translationally either chemically or by cellular biosynthetic mechanisms, wherein the later incorporates the use of known glycosylation motifs, which can be native to the sequence or can be added as a peptide or added in the nucleic acid coding sequence. The glycosylation can be O-linked or N-linked.

The peptides and polypeptides of the invention, as defined above, include all "mimetic" and "peptidomimetic" forms. The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound which has substantially the same structural and/or functional characteristics of the polypeptides of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogues of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity. As with polypeptides of the invention which are conservative variants or members of a genus of polypeptides of the invention (e.g., having about 50% or more sequence identity to an exemplary sequence of the invention), routine experimentation will determine whether a mimetic is within the scope of the invention, i.e., that its structure and/or function is not substantially altered. Thus, in one aspect, a mimetic composition is within the scope of the invention if it has a polypeptide, enzyme, protein, e.g. structural or binding protein's activity.

Polypeptide mimetic compositions of the invention can contain any combination of non-natural structural components. In alternative aspect, mimetic compositions of the invention include one or all of the following three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, i.e., to induce or stabilize a secondary structure, e.g., a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. For example, a polypeptide of the invention can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, e.g., glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-

diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, e.g., ketomethylene (e.g., $-C(=O)-CH_2-$ for $-C(=O)-NH-$), aminomethylene (CH_2-NH), ethylene, olefin ($CH=CH$), ether (CH_2-O), thioether (CH_2-S), tetrazole (CN_4), thiazole, retroamide, thioamide, or ester (see, e.g., Spatola (1983) in *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. 7, pp 267-357, "Peptide Backbone Modifications," Marcell Dekker, NY).

A polypeptide of the invention can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues. Non-natural residues are well described in the scientific and patent literature; a few exemplary non-natural compositions useful as mimetics of natural amino acid residues and guidelines are described below. Mimetics of aromatic amino acids can be generated by replacing by, e.g., D- or L- naphylalanine; D- or L- phenylglycine; D- or L- 2 thieneylalanine; D- or L-1, -2, 3-, or 4- pyreneylalanine; D- or L-3 thieneylalanine; D- or L-(2-pyridinyl)-alanine; D- or L-(3-pyridinyl)-alanine; D- or L-(2-pyrazinyl)-alanine; D- or L-(4-isopropyl)-phenylglycine; D-(trifluoromethyl)-phenylglycine; D-(trifluoromethyl)-phenylalanine; D-p-fluoro-phenylalanine; D- or L-p-biphenylphenylalanine; D- or L-p-methoxy-biphenylphenylalanine; D- or L-2-indole(alkyl)alanines; and, D- or L-alkylainines, where alkyl can be substituted or unsubstituted methyl, ethyl, propyl, hexyl, butyl, pentyl, isopropyl, iso-butyl, sec-isotyl, iso-pentyl, or a non-acidic amino acids. Aromatic rings of a non-natural amino acid include, e.g., thiazolyl, thiophenyl, pyrazolyl, benzimidazolyl, naphthyl, furanyl, pyrrolyl, and pyridyl aromatic rings.

Mimetics of acidic amino acids can be generated by substitution by, e.g., non-carboxylate amino acids while maintaining a negative charge; (phosphono)alanine; sulfated threonine. Carboxyl side groups (e.g., aspartyl or glutamyl) can also be selectively modified by reaction with carbodiimides ($R'-N-C-N-R'$) such as, e.g., 1-cyclohexyl-3(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3(4-azonia- 4,4-dimetholpentyl) carbodiimide. Aspartyl or glutamyl can also be converted to asparaginy and glutaminyl residues by reaction with ammonium ions. Mimetics of basic amino acids can be generated by substitution with, e.g., (in addition to lysine and arginine) the amino acids ornithine, citrulline, or (guanidino)-acetic acid, or (guanidino)alkyl-acetic acid, where alkyl is defined above. Nitrile derivative (e.g., containing the CN-moiety in place of COOH) can be substituted for asparagine or glutamine. Asparaginy and glutaminyl

residues can be deaminated to the corresponding aspartyl or glutamyl residues. Arginine residue mimetics can be generated by reacting arginyl with, e.g., one or more conventional reagents, including, e.g., phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, or ninhydrin, in one aspect under alkaline conditions. Tyrosine residue mimetics can be generated by reacting tyrosyl with, e.g., aromatic diazonium compounds or tetranitromethane. N-acetylimidizol and tetranitromethane can be used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Cysteine residue mimetics can be generated by reacting cysteinyl residues with, e.g., alpha-haloacetates such as 2-chloroacetic acid or chloroacetamide and corresponding amines; to give carboxymethyl or carboxyamidomethyl derivatives. Cysteine residue mimetics can also be generated by reacting cysteinyl residues with, e.g., bromo-trifluoroacetone, alpha-bromo-beta-(5-imidazolyl) propionic acid; chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide; methyl 2-pyridyl disulfide; p-chloromercuribenzoate; 2-chloromercuri-4-nitrophenol; or, chloro-7-nitrobenzo-oxa-1,3-diazole. Lysine mimetics can be generated (and amino terminal residues can be altered) by reacting lysinyl with, e.g., succinic or other carboxylic acid anhydrides. Lysine and other alpha-amino-containing residue mimetics can also be generated by reaction with imidoesters, such as methyl picolinimidate, pyridoxal phosphate, pyridoxal, chloroborohydride, trinitrobenzenesulfonic acid, O-methylisourea, 2,4, pentanedione, and transamidase-catalyzed reactions with glyoxylate. Mimetics of methionine can be generated by reaction with, e.g., methionine sulfoxide. Mimetics of proline include, e.g., pipecolic acid, thiazolidine carboxylic acid, 3- or 4- hydroxy proline, dehydropyrolidine, 3- or 4-methylproline, or 3,3,-dimethylproline. Histidine residue mimetics can be generated by reacting histidyl with, e.g., diethylprocarbonate or para-bromophenacyl bromide. Other mimetics include, e.g., those generated by hydroxylation of proline and lysine; phosphorylation of the hydroxyl groups of seryl or threonyl residues; methylation of the alpha-amino groups of lysine, arginine and histidine; acetylation of the N-terminal amine; methylation of main chain amide residues or substitution with N-methyl amino acids; or amidation of C-terminal carboxyl groups.

A residue, e.g., an amino acid, of a polypeptide of the invention can also be replaced by an amino acid (or peptidomimetic residue) of the opposite chirality. Thus, any amino acid naturally occurring in the L-configuration (which can also be referred to as the R or S, depending upon the structure of the chemical entity) can be replaced with the amino acid of the same chemical structural type or a peptidomimetic, but of the

opposite chirality, referred to as the D- amino acid, but also can be referred to as the R- or S- form.

The invention also provides methods for modifying the polypeptides of the invention by either natural processes, such as post-translational processing (e.g., phosphorylation, acylation, etc), or by chemical modification techniques, and the resulting modified polypeptides. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide may have many types of modifications. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, cross-linking cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, and transfer-RNA mediated addition of amino acids to protein such as arginylation. See, e.g., Creighton, T.E., *Proteins – Structure and Molecular Properties* 2nd Ed., W.H. Freeman and Company, New York (1993); *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983).

Solid-phase chemical peptide synthesis methods can also be used to synthesize the polypeptide or fragments of the invention. Such method have been known in the art since the early 1960's (Merrifield, R. B., *J. Am. Chem. Soc.*, 85:2149-2154, 1963) (See also Stewart, J. M. and Young, J. D., *Solid Phase Peptide Synthesis*, 2nd Ed., Pierce Chemical Co., Rockford, Ill., pp. 11-12)) and have recently been employed in commercially available laboratory peptide design and synthesis kits (Cambridge Research Biochemicals). Such commercially available laboratory kits have generally utilized the teachings of H. M. Geysen et al, *Proc. Natl. Acad. Sci., USA*, 81:3998 (1984) and provide for synthesizing peptides upon the tips of a multitude of "rods" or "pins" all of which are connected to a single plate. When such a system is utilized, a plate of rods or pins is inverted and inserted into a second plate of corresponding wells or reservoirs, which contain solutions for attaching or anchoring an appropriate amino acid to the pin's or rod's

tips. By repeating such a process step, i.e., inverting and inserting the rod's and pin's tips into appropriate solutions, amino acids are built into desired peptides. In addition, a number of available Fmoc peptide synthesis systems are available. For example, assembly of a polypeptide or fragment can be carried out on a solid support using an Applied Biosystems, Inc. Model 431A™ automated peptide synthesizer. Such equipment provides ready access to the peptides of the invention, either by direct synthesis or by synthesis of a series of fragments that can be coupled using other known techniques.

The polypeptides of the invention include a polypeptide, enzyme, protein, e.g. structural or binding protein, in an active or inactive form. For example, the polypeptides of the invention include proproteins before "maturation" or processing of prepro sequences, e.g., by a proprotein-processing enzyme, such as a proprotein convertase to generate an "active" mature protein. The polypeptides of the invention include a polypeptide, enzyme, protein, e.g. structural or binding protein, inactive for other reasons, e.g., before "activation" by a post-translational processing event, e.g., an endo- or exo-peptidase or proteinase action, a phosphorylation event, an amidation, a glycosylation or a sulfation, a dimerization event, and the like. The polypeptides of the invention include all active forms, including active subsequences, e.g., catalytic domains or active sites, of the enzyme.

The invention includes immobilized polypeptides, enzymes, proteins, e.g. structural or binding proteins, anti-polypeptides, anti-enzymes, anti-proteins, e.g. anti-structural or anti-binding proteins, antibodies and fragments thereof. The invention provides methods for inhibiting a polypeptide, enzyme, protein, e.g. structural or binding protein, activity, e.g., using dominant negative mutants or anti-polypeptide, anti-enzyme, anti-protein, e.g. anti-structural or anti-binding protein antibodies of the invention. The invention includes heterocomplexes, e.g., fusion proteins, heterodimers, etc., comprising the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention.

Polypeptides of the invention can have an enzyme, structural or binding activity under various conditions, e.g., extremes in pH and/or temperature, oxidizing agents, and the like. The invention provides methods leading to alternative a polypeptide, enzyme, protein, e.g. structural or binding protein, preparations with different catalytic efficiencies and stabilities, e.g., towards temperature, oxidizing agents and changing wash conditions. In one aspect, a polypeptide, enzyme, protein, e.g. structural or binding protein, variants can be produced using techniques of site-directed mutagenesis and/or random mutagenesis. In one aspect, directed evolution can be used to produce a great

variety of a polypeptide, enzyme, protein, e.g. structural or binding protein, variants with alternative specificities and stability.

The proteins of the invention are also useful as research reagents to identify a polypeptide, enzyme, protein, e.g. structural or binding protein, modulators, e.g., activators or inhibitors of a polypeptide, enzyme, protein, e.g. structural or binding protein, activity. Briefly, test samples (compounds, broths, extracts, and the like) are added to a polypeptide, enzyme, protein, e.g. structural or binding protein, assays to determine their ability to inhibit substrate cleavage. Inhibitors identified in this way can be used in industry and research to reduce or prevent undesired proteolysis. As with a polypeptide, enzyme, protein, e.g. structural or binding protein, inhibitors can be combined to increase the spectrum of activity.

The enzymes of the invention are also useful as research reagents to digest proteins or in protein sequencing. For example, the polypeptide, enzyme, protein, e.g. structural or binding proteins may be used to break polypeptides into smaller fragments for sequencing using, e.g. an automated sequencer.

The invention also provides methods of discovering new a polypeptide, enzyme, protein, e.g. structural or binding protein, using the nucleic acids, polypeptides and antibodies of the invention. In one aspect, phagemid libraries are screened for expression-based discovery of a polypeptide, enzyme, protein, e.g. structural or binding protein, . In another aspect, lambda phage libraries are screened for expression-based discovery of a polypeptide, enzyme, protein, e.g. structural or binding protein, . Screening of the phage or phagemid libraries can allow the detection of toxic clones; improved access to substrate; reduced need for engineering a host, by-passing the potential for any bias resulting from mass excision of the library; and, faster growth at low clone densities. Screening of phage or phagemid libraries can be in liquid phase or in solid phase. In one aspect, the invention provides screening in liquid phase. This gives a greater flexibility in assay conditions; additional substrate flexibility; higher sensitivity for weak clones; and ease of automation over solid phase screening.

The invention provides screening methods using the proteins and nucleic acids of the invention and robotic automation to enable the execution of many thousands of biocatalytic reactions and screening assays in a short period of time, e.g., per day, as well as ensuring a high level of accuracy and reproducibility (see discussion of arrays, below). As a result, a library of derivative compounds can be produced in a matter of

weeks. For further teachings on modification of molecules, including small molecules, see PCT/US94/09174.

In one aspect, polypeptides or fragments of the invention may be obtained through biochemical enrichment or purification procedures. The sequence of potentially homologous polypeptides or fragments may be determined by a polypeptide, enzyme, protein, e.g. structural or binding protein, assays, gel electrophoresis and/or microsequencing. The sequence of the prospective polypeptide or fragment of the invention can be compared to an exemplary polypeptide of the invention, or a fragment, e.g., comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof using any of the programs described above.

Another aspect of the invention is an assay for identifying fragments or variants of the invention, which retain the enzymatic function of the polypeptides of the invention. For example the fragments or variants of said polypeptides, may be used to catalyze biochemical reactions (e.g., production of a nootkatone from a valencene), which indicate that the fragment or variant retains the enzymatic activity of a polypeptide of the invention.

An exemplary assay for determining if fragments of variants retain the enzymatic activity of the polypeptides of the invention includes the steps of: contacting the polypeptide fragment or variant with a substrate molecule under conditions which allow the polypeptide fragment or variant to function and detecting either a decrease in the level of substrate or an increase in the level of the specific reaction product of the reaction between the polypeptide and substrate.

The present invention exploits the unique catalytic properties of enzymes. Whereas the use of biocatalysts (i.e., purified or crude enzymes, non-living or living cells) in chemical transformations normally requires the identification of a particular biocatalyst that reacts with a specific starting compound, the present invention uses selected biocatalysts and reaction conditions that are specific for functional groups that are present in many starting compounds, such as small molecules. Each biocatalyst is specific for one functional group, or several related functional groups and can react with many starting compounds containing this functional group.

The biocatalytic reactions produce a population of derivatives from a single starting compound. These derivatives can be subjected to another round of biocatalytic reactions to produce a second population of derivative compounds. Thousands of

variations of the original small molecule or compound can be produced with each iteration of biocatalytic derivatization.

Enzymes react at specific sites of a starting compound without affecting the rest of the molecule, a process which is very difficult to achieve using traditional chemical methods. This high degree of biocatalytic specificity provides the means to identify a single active compound within the library. The library is characterized by the series of biocatalytic reactions used to produce it, a so-called "biosynthetic history". Screening the library for biological activities and tracing the biosynthetic history identifies the specific reaction sequence producing the active compound. The reaction sequence is repeated and the structure of the synthesized compound determined. This mode of identification, unlike other synthesis and screening approaches, does not require immobilization technologies and compounds can be synthesized and tested free in solution using virtually any type of screening assay. It is important to note, that the high degree of specificity of enzyme reactions on functional groups allows for the "tracking" of specific enzymatic reactions that make up the biocatalytically produced library.

Many of the procedural steps are performed using robotic automation enabling the execution of many thousands of biocatalytic reactions and screening assays per day as well as ensuring a high level of accuracy and reproducibility. As a result, a library of derivative compounds can be produced in a matter of weeks, which would take years to produce using current chemical methods.

In a particular aspect, the invention provides a method for modifying small molecules, comprising contacting a polypeptide encoded by a polynucleotide described herein or enzymatically active fragments thereof with a small molecule to produce a modified small molecule. A library of modified small molecules is tested to determine if a modified small molecule is present within the library, which exhibits a desired activity. A specific biocatalytic reaction which produces the modified small molecule of desired activity is identified by systematically eliminating each of the biocatalytic reactions used to produce a portion of the library and then testing the small molecules produced in the portion of the library for the presence or absence of the modified small molecule with the desired activity. The specific biocatalytic reactions which produce the modified small molecule of desired activity is optionally repeated. The biocatalytic reactions are conducted with a group of biocatalysts that react with distinct structural moieties found within the structure of a small molecule, each biocatalyst is specific for one structural

moiety or a group of related structural moieties; and each biocatalyst reacts with many different small molecules which contain the distinct structural moiety.

A polypeptide, enzyme, protein, e.g. structural or binding protein, signal sequences, prepro and catalytic domains

The invention provides a polypeptide, enzyme, protein, e.g. structural or binding protein, signal sequences (e.g., signal peptides (SPs)), prepro domains and catalytic domains (CDs). The SPs, prepro domains and/or CDs of the invention can be isolated or recombinant peptides or can be part of a fusion protein, e.g., as a heterologous domain in a chimeric protein. The invention provides nucleic acids encoding these catalytic domains (CDs), prepro domains and signal sequences (SPs, e.g., a peptide having a sequence comprising/ consisting of amino terminal residues of a polypeptide of the invention).

The invention provides isolated or recombinant signal sequences (e.g., signal peptides) consisting of or comprising a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44, 1 to 45, 1 to 46, or 1 to 47, or more, of a polypeptide of the invention, e.g., SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, and all polypeptides disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:3 through SEQ ID NO:26,898. In one aspect, the invention provides signal sequences comprising the first 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70 or more amino terminal residues of a polypeptide of the invention.

The invention also provides isolated or recombinant signal sequences comprising/ consisting of the signal sequences set forth in Table 4, and polypeptides comprising these signal sequences. The polypeptide can be enzyme or protein of the invention. For example, reading Table 4, the invention provides an isolated or recombinant signal sequence as set forth by residues 1 to 16 of SEQ ID NO:10010. This can be determined by reading the second column for the first row, "Probability: 0.992 AA1: 16 AA2: 17", wherein the cleavage of signal sequence takes place between amino acid 16 (AA16) and amino acid 17 (AA17), with a probability of 0.992 that this is the correct cleavage site. Therefore, the signal sequence is predicted to be from the amino acid in position 1 of SEQ ID NO:10010 up to and including the amino acid in position 16 of SEQ ID NO:10010. This signal sequence, in one aspect, is encoded by a subsequence of SEQ ID NO:10009.

Table 4

| SEQ ID NO: | Signalp Cleavage Site | Predicted Signal Sequence |
|--------------|------------------------------------|---------------------------|
| 10009, 10010 | Probability: 0.992 AA1: 16 AA2: 17 | MKSYFLLLLFLLPLFA |
| 10111, 10112 | Probability: 0.964 AA1: 17 AA2: 18 | MKYIFILVFLTTTLFA |
| 1013, 1014 | Probability: 0.584 AA1: 20 AA2: 21 | MKRVLLAIIIGIILAIIVVVG |
| 10147, 10148 | Probability: 0.999 AA1: 19 AA2: 20 | MNKILIFIIISLFSNLISA |
| 10157, 10158 | Probability: 0.941 AA1: 19 AA2: 20 | MLKRIFILSLAILICSNG |
| 10217, 10218 | Probability: 0.999 AA1: 18 AA2: 19 | MKKISILIIFILSTLTLS |
| 10309, 10310 | Probability: 0.994 AA1: 20 AA2: 21 | MRANLKKSYYLIGLLLLFSLA |
| 10327, 10328 | Probability: 0.647 AA1: 16 AA2: 17 | MRYLFSLFIFTTLIFA |
| 10355, 10356 | Probability: 0.592 AA1: 19 AA2: 20 | MTKKVIVLSLIILLFINSS |
| 10441, 10442 | Probability: 0.683 AA1: 17 AA2: 18 | MKRTFLTITAAAFILVG |
| 10447, 10448 | Probability: 0.928 AA1: 17 AA2: 18 | MKNKLIILFIFSLFLLA |
| 10525, 10526 | Probability: 0.728 AA1: 16 AA2: 17 | MRVLFFIFISLTTLFA |
| 10537, 10538 | Probability: 0.998 AA1: 17 AA2: 18 | MKKIILLSTLLFLALNA |
| 10543, 10544 | Probability: 0.991 AA1: 17 AA2: 18 | MKRKWFIFILTALVTIA |
| 10591, 10592 | Probability: 0.922 AA1: 17 AA2: 18 | MFKLLIGIFISVAYS |
| 10659, 10660 | Probability: 0.967 AA1: 20 AA2: 21 | MKDVIIGAGGAGLSAGLSA |
| 10673, 10674 | Probability: 0.711 AA1: 19 AA2: 20 | MKIWSTIKLVFISLVALVA |
| 10711, 10712 | Probability: 0.876 AA1: 16 AA2: 17 | MMKGISPGAALVFLMA |
| 10731, 10732 | Probability: 0.997 AA1: 19 AA2: 20 | MLKLLMITILLSTSGVANS |
| 1079, 1080 | Probability: 0.929 AA1: 17 AA2: 18 | MRIIKLFALFFLTACN |
| 10915, 10916 | Probability: 0.934 AA1: 17 AA2: 18 | MKSRLLLSGFFIFVLMS |
| 11047, 11048 | Probability: 0.530 AA1: 16 AA2: 17 | MPEAAFSMSLPSKVFA |
| 1109, 1110 | Probability: 0.777 AA1: 18 AA2: 19 | MKVLLYILILFSGFKSFG |
| 1111, 1112 | Probability: 0.765 AA1: 18 AA2: 19 | MKVLLYILILFSGFKSFG |
| 1119, 1120 | Probability: 0.870 AA1: 18 AA2: 19 | MKKLFILCIFFSVESFS |
| 11209, 11210 | Probability: 0.910 AA1: 19 AA2: 20 | MKQIILLFSILFIVGKSYS |
| 11253, 11254 | Probability: 0.987 AA1: 19 AA2: 20 | MKNIFFFSILLFLSFTGKA |
| 11339, 11340 | Probability: 0.510 AA1: 19 AA2: 20 | MLKSISLFILITIVTGCSV |
| 1137, 1138 | Probability: 0.992 AA1: 18 AA2: 19 | MKILTIVFLVGFFCFVQA |
| 11401, 11402 | Probability: 0.992 AA1: 19 AA2: 20 | MTISKNKLLIASLLSVAFT |
| 11495, 11496 | Probability: 0.647 AA1: 16 AA2: 17 | MRYLFSLFIFTTLIFA |

| | | |
|--------------|------------------------------------|------------------------|
| 11719, 11720 | Probability: 0.998 AA1: 17 AA2: 18 | MKIILLIFFLLLSFSFA |
| 11745, 11746 | Probability: 0.972 AA1: 18 AA2: 19 | MKYKIIFFIAAFMAFSTLV |
| 1177, 1178 | Probability: 0.995 AA1: 20 AA2: 21 | MDQKKSLSLLFLIPAVSVIA |
| 11821, 11822 | Probability: 0.663 AA1: 18 AA2: 19 | MSNKSIVSTLIISIFFTA |
| 11827, 11828 | Probability: 0.727 AA1: 19 AA2: 20 | MYVMKILLISILFYCLLA |
| 11935, 11936 | Probability: 1.000 AA1: 20 AA2: 21 | MKKTILIASLFVAAFVIGQA |
| 11965, 11966 | Probability: 0.999 AA1: 19 AA2: 20 | MKKILVLSVLLTVCLISFA |
| 12071, 12072 | Probability: 0.773 AA1: 19 AA2: 20 | MNKELLSFFSIFIALFVGA |
| 12157, 12158 | Probability: 0.983 AA1: 16 AA2: 17 | MRLLLLLSLLVYTVFA |
| 12377, 12378 | Probability: 0.562 AA1: 15 AA2: 16 | MASTTMIVSLIVAVA |
| 12709, 12710 | Probability: 0.993 AA1: 18 AA2: 19 | MNNLKQILAIVMLLSVTA |
| 13005, 13006 | Probability: 0.977 AA1: 20 AA2: 21 | MFLRRLSILILLFVFFTA |
| 13017, 13018 | Probability: 0.995 AA1: 17 AA2: 18 | MFKNIIMSLLLCTFLSA |
| 13139, 13140 | Probability: 0.849 AA1: 17 AA2: 18 | MRVVVLVLFSLHFLFA |
| 13307, 13308 | Probability: 0.995 AA1: 19 AA2: 20 | MKKLILLILGFSTNLIFS |
| 13347, 13348 | Probability: 0.788 AA1: 18 AA2: 19 | MLLILICAVYSVGCALA |
| 1343, 1344 | Probability: 0.708 AA1: 18 AA2: 19 | MKSIIIFSLILFFTACK |
| 13475, 13476 | Probability: 0.998 AA1: 17 AA2: 18 | MKIILLIFFLLLSFSFA |
| 13531, 13532 | Probability: 0.651 AA1: 17 AA2: 18 | MSHLLFSTSVLILLVVS |
| 13543, 13544 | Probability: 0.995 AA1: 19 AA2: 20 | MKFILTTLMMAYLILPGMA |
| 13603, 13604 | Probability: 0.734 AA1: 18 AA2: 19 | MNFKNILYSLLISGCLYG |
| 13607, 13608 | Probability: 0.840 AA1: 19 AA2: 20 | MKKIILSLGVATLLLTNL |
| 13699, 13700 | Probability: 0.544 AA1: 21 AA2: 22 | MMKLHTLISLIFAVLMFIFCM |
| 13711, 13712 | Probability: 0.815 AA1: 20 AA2: 21 | MSNKSIVSTLIISIFFTACT |
| 13719, 13720 | Probability: 1.000 AA1: 20 AA2: 21 | MKLTKIITVFMVFSLSLMA |
| 13777, 13778 | Probability: 0.682 AA1: 19 AA2: 20 | MKSMRTIFISFLIILLQG |
| 13829, 13830 | Probability: 0.940 AA1: 19 AA2: 20 | MKNLGLILLVFLGLISTS |
| 13891, 13892 | Probability: 0.993 AA1: 16 AA2: 17 | MKYFLLLLLIITLNA |
| 13915, 13916 | Probability: 1.000 AA1: 20 AA2: 21 | MKKFFLALFLTSIVTISIAA |
| 13933, 13934 | Probability: 0.962 AA1: 19 AA2: 20 | MFMNKKVYISLITALVNA |
| 14081, 14082 | Probability: 0.918 AA1: 18 AA2: 19 | MTYLFLAIAIGLITAASK |
| 14133, 14134 | Probability: 0.989 AA1: 20 AA2: 21 | MNNLIKILLITLSFSLLS |
| 14197, 14198 | Probability: 0.995 AA1: 18 AA2: 19 | MKKITLILFAIFTALSMS |
| 14267, 14268 | Probability: 0.815 AA1: 20 AA2: 21 | MSNKSIVSTLIISIFFTACT |
| 14369, 14370 | Probability: 0.669 AA1: 17 AA2: 18 | MKKYIIIFCIFSGLYG |
| 14505, 14506 | Probability: 0.951 AA1: 20 AA2: 21 | MIRFGSSSSSILYFFRNTMA |
| 14573, 14574 | Probability: 0.992 AA1: 19 AA2: 20 | MLRWFILLISVIVCLNVNA |
| 1461, 1462 | Probability: 0.908 AA1: 19 AA2: 20 | MKKFLIFCLFLFNKPLIS |
| 14655, 14656 | Probability: 0.773 AA1: 22 AA2: 23 | MAQAVAIISIAFFSVLLSLLFN |
| 14705, 14706 | Probability: 0.599 AA1: 21 AA2: 22 | MGGLIAIILSSRTVAPLGQA |
| 14835, 14836 | Probability: 0.999 AA1: 17 AA2: 18 | MVKKLLFLALAFSISFA |
| 14857, 14858 | Probability: 1.000 AA1: 21 AA2: 22 | MIRQKIVLTMLLFCFSLITVA |
| 14863, 14864 | Probability: 0.990 AA1: 17 AA2: 18 | MRKYFLVLLLFCTSLLS |
| 15045, 15046 | Probability: 0.984 AA1: 21 AA2: 22 | MKNIILSTLAFVLALFFSGCT |
| 15049, 15050 | Probability: 0.845 AA1: 19 AA2: 20 | MNFFIMPFLMFLFIGIFA |
| 15055, 15056 | Probability: 0.669 AA1: 15 AA2: 16 | MKFNLNSFLMSVSLA |
| 15111, 15112 | Probability: 0.835 AA1: 17 AA2: 18 | MIKRLFSIVLSLGLVFN |
| 15135, 15136 | Probability: 0.853 AA1: 15 AA2: 16 | MKYLLALCIFLLLTG |
| 15173, 15174 | Probability: 0.513 AA1: 19 AA2: 20 | MKKLNVAIYIVILSLFS |
| 15179, 15180 | Probability: 0.645 AA1: 16 AA2: 17 | MRYLFSLFIFTTLIFA |
| 15201, 15202 | Probability: 0.883 AA1: 20 AA2: 21 | MKLLGIGSILLQVLLCSVSA |
| 15235, 15236 | Probability: 0.792 AA1: 19 AA2: 20 | MNFKQLFLSVLLILTIVLS |
| 15251, 15252 | Probability: 0.998 AA1: 17 AA2: 18 | MKIILLIFFLLLSFSFA |
| 153, 154 | Probability: 0.824 AA1: 20 AA2: 21 | MIKTIXSLARCIIAFGILNA |
| 15329, 15330 | Probability: 0.557 AA1: 20 AA2: 21 | MKNIIYKILLSLIISILG |

| | | |
|--------------|------------------------------------|-----------------------|
| 1541, 1542 | Probability: 1.000 AA1: 19 AA2: 20 | MKRNSLLLVLLALSFTAA |
| 15473, 15474 | Probability: 0.934 AA1: 19 AA2: 20 | MRGTICSILISFIFLITA |
| 15475, 15476 | Probability: 0.934 AA1: 20 AA2: 21 | MAAGDFFAIFGIFMSLSLLA |
| 15495, 15496 | Probability: 0.645 AA1: 16 AA2: 17 | MRYLFSLFIFTTLIFA |
| 15521, 15522 | Probability: 0.972 AA1: 18 AA2: 19 | MIKVSIVVLLLSYIHA |
| 15585, 15586 | Probability: 0.993 AA1: 16 AA2: 17 | MKLLLLLFLVLLNVNA |
| 15589, 15590 | Probability: 0.967 AA1: 17 AA2: 18 | MNKKILILMILGLAVA |
| 15623, 15624 | Probability: 0.553 AA1: 18 AA2: 19 | MSSRVFLTSFLIIVPLTA |
| 15635, 15636 | Probability: 1.000 AA1: 19 AA2: 20 | MKNILSIALAVLMIGSLHS |
| 15659, 15660 | Probability: 1.000 AA1: 20 AA2: 21 | MYKFITALISLFLTTTHSYA |
| 15697, 15698 | Probability: 0.561 AA1: 18 AA2: 19 | MISIKTAIAIILVIVATN |
| 15765, 15766 | Probability: 0.936 AA1: 18 AA2: 19 | MKFHKSLLLLLLSFIVS |
| 15783, 15784 | Probability: 0.951 AA1: 20 AA2: 21 | MKIAVLGAGISGLGSAYLLS |
| 1585, 1586 | Probability: 0.668 AA1: 19 AA2: 20 | MMFFTSISIXSFXPIXIXLX |
| 15855, 15856 | Probability: 0.677 AA1: 18 AA2: 19 | MKKLKLILGSVLSIVAF |
| 15873, 15874 | Probability: 0.784 AA1: 16 AA2: 17 | MIFFFIFVILFTFSVA |
| 15907, 15908 | Probability: 0.998 AA1: 20 AA2: 21 | MSLKKYIFILTLFISNLFA |
| 15909, 15910 | Probability: 0.935 AA1: 20 AA2: 21 | MKQKLLKITLTLTLLTSAIA |
| 16005, 16006 | Probability: 0.932 AA1: 20 AA2: 21 | MLKNLKNILFFLFFLIFCLN |
| 16015, 16016 | Probability: 0.541 AA1: 16 AA2: 17 | MIIAISALIATTIIA |
| 16171, 16172 | Probability: 0.985 AA1: 20 AA2: 21 | MKLNLGKIFLLIFPIITFA |
| 16175, 16176 | Probability: 0.957 AA1: 17 AA2: 18 | MMKTFIVFCVMSISIFA |
| 16183, 16184 | Probability: 0.999 AA1: 20 AA2: 21 | MKLISKILLILAITSGVLS |
| 16237, 16238 | Probability: 0.792 AA1: 19 AA2: 20 | MNFKQLFLSVLLILTIVLS |
| 16289, 16290 | Probability: 0.995 AA1: 16 AA2: 17 | MRISILLAVVSSIIFA |
| 163, 164 | Probability: 0.860 AA1: 20 AA2: 21 | MQINRLIVLLIMISHKNFA |
| 1633, 1634 | Probability: 0.993 AA1: 19 AA2: 20 | MKIYVILALLIFSSRSIYS |
| 16339, 16340 | Probability: 1.000 AA1: 18 AA2: 19 | MKKLLLIYILLSTITFA |
| 16345, 16346 | Probability: 0.776 AA1: 19 AA2: 20 | MGNIVILVFISLFLIAIT |
| 16373, 16374 | Probability: 0.995 AA1: 16 AA2: 17 | MRISILLAVVSSIIFA |
| 1641, 1642 | Probability: 0.879 AA1: 18 AA2: 19 | MKKFILFLGFFYLISFFA |
| 16455, 16456 | Probability: 0.890 AA1: 19 AA2: 20 | MKKFNKILIIIFISSLFLA |
| 16467, 16468 | Probability: 0.681 AA1: 20 AA2: 21 | MERRFLKKGATILASSAVIA |
| 1647, 1648 | Probability: 0.812 AA1: 20 AA2: 21 | MRLKLSLLILLFSGINGIA |
| 16487, 16488 | Probability: 0.987 AA1: 19 AA2: 20 | MRIFNYLIMSILLSVTLMA |
| 1669, 1670 | Probability: 0.999 AA1: 18 AA2: 19 | MRATFIVLSVLLTSSVMS |
| 16711, 16712 | Probability: 0.626 AA1: 17 AA2: 18 | MFKTILFTFILITNIFS |
| 16747, 16748 | Probability: 0.628 AA1: 19 AA2: 20 | MKNIFFLFIIVLILSNCKN |
| 16825, 16826 | Probability: 0.975 AA1: 18 AA2: 19 | MFKKALLVFYIFLGITMA |
| 16833, 16834 | Probability: 0.857 AA1: 20 AA2: 21 | MNNKTKIFLPILLAMAIVLG |
| 16885, 16886 | Probability: 0.993 AA1: 16 AA2: 17 | MKLLLLLFLVLLNVNA |
| 16967, 16968 | Probability: 0.888 AA1: 20 AA2: 21 | MKPTKLLFGLFILIFTFTTS |
| 17035, 17036 | Probability: 0.977 AA1: 16 AA2: 17 | MMKKYIIALISTFLYA |
| 17065, 17066 | Probability: 0.982 AA1: 17 AA2: 18 | MKHFLLCVLLLGVLDA |
| 171, 172 | Probability: 0.956 AA1: 21 AA2: 22 | MKRIIYIILLFSVAVILSSCT |
| 17157, 17158 | Probability: 0.952 AA1: 16 AA2: 17 | MKILLIVLFISSLFS |
| 17331, 17332 | Probability: 0.981 AA1: 17 AA2: 18 | MLKKLLILTFTTISFA |
| 17347, 17348 | Probability: 0.999 AA1: 16 AA2: 17 | MSKIIILISFLIANA |
| 17353, 17354 | Probability: 0.993 AA1: 20 AA2: 21 | MKLKYLLIIIIITLGQFVIA |
| 17359, 17360 | Probability: 0.932 AA1: 19 AA2: 20 | MKIKHFILLFLFSIALYS |
| 17367, 17368 | Probability: 0.912 AA1: 20 AA2: 21 | MKKSILFLLLTLLIIMGIG |
| 1749, 1750 | Probability: 0.990 AA1: 18 AA2: 19 | MNRIFLIVVLFISSTCFS |
| 17537, 17538 | Probability: 0.999 AA1: 17 AA2: 18 | MKFFFILLILFMFNALS |
| 17547, 17548 | Probability: 0.959 AA1: 19 AA2: 20 | MKNIIITYLFMLMSLFLLS |
| 1771, 1772 | Probability: 0.931 AA1: 20 AA2: 21 | MVMKSILGIVSFLIGLSLIA |

| | | |
|--------------|------------------------------------|----------------------|
| 17751, 17752 | Probability: 0.561 AA1: 18 AA2: 19 | MKYLLILLLVFTGCNNV |
| 17783, 17784 | Probability: 0.987 AA1: 19 AA2: 20 | MTKIKVVGLLVILSIALA |
| 1785, 1786 | Probability: 0.716 AA1: 17 AA2: 18 | MKLLSATFFMVVFSVIS |
| 17915, 17916 | Probability: 0.898 AA1: 17 AA2: 18 | MVKIFLSIILFVNIVFA |
| 18019, 18020 | Probability: 0.993 AA1: 18 AA2: 19 | MKKITFLLILFVTTFSFS |
| 18039, 18040 | Probability: 0.867 AA1: 19 AA2: 20 | MQKVILTLVCIITSFFFQA |
| 18057, 18058 | Probability: 0.874 AA1: 19 AA2: 20 | MRFLFVLFTFLIFSCSKNS |
| 18131, 18132 | Probability: 1.000 AA1: 19 AA2: 20 | MKKTQIILLILLSMASHA |
| 18237, 18238 | Probability: 0.975 AA1: 18 AA2: 19 | MKKVLIFYCVLFSLQGFS |
| 18249, 18250 | Probability: 0.719 AA1: 18 AA2: 19 | MKTKTLLTVLTILFSLQS |
| 18329, 18330 | Probability: 0.988 AA1: 17 AA2: 18 | MSKLAVLFLFLACNN |
| 18377, 18378 | Probability: 0.983 AA1: 18 AA2: 19 | MKKARIILSFFIGMVAA |
| 18403, 18404 | Probability: 1.000 AA1: 19 AA2: 20 | MKKTILVLICLFSISALFA |
| 18435, 18436 | Probability: 0.611 AA1: 19 AA2: 20 | MKIGFILILSIAICTSCKV |
| 18489, 18490 | Probability: 0.914 AA1: 17 AA2: 18 | MKKLTYLFLSITLLSFG |
| 18495, 18496 | Probability: 0.627 AA1: 19 AA2: 20 | MKNSIAFLFLSLLIFTGCK |
| 18507, 18508 | Probability: 0.783 AA1: 20 AA2: 21 | MKKIYLILASTIVLASCNGK |
| 1851, 1852 | Probability: 0.998 AA1: 18 AA2: 19 | MKKFLAIFLFFIAFHGNA |
| 18529, 18530 | Probability: 0.999 AA1: 19 AA2: 20 | MKKNTILLFGIVLVFAAYG |
| 18587, 18588 | Probability: 0.956 AA1: 19 AA2: 20 | MSFFKPSFVLFFCLLGLHG |
| 18607, 18608 | Probability: 0.636 AA1: 18 AA2: 19 | MHGLHSIFSLLFLCTLSA |
| 18713, 18714 | Probability: 1.000 AA1: 18 AA2: 19 | MKKTLLFLFLSTLVVQA |
| 18747, 18748 | Probability: 0.985 AA1: 18 AA2: 19 | MKKIYIFVILLSVSVSG |
| 18825, 18826 | Probability: 0.999 AA1: 18 AA2: 19 | MKFILLAFFTLISNYALS |
| 18841, 18842 | Probability: 1.000 AA1: 19 AA2: 20 | MLKSAIFVLVLSLVGSAFG |
| 18919, 18920 | Probability: 0.995 AA1: 20 AA2: 21 | MHIFLKSFILFIFLSFILQA |
| 18921, 18922 | Probability: 0.998 AA1: 18 AA2: 19 | MKNLIVLIFVVLTLQLSVA |
| 18957, 18958 | Probability: 0.719 AA1: 18 AA2: 19 | MKTKTLLTVLTILFSLQS |
| 18971, 18972 | Probability: 0.775 AA1: 17 AA2: 18 | MKKLIALFFLCILISCN |
| 18977, 18978 | Probability: 1.000 AA1: 17 AA2: 18 | MKKLFLILMLPFSLLA |
| 19079, 19080 | Probability: 0.895 AA1: 19 AA2: 20 | MKFFSALLILTLVITSCKS |
| 19143, 19144 | Probability: 0.610 AA1: 18 AA2: 19 | MKKNQLSFLLLVFLISNT |
| 1919, 1920 | Probability: 0.996 AA1: 19 AA2: 20 | MKTLIFFLILFFGSIPSYS |
| 19211, 19212 | Probability: 0.517 AA1: 19 AA2: 20 | MFNKKQAITLFSGLLFCFT |
| 19265, 19266 | Probability: 1.000 AA1: 19 AA2: 20 | MKKTILVLICLFSISALFA |
| 19277, 19278 | Probability: 0.945 AA1: 19 AA2: 20 | MKFTSYLFFLFFIFMNCTA |
| 19385, 19386 | Probability: 0.835 AA1: 18 AA2: 19 | MKKIIPYILSCMLLSLAA |
| 19391, 19392 | Probability: 0.999 AA1: 19 AA2: 20 | MKSFLTILFSLFLTGSINS |
| 19421, 19422 | Probability: 0.998 AA1: 20 AA2: 21 | MRKHQLLILILMLTSVSNS |
| 19467, 19468 | Probability: 0.994 AA1: 20 AA2: 21 | MSNYLLSVILLAFILASCST |
| 19475, 19476 | Probability: 0.998 AA1: 19 AA2: 20 | MKIRFYLSALFACLLFASS |
| 19527, 19528 | Probability: 0.998 AA1: 17 AA2: 18 | MKKILLLLPLISILSYA |
| 19535, 19536 | Probability: 0.596 AA1: 20 AA2: 21 | MKSIKKLFIFILVLYL |
| 1955, 1956 | Probability: 1.000 AA1: 19 AA2: 20 | MRKIYGLLAFCLLMNTAKA |
| 19563, 19564 | Probability: 0.940 AA1: 20 AA2: 21 | MKNSIAFLFLSLLIFTGCKS |
| 19657, 19658 | Probability: 0.994 AA1: 20 AA2: 21 | MIAKKITLLILFVNQYVIA |
| 19733, 19734 | Probability: 0.938 AA1: 20 AA2: 21 | MNITHGSGYVGLVSGTCFA |
| 19785, 19786 | Probability: 0.936 AA1: 19 AA2: 20 | MRTLSFLIVTFSVLISGCA |
| 19797, 19798 | Probability: 1.000 AA1: 18 AA2: 19 | MKTALFILFCTLGQMSLA |
| 19915, 19916 | Probability: 0.999 AA1: 17 AA2: 18 | MKKLLILLFLFNSNLFA |
| 19919, 19920 | Probability: 0.676 AA1: 20 AA2: 21 | MRISVFFYISLFIISSTKFS |
| 19953, 19954 | Probability: 1.000 AA1: 19 AA2: 20 | MKKFLLLFLVPLLAISGFA |
| 19993, 19994 | Probability: 0.575 AA1: 20 AA2: 21 | MRTTLKRIAFLFFFSFLIFS |
| 20001, 20002 | Probability: 0.674 AA1: 18 AA2: 19 | MKKIIFLLVTLIIFNSCK |
| 2003, 2004 | Probability: 1.000 AA1: 18 AA2: 19 | MKVRYLLAFLIISASLA |

| | | |
|--------------|------------------------------------|----------------------|
| 20069, 20070 | Probability: 1.000 AA1: 20 AA2: 21 | MKIKIRCLLIFLTLSPFVQA |
| 20083, 20084 | Probability: 0.637 AA1: 20 AA2: 21 | MILGLLLALIAIVFLFLK |
| 20111, 20112 | Probability: 1.000 AA1: 19 AA2: 20 | MRKILFTCFLLILSLFSYA |
| 20143, 20144 | Probability: 0.946 AA1: 17 AA2: 18 | MKKFIFSVLTLVLVGLS |
| 20161, 20162 | Probability: 0.602 AA1: 19 AA2: 20 | MKSIYMAALILSVKGTS |
| 20187, 20188 | Probability: 0.585 AA1: 20 AA2: 21 | MKPMRNLLFLVLIANTSLL |
| 20225, 20226 | Probability: 1.000 AA1: 20 AA2: 21 | MLQKTILVLLFLLTTSNSFS |
| 20229, 20230 | Probability: 0.522 AA1: 20 AA2: 21 | MKFIINPILILLAVIILSLN |
| 20253, 20254 | Probability: 0.906 AA1: 20 AA2: 21 | MKTILRLTICGLILLNASLA |
| 203, 204 | Probability: 0.824 AA1: 19 AA2: 20 | MENKMKRLLTIFVFLIVFS |
| 20301, 20302 | Probability: 0.675 AA1: 19 AA2: 20 | MIRIISFLLPLLFFLNCQK |
| 20309, 20310 | Probability: 0.989 AA1: 19 AA2: 20 | MKMKFTFLLLIISTISIYG |
| 20349, 20350 | Probability: 0.967 AA1: 19 AA2: 20 | MKKHLLFFLTILSISGYS |
| 20371, 20372 | Probability: 0.605 AA1: 18 AA2: 19 | MNKLISIVLVCITLMSTG |
| 2045, 2046 | Probability: 0.906 AA1: 20 AA2: 21 | MKKHLFITALLMLTVINYTG |
| 20485, 20486 | Probability: 0.951 AA1: 17 AA2: 18 | MKNLFLFLTILSLSCMQ |
| 20487, 20488 | Probability: 0.951 AA1: 17 AA2: 18 | MKNLFLFLTILSLSCMQ |
| 20531, 20532 | Probability: 0.895 AA1: 19 AA2: 20 | MFSFLGVILIAFFGFIGFS |
| 20569, 20570 | Probability: 0.819 AA1: 19 AA2: 20 | MKILLRISLLITTISCTS |
| 20571, 20572 | Probability: 0.819 AA1: 19 AA2: 20 | MKILLRISLLITTISCTS |
| 20665, 20666 | Probability: 0.989 AA1: 18 AA2: 19 | MRKKIFLVLIILMSLSLG |
| 2071, 2072 | Probability: 0.994 AA1: 19 AA2: 20 | MKKIVSILVFVLLANLSQA |
| 20735, 20736 | Probability: 1.000 AA1: 18 AA2: 19 | MKLFVTLVSVLFFCVFATA |
| 20743, 20744 | Probability: 0.998 AA1: 19 AA2: 20 | MKNVIVLFSVAMAFSCFS |
| 20805, 20806 | Probability: 0.962 AA1: 19 AA2: 20 | MMLKKSILLSIAALFISSA |
| 20881, 20882 | Probability: 0.574 AA1: 18 AA2: 19 | MRVFILISLFFTLFSCQ |
| 2093, 2094 | Probability: 0.641 AA1: 18 AA2: 19 | MNFIIFCFVLLSGFLTG |
| 21115, 21116 | Probability: 0.990 AA1: 19 AA2: 20 | MMKLYLFVFFFVIVAAGYA |
| 21121, 21122 | Probability: 0.680 AA1: 17 AA2: 18 | MKPIYLIFSLLTFISLS |
| 21133, 21134 | Probability: 0.998 AA1: 19 AA2: 20 | MKRTLVMVFLMTISQIQA |
| 2115, 2116 | Probability: 0.699 AA1: 20 AA2: 21 | MKRHNIIYFAAILFACNGNT |
| 2117, 2118 | Probability: 0.999 AA1: 19 AA2: 20 | MNKLFLSIVLILTCCQLSA |
| 21307, 21308 | Probability: 0.814 AA1: 16 AA2: 17 | MRKIILSILGVLFIIA |
| 21361, 21362 | Probability: 0.856 AA1: 19 AA2: 20 | MKKSLFFFTIIFCILFLSQ |
| 21363, 21364 | Probability: 0.856 AA1: 19 AA2: 20 | MKKSLFFFTIIFCILFLSQ |
| 21395, 21396 | Probability: 0.698 AA1: 19 AA2: 20 | MMKRVIVGLSGGVDSSVAA |
| 21427, 21428 | Probability: 0.971 AA1: 19 AA2: 20 | MRNSVILSLIFVMISNQLS |
| 21563, 21564 | Probability: 0.984 AA1: 18 AA2: 19 | MIRLITILLIISTNIYS |
| 21595, 21596 | Probability: 0.871 AA1: 18 AA2: 19 | MNYSKLVAIFFIAMLSA |
| 21755, 21756 | Probability: 0.998 AA1: 18 AA2: 19 | MKNILLTIALSFVNLFA |
| 21773, 21774 | Probability: 0.895 AA1: 19 AA2: 20 | MKKKKKKKNXSGVSLSFDSA |
| 21777, 21778 | Probability: 0.845 AA1: 19 AA2: 20 | MKYFVFFFSIILCSCSSSE |
| 21845, 21846 | Probability: 0.940 AA1: 19 AA2: 20 | MKMILHTLFILLISIPLYA |
| 21851, 21852 | Probability: 0.976 AA1: 18 AA2: 19 | MKKFFKFLGILLVVLIVA |
| 21863, 21864 | Probability: 0.818 AA1: 16 AA2: 17 | MKALFFIIFVAIAVA |
| 21939, 21940 | Probability: 0.993 AA1: 18 AA2: 19 | MKGIFYLLLFVSALSFS |
| 21987, 21988 | Probability: 0.875 AA1: 16 AA2: 17 | MKKIMVLGILIVVFM |
| 22293, 22294 | Probability: 0.615 AA1: 20 AA2: 21 | MRKSFKILFSILGILLLL |
| 22337, 22338 | Probability: 1.000 AA1: 19 AA2: 20 | MKKIITLVALVFFSVSTFA |
| 22363, 22364 | Probability: 0.997 AA1: 18 AA2: 19 | MKRLIMVIFLFLGVQSI |
| 22455, 22456 | Probability: 1.000 AA1: 18 AA2: 19 | MKTVLLLLSILVSSYSLA |
| 22467, 22468 | Probability: 0.546 AA1: 17 AA2: 18 | MARMRISVLFFMFCVFA |
| 22491, 22492 | Probability: 1.000 AA1: 18 AA2: 19 | MKKKFLLLLLVTSATFA |
| 22509, 22510 | Probability: 1.000 AA1: 18 AA2: 19 | MKKTLFFIALLTFNSNA |
| 22513, 22514 | Probability: 0.542 AA1: 13 AA2: 14 | MKKILTGVILTLA |

| | | |
|--------------|------------------------------------|-----------------------|
| 22657, 22658 | Probability: 1.000 AA1: 19 AA2: 20 | MTKNLILLILVLIFNIGFA |
| 22701, 22702 | Probability: 0.970 AA1: 17 AA2: 18 | MKKHALLVLVSLFSCG |
| 22703, 22704 | Probability: 0.984 AA1: 16 AA2: 17 | MIYKKIVFLVTLLAFA |
| 22767, 22768 | Probability: 0.988 AA1: 14 AA2: 15 | MRLILLFTLCLAMA |
| 22803, 22804 | Probability: 0.575 AA1: 19 AA2: 20 | MKKTTLIAIFLLIGLKIN |
| 2281, 2282 | Probability: 0.999 AA1: 18 AA2: 19 | MKLFISLSLLFISIFVIA |
| 22817, 22818 | Probability: 0.934 AA1: 18 AA2: 19 | MKKSIISAIVLGFSLVLS |
| 22903, 22904 | Probability: 0.996 AA1: 20 AA2: 21 | MKKLFTLLIMSLVSSCTDA |
| 22953, 22954 | Probability: 0.593 AA1: 18 AA2: 19 | MTKILMVCLGNICRSPLA |
| 22993, 22994 | Probability: 1.000 AA1: 19 AA2: 20 | MKNLVLSLFLAISISAFS |
| 23055, 23056 | Probability: 0.757 AA1: 18 AA2: 19 | MKSIKFILVLFITVSIFS |
| 23107, 23108 | Probability: 0.782 AA1: 18 AA2: 19 | MKKLFITFTLLLLIACK |
| 23167, 23168 | Probability: 0.816 AA1: 18 AA2: 19 | MKKFLLIVCIGLLMFSFT |
| 23175, 23176 | Probability: 0.631 AA1: 18 AA2: 19 | MNRLLLIFSIFLISCYN |
| 2321, 2322 | Probability: 1.000 AA1: 20 AA2: 21 | MFRKTILGGLAIIAALTINA |
| 23253, 23254 | Probability: 0.930 AA1: 19 AA2: 20 | MKKIIFVLLIVLLFASCSK |
| 23277, 23278 | Probability: 0.814 AA1: 16 AA2: 17 | MRKIILSILGVLFIIA |
| 23279, 23280 | Probability: 0.771 AA1: 18 AA2: 19 | MKQYLVITFLLSLTLGFS |
| 23323, 23324 | Probability: 0.536 AA1: 19 AA2: 20 | MKYYSILITVLITCNNHS |
| 23339, 23340 | Probability: 0.821 AA1: 18 AA2: 19 | MMKKISLLILIIIGSCQT |
| 2339, 2340 | Probability: 1.000 AA1: 18 AA2: 19 | MKKIFLSFCLLSSFIGFA |
| 23415, 23416 | Probability: 0.882 AA1: 19 AA2: 20 | MIKSIYLLFLIFSLTIIA |
| 23431, 23432 | Probability: 0.926 AA1: 16 AA2: 17 | MKNTILLSVILLLLFS |
| 23549, 23550 | Probability: 0.516 AA1: 17 AA2: 18 | MNKLAVILLVVIVAFLS |
| 23559, 23560 | Probability: 0.998 AA1: 20 AA2: 21 | MKKLFCILSILIFGCGSTS |
| 23587, 23588 | Probability: 0.862 AA1: 18 AA2: 19 | MKKICFLFFCFMITYIavg |
| 23631, 23632 | Probability: 0.676 AA1: 18 AA2: 19 | MKKLAVLIVLVCTILSCN |
| 23635, 23636 | Probability: 0.886 AA1: 16 AA2: 17 | MKKIAVVFLLLIVVIS |
| 23649, 23650 | Probability: 0.993 AA1: 16 AA2: 17 | MKKILTSLFFLLVLTA |
| 23723, 23724 | Probability: 0.996 AA1: 18 AA2: 19 | MKLLKKILFALVILLAIA |
| 23817, 23818 | Probability: 0.635 AA1: 19 AA2: 20 | MIMNKRISISVLLIAMMALL |
| 23827, 23828 | Probability: 0.871 AA1: 17 AA2: 18 | MKNYILTTAALLAFLFT |
| 23841, 23842 | Probability: 0.647 AA1: 19 AA2: 20 | MKKYFLIFMISALYSCGSA |
| 23851, 23852 | Probability: 0.861 AA1: 18 AA2: 19 | MKKIITFLLLTIVLVSCG |
| 23879, 23880 | Probability: 0.710 AA1: 19 AA2: 20 | MKEILSFILFTSVAINIIA |
| 23913, 23914 | Probability: 1.000 AA1: 19 AA2: 20 | MKKSIIVIVLIFGFSVNA |
| 23937, 23938 | Probability: 0.997 AA1: 19 AA2: 20 | MKKTILLITCLLSIFSIS |
| 23941, 23942 | Probability: 0.988 AA1: 17 AA2: 18 | MKYIYLCLFLFSSFTFS |
| 23967, 23968 | Probability: 0.991 AA1: 19 AA2: 20 | MKKFLITLVLPFFGIAQT |
| 24023, 24024 | Probability: 0.572 AA1: 20 AA2: 21 | MNKYFIILIFICFDSGSQN |
| 24063, 24064 | Probability: 1.000 AA1: 17 AA2: 18 | MKKILFLLLISSTVSA |
| 2411, 2412 | Probability: 1.000 AA1: 21 AA2: 22 | MKKIVVLLALITAMVPAGVFA |
| 24141, 24142 | Probability: 0.985 AA1: 20 AA2: 21 | MNMMKGFLLFFLFSVHILSA |
| 2415, 2416 | Probability: 0.907 AA1: 20 AA2: 21 | MIMNQRIKKIVGIMLLSVVA |
| 24159, 24160 | Probability: 0.994 AA1: 20 AA2: 21 | MNKIKYFLLTITFLSLSACT |
| 24161, 24162 | Probability: 0.578 AA1: 20 AA2: 21 | MNKFLQRISFTLLSCILLG |
| 24267, 24268 | Probability: 0.993 AA1: 20 AA2: 21 | MKQLLALALLVLCACKSTK |
| 2429, 2430 | Probability: 0.925 AA1: 18 AA2: 19 | MKYCLILFSIVNSLFTNA |
| 24317, 24318 | Probability: 0.592 AA1: 21 AA2: 22 | MLFIAPLVFYILLTGTNNFA |
| 2435, 2436 | Probability: 0.594 AA1: 20 AA2: 21 | MKKKINYIAFIILLICSVPA |
| 24359, 24360 | Probability: 0.943 AA1: 18 AA2: 19 | MKKLIHLALILISVSFS |
| 24367, 24368 | Probability: 0.968 AA1: 20 AA2: 21 | MNMKILLSILSLFLLFNCVN |
| 24397, 24398 | Probability: 1.000 AA1: 20 AA2: 21 | MKLKIVLLILFVSITTLVNA |
| 24469, 24470 | Probability: 0.998 AA1: 18 AA2: 19 | MKKILLIAIFLWSWVSTA |
| 24473, 24474 | Probability: 0.996 AA1: 18 AA2: 19 | MKLLKKILFALVILLAIA |

| | | |
|--------------|------------------------------------|-----------------------|
| 24525, 24526 | Probability: 0.992 AA1: 19 AA2: 20 | MNRIKPFLLILLFLTSLTYS |
| 24535, 24536 | Probability: 1.000 AA1: 18 AA2: 19 | MKKLILICALLISVFSTA |
| 24579, 24580 | Probability: 0.998 AA1: 19 AA2: 20 | MRKNMLIIIFVFLTITISFG |
| 24607, 24608 | Probability: 0.998 AA1: 19 AA2: 20 | MKNVLFILIMTFGILSCNA |
| 24633, 24634 | Probability: 0.537 AA1: 19 AA2: 20 | MKLKKYIALMLFCLFIGFV |
| 24655, 24656 | Probability: 1.000 AA1: 21 AA2: 22 | MKKLSPALLILLFLIPNFLQA |
| 24707, 24708 | Probability: 0.704 AA1: 18 AA2: 19 | MKLTTHIILIPFXCFÄ |
| 24719, 24720 | Probability: 0.989 AA1: 19 AA2: 20 | MNKRHISILMLAMTALLSG |
| 24821, 24822 | Probability: 0.945 AA1: 19 AA2: 20 | MQKILLIIVMFVFTIKVYS |
| 24823, 24824 | Probability: 0.975 AA1: 18 AA2: 19 | MKNSITFFILLTIIVSA |
| 24853, 24854 | Probability: 1.000 AA1: 21 AA2: 22 | MRVFFINCLMVFLSSCTSYA |
| 24879, 24880 | Probability: 0.996 AA1: 18 AA2: 19 | MNRLIILILIFFSQISIA |
| 25057, 25058 | Probability: 0.548 AA1: 20 AA2: 21 | MTFHLKPILVFALLFMSCNT |
| 25085, 25086 | Probability: 0.900 AA1: 19 AA2: 20 | MQKKLYFSSLLFFLIVSFT |
| 25115, 25116 | Probability: 0.748 AA1: 18 AA2: 19 | MKNSILIFTTLFSFICGT |
| 25169, 25170 | Probability: 0.703 AA1: 19 AA2: 20 | MKTLKQLLFITAFALLSFT |
| 25203, 25204 | Probability: 0.505 AA1: 18 AA2: 19 | MRLTFIFTLLIIGQFSYG |
| 25225, 25226 | Probability: 0.998 AA1: 19 AA2: 20 | MSKTIFLFLITTVLSAQN |
| 25299, 25300 | Probability: 0.513 AA1: 17 AA2: 18 | MKKFLVGSCFSITMLMG |
| 25307, 25308 | Probability: 1.000 AA1: 19 AA2: 20 | MKKHIITLLVLVFSFSAIA |
| 25311, 25312 | Probability: 0.999 AA1: 20 AA2: 21 | MKKSITIIILLVFVATQSFA |
| 25355, 25356 | Probability: 0.751 AA1: 16 AA2: 17 | MKKIFLLLIIVFVSCS |
| 25361, 25362 | Probability: 0.708 AA1: 18 AA2: 19 | MNRLIILLIFSIFLISCYN |
| 25395, 25396 | Probability: 0.982 AA1: 18 AA2: 19 | MKSCFVLIILLCSSFCIS |
| 25449, 25450 | Probability: 0.969 AA1: 19 AA2: 20 | MKKLAVLIVLVCTILSCNE |
| 25563, 25564 | Probability: 0.960 AA1: 19 AA2: 20 | MKPIFSFFICMSICTTIFS |
| 25571, 25572 | Probability: 0.997 AA1: 20 AA2: 21 | MHSRYFIILLVLFTINSFS |
| 25615, 25616 | Probability: 0.955 AA1: 20 AA2: 21 | MMSVVLGLIASVITQYVAS |
| 25621, 25622 | Probability: 0.511 AA1: 21 AA2: 22 | MIKNRPRKTYTILSLLVASYS |
| 2571, 2572 | Probability: 0.871 AA1: 20 AA2: 21 | MKKLKLTLSSLAFSTVPV |
| 25761, 25762 | Probability: 0.989 AA1: 19 AA2: 20 | MNKRHISILMLAMTALLSG |
| 25797, 25798 | Probability: 0.999 AA1: 18 AA2: 19 | MKNLILILALSIGFNAFS |
| 25833, 25834 | Probability: 0.998 AA1: 18 AA2: 19 | MKKITLLILFTSIISFS |
| 25865, 25866 | Probability: 0.745 AA1: 15 AA2: 16 | MKKIIIALATTLVFG |
| 25867, 25868 | Probability: 0.949 AA1: 18 AA2: 19 | MKKTIVILLIFISCSSTK |
| 25899, 25900 | Probability: 1.000 AA1: 19 AA2: 20 | MKKIITLVALVFFSVSTFA |
| 25985, 25986 | Probability: 0.776 AA1: 20 AA2: 21 | MNFKASLFFVVTIFSIGLMS |
| 26069, 26070 | Probability: 0.730 AA1: 18 AA2: 19 | MKKNIYRIFLTILSIALA |
| 26081, 26082 | Probability: 1.000 AA1: 18 AA2: 19 | MKNLFFTAIFLFCPLALA |
| 26085, 26086 | Probability: 0.980 AA1: 17 AA2: 18 | MKWSFLILFVLSFPSSA |
| 26127, 26128 | Probability: 0.985 AA1: 17 AA2: 18 | MKRNLAILLILTTVLS |
| 26133, 26134 | Probability: 0.846 AA1: 20 AA2: 21 | MPMKNASFLIVLLFFSACK |
| 26249, 26250 | Probability: 0.999 AA1: 17 AA2: 18 | MKQILILFSLLYFSAQA |
| 26305, 26306 | Probability: 0.998 AA1: 18 AA2: 19 | MASGLLVFLALHPTQSNA |
| 26341, 26342 | Probability: 0.629 AA1: 20 AA2: 21 | MKKSNSIYYLLSLTLFFSS |
| 26431, 26432 | Probability: 0.663 AA1: 18 AA2: 19 | MNIVILFFLSFLALVLS |
| 26445, 26446 | Probability: 0.527 AA1: 13 AA2: 14 | MKTKSLSFFMAHN |
| 26489, 26490 | Probability: 0.999 AA1: 20 AA2: 21 | MKRTFSMSIILILALSFFNA |
| 26595, 26596 | Probability: 0.979 AA1: 19 AA2: 20 | MKYLLFILLVGLSTTFGFS |
| 26609, 26610 | Probability: 0.997 AA1: 20 AA2: 21 | MHSRYFIILLVLFTINSFS |
| 26625, 26626 | Probability: 0.901 AA1: 20 AA2: 21 | MKRSTLSLFLVITLSLFQIG |
| 26627, 26628 | Probability: 0.998 AA1: 19 AA2: 20 | MNKYIPLMLVLFANLSFS |
| 26675, 26676 | Probability: 0.939 AA1: 17 AA2: 18 | MKKLLICMSALAIVACK |
| 26681, 26682 | Probability: 0.715 AA1: 18 AA2: 19 | MKRTVILTIVFLPLILIG |
| 26719, 26720 | Probability: 0.996 AA1: 18 AA2: 19 | MNKFILLIGLCVCSNIFS |

| | | |
|--------------|------------------------------------|-----------------------|
| 26747, 26748 | Probability: 0.689 AA1: 18 AA2: 19 | MIKVFKLVVALLCLACK |
| 2675, 2676 | Probability: 1.000 AA1: 18 AA2: 19 | MKKTMSLLFFVSAIAFS |
| 2683, 2684 | Probability: 0.939 AA1: 19 AA2: 20 | MKKIILSFLFLLYCTFVQN |
| 26855, 26856 | Probability: 0.619 AA1: 18 AA2: 19 | MNKLGIIGLLIGLGLFG |
| 26857, 26858 | Probability: 0.501 AA1: 20 AA2: 21 | MYVMKSIFFLFFLMCMNISON |
| 275, 276 | Probability: 0.999 AA1: 21 AA2: 22 | MLKNISIFSILFILLINASNA |
| 2761, 2762 | Probability: 0.980 AA1: 17 AA2: 18 | MKKIHIVFLILIVAALA |
| 2927, 2928 | Probability: 0.964 AA1: 18 AA2: 19 | MLKNISIFSILFILLINA |
| 2941, 2942 | Probability: 0.997 AA1: 19 AA2: 20 | MKSTLVTFFILLFSQFIVA |
| 2985, 2986 | Probability: 0.957 AA1: 19 AA2: 20 | MLRSKWGFLALCALLISWQ |
| 303, 304 | Probability: 0.997 AA1: 19 AA2: 20 | MSKIFLAVLTVFTGIGVQA |
| 3055, 3056 | Probability: 0.545 AA1: 19 AA2: 20 | MNSMNKVLIFIILLFSSVS |
| 3113, 3114 | Probability: 0.978 AA1: 19 AA2: 20 | MKRAILITFIIFTNQLYA |
| 3117, 3118 | Probability: 0.623 AA1: 19 AA2: 20 | MKTKTIFILFFSIVSFCFK |
| 3119, 3120 | Probability: 0.999 AA1: 20 AA2: 21 | MKIILLYAAIVGSLFVSCNA |
| 3221, 3222 | Probability: 0.995 AA1: 20 AA2: 21 | MIKAKIFSGLLLFISTALFS |
| 3231, 3232 | Probability: 0.992 AA1: 19 AA2: 20 | MRHIAIILIVLPLISQG |
| 3233, 3234 | Probability: 1.000 AA1: 20 AA2: 21 | MKKDLILTLLIFLFTVSLTA |
| 3235, 3236 | Probability: 1.000 AA1: 20 AA2: 21 | MKKDLILTLLIFLXTVSLTA |
| 3245, 3246 | Probability: 0.975 AA1: 19 AA2: 20 | MKTNLKFLIMLSISIEA |
| 3277, 3278 | Probability: 0.979 AA1: 20 AA2: 21 | MRNSLTLLIFALLLTNCNNS |
| 3337, 3338 | Probability: 0.994 AA1: 19 AA2: 20 | MKKIVSILVFVLLANLSQA |
| 3397, 3398 | Probability: 0.643 AA1: 19 AA2: 20 | MEESMRLFVLLFLIFPVVA |
| 3405, 3406 | Probability: 0.534 AA1: 20 AA2: 21 | MIKKGLSLLRGILSPSITWK |
| 3471, 3472 | Probability: 0.954 AA1: 19 AA2: 20 | MKRIFFAFSILFISVCGFA |
| 3515, 3516 | Probability: 0.686 AA1: 19 AA2: 20 | MAFIFFALVIGTMVIGISMT |
| 3525, 3526 | Probability: 0.873 AA1: 20 AA2: 21 | MKRKIFFYTLMSILLAGIFA |
| 3565, 3566 | Probability: 0.646 AA1: 19 AA2: 20 | MKRFSYLFLILLINQCRN |
| 365, 366 | Probability: 0.540 AA1: 21 AA2: 22 | MHNSSPMKNLLIFASFILSS |
| 3705, 3706 | Probability: 0.845 AA1: 19 AA2: 20 | MKPTLLIMAAGMASRYGSM |
| 3711, 3712 | Probability: 0.994 AA1: 19 AA2: 20 | MKKIVSILVFVLLANLSQA |
| 373, 374 | Probability: 0.665 AA1: 20 AA2: 21 | MNKRHILISATVVSISLQV |
| 3771, 3772 | Probability: 0.860 AA1: 20 AA2: 21 | MQINRLIVLLIMISHKNFA |
| 3843, 3844 | Probability: 1.000 AA1: 19 AA2: 20 | MKSFIFFLFFVLAFSVANA |
| 3871, 3872 | Probability: 0.973 AA1: 18 AA2: 19 | MNKSVLVVGAGLGGMALA |
| 3913, 3914 | Probability: 0.999 AA1: 19 AA2: 20 | MNRFLIFIVICFCGTAVS |
| 397, 398 | Probability: 0.978 AA1: 18 AA2: 19 | MIRFVIPVFFLLPFFSNA |
| 4037, 4038 | Probability: 0.904 AA1: 19 AA2: 20 | MKKEFLKIGIAILVLAIA |
| 4087, 4088 | Probability: 1.000 AA1: 18 AA2: 19 | MRKIFAVAALFTSSQLAA |
| 4153, 4154 | Probability: 0.515 AA1: 18 AA2: 19 | MLKSLFLFTSFSSFFLLV |
| 4167, 4168 | Probability: 0.784 AA1: 17 AA2: 18 | MARLVLVFILLHQTIVA |
| 419, 420 | Probability: 0.708 AA1: 18 AA2: 19 | MKSLIIFSLILFFTACK |
| 4223, 4224 | Probability: 0.659 AA1: 19 AA2: 20 | MRSKIFLLMLXTASFYSPS |
| 4241, 4242 | Probability: 1.000 AA1: 20 AA2: 21 | MKKKITILILFFICLFALS |
| 4259, 4260 | Probability: 0.788 AA1: 17 AA2: 18 | MKTHIITILITSCA |
| 4273, 4274 | Probability: 0.987 AA1: 19 AA2: 20 | MKAHIRIILLALFFGTAVQ |
| 4291, 4292 | Probability: 1.000 AA1: 18 AA2: 19 | MKKIFLSFCLLSSFIGFA |
| 4309, 4310 | Probability: 0.924 AA1: 18 AA2: 19 | MKYCLILFSIVNSLFTNA |
| 4313, 4314 | Probability: 0.834 AA1: 18 AA2: 19 | MKNKVLLSFLCFFLYTHV |
| 4319, 4320 | Probability: 0.670 AA1: 15 AA2: 16 | MKLAALILLIIFTQS |
| 4337, 4338 | Probability: 0.537 AA1: 20 AA2: 21 | MKKLTVILFFVIGVTYQVIG |
| 4361, 4362 | Probability: 0.850 AA1: 17 AA2: 18 | MKKILFSLIVCVFCLSS |
| 4405, 4406 | Probability: 0.873 AA1: 20 AA2: 21 | MKRKIFFYTLMSILLAGIFA |
| 4415, 4416 | Probability: 0.923 AA1: 18 AA2: 19 | MKQMLAAIFCFCFFISHS |
| 4483, 4484 | Probability: 0.575 AA1: 18 AA2: 19 | MRTIVILYLVMFSLSCQQ |

| | | |
|------------|------------------------------------|-------------------------|
| 4623, 4624 | Probability: 0.540 AA1: 21 AA2: 22 | MHNSSPMKNLLILFASFILSS |
| 463, 464 | Probability: 0.643 AA1: 21 AA2: 22 | MIRTKGXXXXXXXXXXXXXXXXX |
| 4641, 4642 | Probability: 0.976 AA1: 20 AA2: 21 | MKRMIITGMLAFLGTTGFG |
| 4771, 4772 | Probability: 0.998 AA1: 19 AA2: 20 | MSKIFLAVLTVFTGIGVQA |
| 4903, 4904 | Probability: 0.998 AA1: 17 AA2: 18 | MFRFIIVSVFAISVSFA |
| 4937, 4938 | Probability: 0.977 AA1: 19 AA2: 20 | MTIMKYKLITLFLLFQTLA |
| 4939, 4940 | Probability: 0.600 AA1: 19 AA2: 20 | MKTTVRILCVCILVCSSVS |
| 495, 496 | Probability: 0.674 AA1: 20 AA2: 21 | MGRHAVCXXXXXXXXXXXXXXXX |
| 5031, 5032 | Probability: 0.713 AA1: 18 AA2: 19 | MKKSLTMTLFAGLFLINS |
| 5037, 5038 | Probability: 0.987 AA1: 19 AA2: 20 | MKAHIRIILLALFFGTAVQ |
| 5057, 5058 | Probability: 0.990 AA1: 19 AA2: 20 | MRNYILTILTFFFSITLFA |
| 509, 510 | Probability: 0.558 AA1: 18 AA2: 19 | MKVLLSTALPIALCCLLL |
| 5261, 5262 | Probability: 0.558 AA1: 18 AA2: 19 | MKVLLSTALPIALCCLLL |
| 5289, 5290 | Probability: 0.979 AA1: 15 AA2: 16 | MANKYLLCCLFLVSA |
| 5351, 5352 | Probability: 0.928 AA1: 18 AA2: 19 | MKFLALLIITCSDICTA |
| 5371, 5372 | Probability: 0.588 AA1: 20 AA2: 21 | MKKLILLPFLALLLGFILPG |
| 5421, 5422 | Probability: 1.000 AA1: 19 AA2: 20 | MLKILLAVTVAFSFLPAFS |
| 5571, 5572 | Probability: 0.836 AA1: 18 AA2: 19 | MKLTVTAIFLCVAIQAIS |
| 5573, 5574 | Probability: 0.985 AA1: 20 AA2: 21 | MKKYFGILLITSLICLVQLQ |
| 5575, 5576 | Probability: 0.999 AA1: 19 AA2: 20 | MRTNCILLSVLLFTFSTSS |
| 5617, 5618 | Probability: 0.968 AA1: 19 AA2: 20 | MKNKIIAFLPLICAGVIT |
| 5693, 5694 | Probability: 0.992 AA1: 18 AA2: 19 | MKILTIVFLVGFFCFVQA |
| 5801, 5802 | Probability: 1.000 AA1: 20 AA2: 21 | MKKILFIAATAVLFSTTTMA |
| 5811, 5812 | Probability: 0.875 AA1: 18 AA2: 19 | MKSFYFLIAMGISLNASA |
| 5943, 5944 | Probability: 0.983 AA1: 16 AA2: 17 | MTTNTILLLLLSLVIA |
| 5951, 5952 | Probability: 0.722 AA1: 20 AA2: 21 | MKLKKGIIILIAFLGFGLSN |
| 5953, 5954 | Probability: 0.973 AA1: 20 AA2: 21 | MMPKLKLLLGCLLILLKNA |
| 6027, 6028 | Probability: 0.682 AA1: 18 AA2: 19 | MKSLIIIFSLILFFTACK |
| 6041, 6042 | Probability: 0.873 AA1: 18 AA2: 19 | MTTSKTLFILFLVMTQL |
| 6185, 6186 | Probability: 0.997 AA1: 19 AA2: 20 | MKSTLVTFILLFSQFIVA |
| 6245, 6246 | Probability: 0.854 AA1: 17 AA2: 18 | MKYFLFIFLLSCPVTLS |
| 6289, 6290 | Probability: 0.999 AA1: 19 AA2: 20 | MKKLFPVVLFLSMNVLQA |
| 6323, 6324 | Probability: 1.000 AA1: 20 AA2: 21 | MKFFSLFYCFLLLGLNFALA |
| 6469, 6470 | Probability: 0.997 AA1: 19 AA2: 20 | MKSTLVTFILLFSQFIVA |
| 6667, 6668 | Probability: 0.912 AA1: 18 AA2: 19 | MRKNFQIVLAFAMTIATS |
| 6719, 6720 | Probability: 1.000 AA1: 18 AA2: 19 | MRKVLLTMLFLSCFSGNA |
| 6741, 6742 | Probability: 0.551 AA1: 18 AA2: 19 | MKKVLLTGCLLITIISTG |
| 6755, 6756 | Probability: 0.909 AA1: 19 AA2: 20 | MKKFLIFCLFLFNKPLIS |
| 6789, 6790 | Probability: 0.707 AA1: 18 AA2: 19 | MRAFLSITVCFFLFVNFA |
| 6885, 6886 | Probability: 0.693 AA1: 19 AA2: 20 | MKILKLFFLLFILPITTLQ |
| 6893, 6894 | Probability: 0.911 AA1: 16 AA2: 17 | MKYLILIALCTLTFS |
| 6943, 6944 | Probability: 1.000 AA1: 18 AA2: 19 | MKKLILSLFILISLNVFA |
| 6951, 6952 | Probability: 0.903 AA1: 19 AA2: 20 | MLFMKKIILLIVTAVVVS |
| 7029, 7030 | Probability: 0.852 AA1: 16 AA2: 17 | MKKIFLLIFTFIYLN |
| 711, 712 | Probability: 0.936 AA1: 19 AA2: 20 | MKNQIFSGFLLFIVNQVA |
| 7357, 7358 | Probability: 0.610 AA1: 16 AA2: 17 | MLRVILISIFVLNIYA |
| 7389, 7390 | Probability: 0.987 AA1: 19 AA2: 20 | MKYFTLIFLFTYLSLSSFG |
| 7491, 7492 | Probability: 0.682 AA1: 19 AA2: 20 | MKSMRTIFISFLIILLQG |
| 7505, 7506 | Probability: 0.995 AA1: 19 AA2: 20 | MRRILALMCVILLSSFFV |
| 7543, 7544 | Probability: 0.997 AA1: 19 AA2: 20 | MLIKNIVLSFLFVLFAGG |
| 759, 760 | Probability: 0.711 AA1: 19 AA2: 20 | MKFKLAIFALILISINLIS |
| 7765, 7766 | Probability: 0.529 AA1: 18 AA2: 19 | MKICIIGLGYVGLPLAHA |
| 7785, 7786 | Probability: 0.983 AA1: 19 AA2: 20 | MFKKVIGILLIALSLVVL |
| 7835, 7836 | Probability: 0.878 AA1: 15 AA2: 16 | MRIIFLVLSISFLYA |
| 7907, 7908 | Probability: 0.926 AA1: 19 AA2: 20 | MKKSSLLLLITFVVVLFQG |

| | | |
|------------|------------------------------------|----------------------|
| 821, 822 | Probability: 1.000 AA1: 20 AA2: 21 | MKKWRFSLISFLFVCVTCLA |
| 8247, 8248 | Probability: 0.995 AA1: 16 AA2: 17 | MRISILLAVVSSIIFA |
| 827, 828 | Probability: 1.000 AA1: 19 AA2: 20 | MKKFFSLIIFLIFSFAFA |
| 8279, 8280 | Probability: 0.672 AA1: 15 AA2: 16 | MKFNLNSFLMSVSLA |
| 8313, 8314 | Probability: 0.992 AA1: 19 AA2: 20 | MKHIKKALLILLFLFLSFS |
| 8349, 8350 | Probability: 0.562 AA1: 17 AA2: 18 | MFKTILFTIVFVTNIFS |
| 8437, 8438 | Probability: 0.820 AA1: 16 AA2: 17 | MKKRVMSSMKSGGVVA |
| 8461, 8462 | Probability: 0.857 AA1: 17 AA2: 18 | MKKYLALFAFILLVLSS |
| 8513, 8514 | Probability: 0.993 AA1: 16 AA2: 17 | MKLLLLLFLVLLNVNA |
| 8561, 8562 | Probability: 0.618 AA1: 17 AA2: 18 | MKLNAGAILVLSGPGSA |
| 8585, 8586 | Probability: 0.997 AA1: 17 AA2: 18 | MKKFTLSILISSSLAFG |
| 8727, 8728 | Probability: 0.825 AA1: 19 AA2: 20 | MKKITKILLIFALVAIFSG |
| 8793, 8794 | Probability: 0.582 AA1: 19 AA2: 20 | MKNKCLLIILLRVISTFLL |
| 8853, 8854 | Probability: 0.649 AA1: 17 AA2: 18 | MMKILILTITTTAILCA |
| 9021, 9022 | Probability: 0.998 AA1: 19 AA2: 20 | MNYKSFLALTAAVIISFSA |
| 9039, 9040 | Probability: 0.977 AA1: 19 AA2: 20 | MQKAFYILILLSVSLSSFG |
| 9213, 9214 | Probability: 0.772 AA1: 17 AA2: 18 | MKKKILVGGGTAGTMT |
| 9351, 9352 | Probability: 0.744 AA1: 18 AA2: 19 | MIKRTTGILLIFISIFA |
| 9373, 9374 | Probability: 0.931 AA1: 17 AA2: 18 | MKHILFITLFFLTSLFA |
| 9413, 9414 | Probability: 0.540 AA1: 15 AA2: 16 | MSNIALSLGSCFTIA |
| 9613, 9614 | Probability: 0.998 AA1: 17 AA2: 18 | MKIFSLIFILLFTSLSA |
| 9713, 9714 | Probability: 0.911 AA1: 17 AA2: 18 | MKKVITLSLITLNLFA |
| 9829, 9830 | Probability: 0.768 AA1: 19 AA2: 20 | MKNILKIIFILFSSCQT |
| 9881, 9882 | Probability: 0.963 AA1: 19 AA2: 20 | MNKNLITAALLFVFGYTML |
| 9925, 9926 | Probability: 0.751 AA1: 18 AA2: 19 | MLQKSFISILLSLLLSLS |
| 9979, 9980 | Probability: 0.799 AA1: 19 AA2: 20 | MIMKDLILTLLLSVYCLV |

Methods for identifying "prepro" domain sequences and signal sequences are well known in the art, see, e.g., Van de Ven (1993) Crit. Rev. Oncog. 4(2):115-136. For example, to identify a prepro sequence, the protein is purified from the extracellular space and the N-terminal protein sequence is determined and compared to the unprocessed form.

The invention includes polypeptides with or without a signal sequence and/or a prepro sequence. The invention includes polypeptides with heterologous signal sequences and/or prepro sequences. The prepro sequence (including a sequence of the invention used as a heterologous prepro domain) can be located on the amino terminal or the carboxy terminal end of the protein. The invention also includes isolated or recombinant signal sequences, prepro sequences and catalytic domains (e.g., "active sites") comprising sequences of the invention. The polypeptide comprising a signal sequence of the invention can be a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention or another polypeptide, enzyme, protein, e.g. structural or binding protein, or another enzyme or other polypeptide.

The polypeptide, enzyme, protein, e.g. structural or binding protein signal sequences (SPs) and/or prepro sequences of the invention can be isolated peptides, or,

sequences joined to another a polypeptide, enzyme, protein, e.g. structural or binding protein, or a non-polypeptide, non-enzyme, non-protein, e.g. non-structural or non-binding protein, e.g., as a fusion (chimeric) protein. In one aspect, the invention provides polypeptides comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, signal sequences of the invention. In one aspect, polypeptides comprising polypeptide, enzyme, protein, e.g. structural or binding protein signal sequences SPs and/or prepro of the invention comprise sequences heterologous to a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention (e.g., a fusion protein comprising an SP and/or prepro of the invention and sequences from another a polypeptide, enzyme, protein, e.g. structural or binding protein, or a non-polypeptide, non-enzyme, non-protein, e.g. non-structural or non-binding protein). In one aspect, the invention provides a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention with heterologous SPs and/or prepro sequences, e.g., sequences with a yeast signal sequence. A polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can comprise a heterologous SP and/or prepro in a vector, e.g., a pPIC series vector (Invitrogen, Carlsbad, CA).

In one aspect, SPs and/or prepro sequences of the invention are identified following identification of novel a polypeptide, enzyme, protein, e.g. structural or binding protein. The pathways by which proteins are sorted and transported to their proper cellular location are often referred to as protein targeting pathways. One of the most important elements in all of these targeting systems is a short amino acid sequence at the amino terminus of a newly synthesized polypeptide called the signal sequence. This signal sequence directs a protein to its appropriate location in the cell and is removed during transport or when the protein reaches its final destination. Most lysosomal, membrane, or secreted proteins have an amino-terminal signal sequence that marks them for translocation into the lumen of the endoplasmic reticulum. The signal sequences can vary in length from about 10 to 65, or more, amino acid residues. Various methods of recognition of signal sequences are known to those of skill in the art. For example, in one aspect, novel a polypeptide, enzyme, protein, e.g. structural or binding protein, signal peptides are identified by a method referred to as SignalP. SignalP uses a combined neural network which recognizes both signal peptides and their cleavage sites. (Nielsen (1997) "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites." Protein Engineering 10:1-6.

It should be understood that in some aspects a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention may not have SPs and/or prepro sequences, or "domains." In one aspect, the invention provides the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention lacking all or part of an SP and/or a prepro domain. In one aspect, the invention provides a nucleic acid sequence encoding a signal sequence (SP) and/or prepro from one a polypeptide, enzyme, protein, e.g. structural or binding protein, operably linked to a nucleic acid sequence of a different a polypeptide, enzyme, protein, e.g. structural or binding protein, or, optionally, a signal sequence (SPs) and/or prepro domain from a non-enzyme or non-protein, e.g. non-structural or non-binding protein, may be desired.

The invention also provides isolated or recombinant polypeptides comprising signal sequences (SPs), prepro domain and/or catalytic domains (CDs) of the invention and heterologous sequences. The heterologous sequences are sequences not naturally associated (e.g., to a enzyme) with an SP, prepro domain and/or CD. The sequence to which the SP, prepro domain and/or CD are not naturally associated can be on the SP's, prepro domain and/or CD's amino terminal end, carboxy terminal end, and/or on both ends of the SP and/or CD. In one aspect, the invention provides an isolated or recombinant polypeptide comprising (or consisting of) a polypeptide comprising a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention with the proviso that it is not associated with any sequence to which it is naturally associated (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, sequence). Similarly in one aspect, the invention provides isolated or recombinant nucleic acids encoding these polypeptides. Thus, in one aspect, the isolated or recombinant nucleic acid of the invention comprises coding sequence for a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention and a heterologous sequence (i.e., a sequence not naturally associated with the a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention). The heterologous sequence can be on the 3' terminal end, 5' terminal end, and/or on both ends of the SP, prepro domain and/or CD coding sequence.

Hybrid (chimeric) a polypeptide, enzyme, protein, e.g. structural or binding protein, and peptide libraries

In one aspect, the invention provides hybrid a polypeptide, enzyme, protein, e.g. structural or binding protein, and fusion proteins, including peptide libraries, comprising sequences of the invention. The peptide libraries of the invention can be used

to isolate peptide modulators (e.g., activators or inhibitors) of targets, such as a polypeptide, enzyme, protein, e.g. structural or binding protein, substrates, receptors, enzymes. The peptide libraries of the invention can be used to identify formal binding partners of targets, such as ligands, e.g., cytokines, hormones and the like. In one aspect, the invention provides chimeric proteins comprising a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention or a combination thereof and a heterologous sequence (see above).

In one aspect, the fusion proteins of the invention (e.g., the peptide moiety) are conformationally stabilized (relative to linear peptides) to allow a higher binding affinity for targets. The invention provides fusions of a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention and other peptides, including known and random peptides. They can be fused in such a manner that the structure of the polypeptide, enzyme, protein, e.g. structural or binding proteins is not significantly perturbed and the peptide is metabolically or structurally conformationally stabilized. This allows the creation of a peptide library that is easily monitored both for its presence within cells and its quantity.

Amino acid sequence variants of the invention can be characterized by a predetermined nature of the variation, a feature that sets them apart from a naturally occurring form, e.g., an allelic or interspecies variation of a polypeptide, enzyme, protein, e.g. structural or binding protein, sequence. In one aspect, the variants of the invention exhibit the same qualitative biological activity as the naturally occurring analogue. Alternatively, the variants can be selected for having modified characteristics. In one aspect, while the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed a polypeptide, enzyme, protein, e.g. structural or binding protein, variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, as discussed herein for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants can be done using, e.g., assays of glucan hydrolysis. In alternative aspects, amino acid substitutions can be single residues; insertions can be on the order of from about 1 to 20 amino acids, although considerably larger insertions can be done. Deletions can range from about 1 to about 20, 30, 40, 50, 60, 70 residues or more. To obtain a final derivative with the optimal

properties, substitutions, deletions, insertions or any combination thereof may be used. Generally, these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances.

The invention provides a polypeptide, enzyme, protein, e.g. structural or binding protein, where the structure of the polypeptide backbone, the secondary or the tertiary structure, e.g., an alpha-helical or beta-sheet structure, has been modified. In one aspect, the charge or hydrophobicity has been modified. In one aspect, the bulk of a side chain has been modified. Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative. For example, substitutions can be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example a alpha-helical or a beta-sheet structure; a charge or a hydrophobic site of the molecule, which can be at an active site; or a side chain. The invention provides substitutions in polypeptide of the invention where (a) a hydrophilic residues, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine. The variants can exhibit the same qualitative biological activity (i.e., an enzyme, structural or binding activity) although variants can be selected to modify the characteristics of the polypeptide, enzyme, protein, e.g. structural or binding proteins as needed.

In one aspect, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention comprise epitopes or purification tags, signal sequences or other fusion sequences, etc. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention can be fused to a random peptide to form a fusion polypeptide. By "fused" or "operably linked" herein is meant that the random peptide and the polypeptide, enzyme, protein, e.g. structural or binding protein are linked together, in such a manner as to minimize the disruption to the stability of the polypeptide, enzyme, protein, e.g. structural or binding protein structure, e.g., it retains a polypeptide, enzyme, protein, e.g. structural or binding protein, activity. The fusion polypeptide (or fusion polynucleotide encoding the fusion polypeptide) can comprise further components as well, including multiple peptides at multiple loops.

In one aspect, the peptides and nucleic acids encoding them are randomized, either fully randomized or they are biased in their randomization, e.g. in nucleotide/residue frequency generally or per position. "Randomized" means that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. In one aspect, the nucleic acids which give rise to the peptides can be chemically synthesized, and thus may incorporate any nucleotide at any position. Thus, when the nucleic acids are expressed to form peptides, any amino acid residue may be incorporated at any position. The synthetic process can be designed to generate randomized nucleic acids, to allow the formation of all or most of the possible combinations over the length of the nucleic acid, thus forming a library of randomized nucleic acids. The library can provide a sufficiently structurally diverse population of randomized expression products to affect a probabilistically sufficient range of cellular responses to provide one or more cells exhibiting a desired response. Thus, the invention provides an interaction library large enough so that at least one of its members will have a structure that gives it affinity for some molecule, protein, or other factor.

In one aspect, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention is a multidomain enzyme that comprises a signal peptide, a carbohydrate binding module, a polypeptide, enzyme, protein, e.g. structural or binding protein, catalytic domain, a linker and/or another catalytic domain.

The invention provides a means for generating chimeric polypeptides which may encode biologically active hybrid polypeptides (e.g., hybrid a polypeptide, enzyme, protein, e.g. structural or binding protein,). In one aspect, the original polynucleotides encode biologically active polypeptides. The method of the invention produces new hybrid polypeptides by utilizing cellular processes which integrate the sequence of the original polynucleotides such that the resulting hybrid polynucleotide encodes a polypeptide demonstrating activities derived from the original biologically active polypeptides. For example, the original polynucleotides may encode a particular enzyme from different microorganisms. An enzyme encoded by a first polynucleotide from one organism or variant may, for example, function effectively under a particular environmental condition, e.g. high salinity. An enzyme encoded by a second polynucleotide from a different organism or variant may function effectively under a different environmental condition, such as extremely high temperatures. A hybrid polynucleotide containing sequences from the first and second original polynucleotides may encode an enzyme which exhibits characteristics of both enzymes encoded by the

original polynucleotides. Thus, the enzyme encoded by the hybrid polynucleotide may function effectively under environmental conditions shared by each of the enzymes encoded by the first and second polynucleotides, *e.g.*, high salinity and extreme temperatures.

A hybrid polypeptide resulting from the method of the invention may exhibit specialized enzyme activity not displayed in the original enzymes. For example, following recombination and/or reductive reassortment of polynucleotides encoding a polypeptide, enzyme, protein, *e.g.* structural or binding protein, the resulting hybrid polypeptide encoded by a hybrid polynucleotide can be screened for specialized non-enzyme, non-structural or non-binding activities, obtained from each of the original enzymes. Thus, for example, the hybrid polypeptide may be screened to ascertain those chemical functionalities which distinguish the hybrid polypeptide from the original parent polypeptides, such as the temperature, pH or salt concentration at which the hybrid polypeptide functions.

In one aspect, the invention relates to a method for producing a biologically active hybrid polypeptide and screening such a polypeptide for enhanced activity by:

- 1) introducing at least a first polynucleotide in operable linkage and a second polynucleotide in operable linkage, the at least first polynucleotide and second polynucleotide sharing at least one region of partial sequence homology, into a suitable host cell;
- 2) growing the host cell under conditions which promote sequence reorganization resulting in a hybrid polynucleotide in operable linkage;
- 3) expressing a hybrid polypeptide encoded by the hybrid polynucleotide;
- 4) screening the hybrid polypeptide under conditions which promote identification of enhanced biological activity; and
- 5) isolating the a polynucleotide encoding the hybrid polypeptide.

Isolating and discovering a polypeptide, enzyme, protein, *e.g.* structural or binding protein

The invention provides methods for isolating and discovering a polypeptide, enzyme, protein, *e.g.* structural or binding protein, and the nucleic acids that encode them. Polynucleotides or enzymes may be isolated from individual organisms ("isolates"), collections of organisms that have been grown in defined media ("enrichment cultures"), or, uncultivated organisms ("environmental samples"). The

organisms can be isolated by, e.g., *in vivo* biopanning (see discussion, below). The use of a culture-independent approach to derive polynucleotides encoding novel bioactivities from environmental samples is most preferable since it allows one to access untapped resources of biodiversity. Polynucleotides or enzymes also can be isolated from any one of numerous organisms, e.g. bacteria. In addition to whole cells, polynucleotides or enzymes also can be isolated from crude enzyme preparations derived from cultures of these organisms, e.g., bacteria.

"Environmental libraries" are generated from environmental samples and represent the collective genomes of naturally occurring organisms archived in cloning vectors that can be propagated in suitable prokaryotic hosts. Because the cloned DNA is initially extracted directly from environmental samples, the libraries are not limited to the small fraction of prokaryotes that can be grown in pure culture. Additionally, a normalization of the environmental DNA present in these samples could allow more equal representation of the DNA from all of the species present in the original sample. This can dramatically increase the efficiency of finding interesting genes from minor constituents of the sample which may be under-represented by several orders of magnitude compared to the dominant species.

For example, gene libraries generated from one or more uncultivated microorganisms are screened for an activity of interest. Potential pathways encoding bioactive molecules of interest are first captured in prokaryotic cells in the form of gene expression libraries. Polynucleotides encoding activities of interest are isolated from such libraries and introduced into a host cell. The host cell is grown under conditions which promote recombination and/or reductive reassortment creating potentially active biomolecules with novel or enhanced activities.

In vivo biopanning may be performed utilizing a FACS-based and non-optical (e.g., magnetic) based machines. Complex gene libraries are constructed with vectors which contain elements which stabilize transcribed RNA. For example, the inclusion of sequences which result in secondary structures such as hairpins which are designed to flank the transcribed regions of the RNA would serve to enhance their stability, thus increasing their half life within the cell. The probe molecules used in the biopanning process consist of oligonucleotides labeled with reporter molecules that only fluoresce upon binding of the probe to a target molecule. These probes are introduced into the recombinant cells from the library using one of several transformation methods. The probe molecules bind to the transcribed target mRNA resulting in DNA/RNA

heteroduplex molecules. Binding of the probe to a target will yield a fluorescent signal which is detected and sorted by the FACS machine during the screening process.

Additionally, subcloning may be performed to further isolate sequences of interest. In subcloning, a portion of DNA is amplified, digested, generally by restriction enzymes, to cut out the desired sequence, the desired sequence is ligated into a recipient vector and is amplified. At each step in subcloning, the portion is examined for the activity of interest, in order to ensure that DNA that encodes the structural protein has not been excluded. The insert may be purified at any step of the subcloning, for example, by gel electrophoresis prior to ligation into a vector or where cells containing the recipient vector and cells not containing the recipient vector are placed on selective media containing, for example, an antibiotic, which will kill the cells not containing the recipient vector. Specific methods of subcloning cDNA inserts into vectors are well-known in the art (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press (1989)). In another aspect, the enzymes of the invention are subclones. Such subclones may differ from the parent clone by, for example, length, a mutation, a tag or a label.

In one aspect, the signal sequences of the invention are identified following identification of a novel polypeptide, enzyme, protein, e.g. structural or binding protein. The pathways by which proteins are sorted and transported to their proper cellular location are often referred to as protein targeting pathways. One of the most important elements in all of these targeting systems is a short amino acid sequence at the amino terminus of a newly synthesized polypeptide called the signal sequence. This signal sequence directs a protein to its appropriate location in the cell and is removed during transport or when the protein reaches its final destination. Most lysosomal, membrane, or secreted proteins have an amino-terminal signal sequence that marks them for translocation into the lumen of the endoplasmic reticulum. More than 100 signal sequences for proteins in this group have been determined. The sequences vary in length from 13 to 36 amino acid residues. Various methods of recognition of signal sequences are known to those of skill in the art. In one aspect, the peptides are identified by a method referred to as SignalP. SignalP uses a combined neural network which recognizes both signal peptides and their cleavage sites. See, e.g., Nielsen (1997) "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites." *Protein Engineering*, vol. 10, no. 1, p. 1-6. It should be understood that some of the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention may or may not

contain signal sequences. It may be desirable to include a nucleic acid sequence encoding a signal sequence from a polypeptide, enzyme, protein, e.g. structural or binding protein, operably linked to a nucleic acid sequence of a different polypeptide, enzyme, protein, e.g. structural or binding protein may be desired.

The microorganisms from which the polynucleotide may be discovered, isolated or prepared include prokaryotic microorganisms, such as *Eubacteria* and *Archaeobacteria* and lower eukaryotic microorganisms such as fungi, some algae and protozoa. Polynucleotides may be discovered, isolated or prepared from environmental samples in which case the nucleic acid may be recovered without culturing of an organism or recovered from one or more cultured organisms. In one aspect, such microorganisms may be extremophiles, such as hyperthermophiles, psychrophiles, psychrotrophs, halophiles, barophiles and acidophiles. Polynucleotides encoding enzymes isolated from extremophilic microorganisms can be used. Such enzymes may function at temperatures above 100°C in terrestrial hot springs and deep seamount vents, at temperatures below 0°C in arctic waters, in the saturated salt environment of the Dead Sea, at pH values around 0 in coal deposits and geothermal sulfur-rich springs, or at pH values greater than 11 in sewage sludge. For example, several esterases and lipases cloned and expressed from extremophilic organisms show high activity throughout a wide range of temperatures and pHs.

Polynucleotides selected and isolated as hereinabove described are introduced into a suitable host cell. A suitable host cell is any cell which is capable of promoting recombination and/or reductive reassortment. The selected polynucleotides are in one aspect already in a vector which includes appropriate control sequences. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or in one aspect, the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis *et al.*, 1986).

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila S2* and *Spodoptera Sf9*; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; and plant cells. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

With particular references to various mammalian cell culture systems that can be employed to express recombinant protein, examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in "SV40-transformed simian cells support the replication of early SV40 mutants" (Gluzman, 1981) and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

In another aspect, it is envisioned the method of the present invention can be used to generate novel polynucleotides encoding biochemical pathways from one or more operons or gene clusters or portions thereof. For example, bacteria and many eukaryotes have a coordinated mechanism for regulating genes whose products are involved in related processes. The genes are clustered, in structures referred to as "gene clusters," on a single chromosome and are transcribed together under the control of a single regulatory sequence, including a single promoter which initiates transcription of the entire cluster. Thus, a gene cluster is a group of adjacent genes that are either identical or related, usually as to their function. An example of a biochemical pathway encoded by gene clusters are polyketides.

Gene cluster DNA can be isolated from different organisms and ligated into vectors, particularly vectors containing expression regulatory sequences which can control and regulate the production of a detectable protein or protein-related array activity from the ligated gene clusters. Use of vectors which have an exceptionally large capacity for exogenous DNA introduction are particularly appropriate for use with such gene clusters and are described by way of example herein to include the f-factor (or fertility factor) of *E. coli*. This f-factor of *E. coli* is a plasmid which affects high-frequency transfer of itself during conjugation and is ideal to achieve and stably propagate large DNA fragments, such as gene clusters from mixed microbial samples. One aspect is to use cloning vectors, referred to as "fosmids" or bacterial artificial chromosome (BAC) vectors. These are derived from *E. coli* f-factor which is able to stably integrate large segments of genomic DNA. When integrated with DNA from a mixed uncultured environmental sample, this makes it possible to achieve large genomic fragments in the

form of a stable “environmental DNA library.” Another type of vector for use in the present invention is a cosmid vector. Cosmid vectors were originally designed to clone and propagate large segments of genomic DNA. Cloning into cosmid vectors is described in detail in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press (1989). Once ligated into an appropriate vector, two or more vectors containing different polyketide synthase gene clusters can be introduced into a suitable host cell. Regions of partial sequence homology shared by the gene clusters will promote processes which result in sequence reorganization resulting in a hybrid gene cluster. The novel hybrid gene cluster can then be screened for enhanced activities not found in the original gene clusters.

Methods for screening for various enzyme activities are known to those of skill in the art and are discussed throughout the present specification. Such methods may be employed when isolating the polypeptides and polynucleotides of the invention.

In one aspect, the invention provides methods for discovering and isolating polypeptides, enzymes, proteins, e.g. structural or binding proteins or compounds to modify the enzymatic activity, using a whole cell approach. Putative clones encoding polypeptides, enzymes, proteins, e.g. structural or binding proteins from genomic DNA library can be screened.

Screening Methodologies and “On-line” Monitoring Devices

In practicing the methods of the invention, a variety of apparatus and methodologies can be used to in conjunction with the polypeptides and nucleic acids of the invention, e.g., to screen polypeptides for a polypeptide, enzyme, protein, e.g. structural or binding protein, activity, to screen compounds as potential modulators, e.g., activators or inhibitors, of an enzyme, structural or binding activity, for antibodies that bind to a polypeptide of the invention, for nucleic acids that hybridize to a nucleic acid of the invention, to screen for cells expressing a polypeptide of the invention and the like. In addition to the array formats described in detail below for screening samples, alternative formats can also be used to practice the methods of the invention. Such formats include, for example, mass spectrometers, chromatographs, e.g., high-throughput HPLC and other forms of liquid chromatography, and smaller formats, such as 1536-well plates, 384-well plates and so on. High throughput screening apparatus can be adapted and used to practice the methods of the invention, see, e.g., U.S. Patent Application No. 20020001809.

Capillary Arrays

Nucleic acids or polypeptides of the invention can be immobilized to or applied to an array. Arrays can be used to screen for or monitor libraries of compositions (e.g., small molecules, antibodies, nucleic acids, etc.) for their ability to bind to or modulate the activity of a nucleic acid or a polypeptide of the invention. Capillary arrays, such as the GIGAMATRIX™, Diversa Corporation, San Diego, CA; and arrays described in, e.g., U.S. Patent Application No. 20020080350 A1; WO 0231203 A; WO 0244336 A, provide an alternative apparatus for holding and screening samples. In one aspect, the capillary array includes a plurality of capillaries formed into an array of adjacent capillaries, wherein each capillary comprises at least one wall defining a lumen for retaining a sample. The lumen may be cylindrical, square, hexagonal or any other geometric shape so long as the walls form a lumen for retention of a liquid or sample. The capillaries of the capillary array can be held together in close proximity to form a planar structure. The capillaries can be bound together, by being fused (e.g., where the capillaries are made of glass), glued, bonded, or clamped side-by-side. Additionally, the capillary array can include interstitial material disposed between adjacent capillaries in the array, thereby forming a solid planar device containing a plurality of through-holes.

A capillary array can be formed of any number of individual capillaries, for example, a range from 100 to 4,000,000 capillaries. Further, a capillary array having about 100,000 or more individual capillaries can be formed into the standard size and shape of a Microtiter® plate for fitment into standard laboratory equipment. The lumens are filled manually or automatically using either capillary action or microinjection using a thin needle. Samples of interest may subsequently be removed from individual capillaries for further analysis or characterization. For example, a thin, needle-like probe is positioned in fluid communication with a selected capillary to either add or withdraw material from the lumen.

In a single-pot screening assay, the assay components are mixed yielding a solution of interest, prior to insertion into the capillary array. The lumen is filled by capillary action when at least a portion of the array is immersed into a solution of interest. Chemical or biological reactions and/or activity in each capillary are monitored for detectable events. A detectable event is often referred to as a "hit", which can usually be distinguished from "non-hit" producing capillaries by optical detection. Thus, capillary arrays allow for massively parallel detection of "hits".

In a multi-pot screening assay, a polypeptide or nucleic acid, e.g., a ligand, can be introduced into a first component, which is introduced into at least a portion of a capillary of a capillary array. An air bubble can then be introduced into the capillary behind the first component. A second component can then be introduced into the capillary, wherein the second component is separated from the first component by the air bubble. The first and second components can then be mixed by applying hydrostatic pressure to both sides of the capillary array to collapse the bubble. The capillary array is then monitored for a detectable event resulting from reaction or non-reaction of the two components.

In a binding screening assay, a sample of interest can be introduced as a first liquid labeled with a detectable particle into a capillary of a capillary array, wherein the lumen of the capillary is coated with a binding material for binding the detectable particle to the lumen. The first liquid may then be removed from the capillary tube, wherein the bound detectable particle is maintained within the capillary, and a second liquid may be introduced into the capillary tube. The capillary is then monitored for a detectable event resulting from reaction or non-reaction of the particle with the second liquid.

Arrays, or "Biochips"

Nucleic acids or polypeptides of the invention can be immobilized to or applied to an array. Arrays can be used to screen for or monitor libraries of compositions (e.g., small molecules, antibodies, nucleic acids, etc.) for their ability to bind to or modulate the activity of a nucleic acid or a polypeptide of the invention. For example, in one aspect of the invention, a monitored parameter is transcript expression of a polypeptide, enzyme, protein, e.g. structural or binding protein, gene. One or more, or, all the transcripts of a cell can be measured by hybridization of a sample comprising transcripts of the cell, or, nucleic acids representative of or complementary to transcripts of a cell, by hybridization to immobilized nucleic acids on an array, or "biochip." By using an "array" of nucleic acids on a microchip, some or all of the transcripts of a cell can be simultaneously quantified. Alternatively, arrays comprising genomic nucleic acid can also be used to determine the genotype of a newly engineered strain made by the methods of the invention. Polypeptide arrays" can also be used to simultaneously quantify a plurality of proteins. The present invention can be practiced with any known "array," also referred to as a "microarray" or "nucleic acid array" or "polypeptide array" or "antibody array" or "biochip," or variation thereof. Arrays are generically a plurality of "spots" or "target elements," each target element comprising a defined amount of one or more biological

molecules, e.g., oligonucleotides, immobilized onto a defined area of a substrate surface for specific binding to a sample molecule, e.g., mRNA transcripts.

The terms "array" or "microarray" or "biochip" or "chip" as used herein is a plurality of target elements, each target element comprising a defined amount of one or more polypeptides (including antibodies) or nucleic acids immobilized onto a defined area of a substrate surface, as discussed in further detail, below.

In practicing the methods of the invention, any known array and/or method of making and using arrays can be incorporated in whole or in part, or variations thereof, as described, for example, in U.S. Patent Nos. 6,277,628; 6,277,489; 6,261,776; 6,258,606; 6,054,270; 6,048,695; 6,045,996; 6,022,963; 6,013,440; 5,965,452; 5,959,098; 5,856,174; 5,830,645; 5,770,456; 5,632,957; 5,556,752; 5,143,854; 5,807,522; 5,800,992; 5,744,305; 5,700,637; 5,556,752; 5,434,049; see also, e.g., WO 99/51773; WO 99/09217; WO 97/46313; WO 96/17958; see also, e.g., Johnston (1998) *Curr. Biol.* 8:R171-R174; Schummer (1997) *Biotechniques* 23:1087-1092; Kern (1997) *Biotechniques* 23:120-124; Solinas-Toldo (1997) *Genes, Chromosomes & Cancer* 20:399-407; Bowtell (1999) *Nature Genetics Supp.* 21:25-32. See also published U.S. patent applications Nos. 20010018642; 20010019827; 20010016322; 20010014449; 20010014448; 20010012537; 20010008765.

Antibodies and Antibody-based screening methods

The invention provides isolated or recombinant antibodies that specifically bind to a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention. These antibodies can be used to isolate, identify or quantify the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention or related polypeptides. These antibodies can be used to isolate other polypeptides within the scope the invention or other related a polypeptide, enzyme, protein, e.g. structural or binding protein, . The antibodies can be designed to bind to an active site of a polypeptide, enzyme, protein, e.g. structural or binding protein. Thus, the invention provides methods of inhibiting a polypeptide, enzyme, protein, e.g. structural or binding protein, using the antibodies of the invention (see discussion above regarding applications for anti-polypeptide, anti-enzyme, anti-protein, e.g., anti-structural or anti-binding protein compositions of the invention).

The invention provides fragments of the enzymes of the invention, including immunogenic fragments of a polypeptide of the invention. The invention provides

compositions comprising a polypeptide or peptide of the invention and adjuvants or carriers and the like.

The term "antibody" includes a peptide or polypeptide derived from, modeled after or substantially encoded by an immunoglobulin gene or immunoglobulin genes, or fragments thereof, capable of specifically binding an antigen or epitope, see, e.g. Fundamental Immunology, Third Edition, W.E. Paul, ed., Raven Press, N.Y. (1993); Wilson (1994) J. Immunol. Methods 175:267-273; Yarmush (1992) J. Biochem. Biophys. Methods 25:85-97. The term antibody includes antigen-binding portions, i.e., "antigen binding sites," (e.g., fragments, subsequences, complementarity determining regions (CDRs)) that retain capacity to bind antigen, including (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a F(ab')₂ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody; (v) a dAb fragment (Ward et al., (1989) Nature 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Single chain antibodies are also included by reference in the term "antibody."

The antibodies can be used in immunoprecipitation, staining, immunoaffinity columns, and the like. If desired, nucleic acid sequences encoding for specific antigens can be generated by immunization followed by isolation of polypeptide or nucleic acid, amplification or cloning and immobilization of polypeptide onto an array of the invention. Alternatively, the methods of the invention can be used to modify the structure of an antibody produced by a cell to be modified, e.g., an antibody's affinity can be increased or decreased. Furthermore, the ability to make or modify antibodies can be a phenotype engineered into a cell by the methods of the invention.

Methods of immunization, producing and isolating antibodies (polyclonal and monoclonal) are known to those of skill in the art and described in the scientific and patent literature, see, e.g., Coligan, CURRENT PROTOCOLS IN IMMUNOLOGY, Wiley/Greene, NY (1991); Stites (eds.) BASIC AND CLINICAL IMMUNOLOGY (7th ed.) Lange Medical Publications, Los Altos, CA ("Stites"); Goding, MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE (2d ed.) Academic Press, New York, NY (1986); Kohler (1975) Nature 256:495; Harlow (1988) ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Publications, New York. Antibodies also can be generated *in vitro*, e.g., using recombinant antibody binding site expressing

phage display libraries, in addition to the traditional *in vivo* methods using animals. See, e.g., Hoogenboom (1997) *Trends Biotechnol.* 15:62-70; Katz (1997) *Annu. Rev. Biophys. Biomol. Struct.* 26:27-45.

The polypeptides of the invention or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof, may also be used to generate antibodies which bind specifically to the polypeptides or fragments. The resulting antibodies may be used in immunoaffinity chromatography procedures to isolate or purify the polypeptide or to determine whether the polypeptide is present in a biological sample. In such procedures, a protein preparation, such as an extract, or a biological sample is contacted with an antibody capable of specifically binding to one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof.

In immunoaffinity procedures, the antibody is attached to a solid support, such as a bead or other column matrix. The protein preparation is placed in contact with the antibody under conditions in which the antibody specifically binds to one of the polypeptides of the invention, or fragment thereof. After a wash to remove non-specifically bound proteins, the specifically bound polypeptides are eluted.

The ability of proteins in a biological sample to bind to the antibody may be determined using any of a variety of procedures familiar to those skilled in the art. For example, binding may be determined by labeling the antibody with a detectable label such as a fluorescent agent, an enzymatic label, or a radioisotope. Alternatively, binding of the antibody to the sample may be detected using a secondary antibody having such a detectable label thereon. Particular assays include ELISA assays, sandwich assays, radioimmunoassays and Western Blots.

Polyclonal antibodies generated against the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, for example, a nonhuman. The antibody so obtained can bind the polypeptide itself. In this manner, even a sequence encoding only a fragment of the polypeptide can be used to generate antibodies which may bind to the whole native polypeptide. Such antibodies can then be used to isolate the polypeptide from cells expressing that polypeptide.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the

hybridoma technique (Kohler and Milstein, *Nature*, 256:495-497, 1975), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* 4:72, 1983) and the EBV-hybridoma technique (Cole, *et al.*, 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. Alternatively, transgenic mice may be used to express humanized antibodies to these polypeptides or fragments thereof.

Antibodies generated against the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in screening for similar polypeptides from other organisms and samples. In such techniques, polypeptides from the organism are contacted with the antibody and those polypeptides which specifically bind the antibody are detected. Any of the procedures described above may be used to detect antibody binding. One such screening assay is described in "Methods for Measuring Cellulase Activities", *Methods in Enzymology*, Vol 160, pp. 87-116.

Kits

The invention provides kits comprising the compositions, e.g., nucleic acids, expression cassettes, vectors, cells, transgenic seeds or plants or plant parts, polypeptides and/or antibodies of the invention. The kits also can contain instructional material teaching the methodologies and uses of the enzymes of the invention (see, e.g., Table 3), including the industrial, experimental, food and feed processing and medical uses of the compositions and methods of the invention, as described herein.

Whole cell engineering and measuring metabolic parameters

The methods of the invention provide whole cell evolution, or whole cell engineering, of a cell to develop a new cell strain having a new phenotype, e.g., a new or modified a polypeptide, enzyme, protein, e.g. structural or binding protein, activity, by modifying the genetic composition of the cell. The genetic composition can be modified by addition to the cell of a nucleic acid of the invention, e.g., a coding sequence for an enzyme of the invention. See, e.g., WO0229032; WO0196551.

To detect the new phenotype, at least one metabolic parameter of a modified cell is monitored in the cell in a "real time" or "on-line" time frame. In one aspect, a plurality

of cells, such as a cell culture, is monitored in "real time" or "on-line." In one aspect, a plurality of metabolic parameters is monitored in "real time" or "on-line." Metabolic parameters can be monitored using the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention.

Metabolic flux analysis (MFA) is based on a known biochemistry framework. A linearly independent metabolic matrix is constructed based on the law of mass conservation and on the pseudo-steady state hypothesis (PSSH) on the intracellular metabolites. In practicing the methods of the invention, metabolic networks are established, including the:

- identity of all pathway substrates, products and intermediary metabolites
- identity of all the chemical reactions interconverting the pathway metabolites, the stoichiometry of the pathway reactions,
- identity of all the enzymes catalyzing the reactions, the enzyme reaction kinetics,
- the regulatory interactions between pathway components, e.g. allosteric interactions, enzyme-enzyme interactions etc,
- intracellular compartmentalization of enzymes or any other supramolecular organization of the enzymes, and,
- the presence of any concentration gradients of metabolites, enzymes or effector molecules or diffusion barriers to their movement.

Once the metabolic network for a given strain is built, mathematic presentation by matrix notion can be introduced to estimate the intracellular metabolic fluxes if the on-line metabolome data is available. Metabolic phenotype relies on the changes of the whole metabolic network within a cell. Metabolic phenotype relies on the change of pathway utilization with respect to environmental conditions, genetic regulation, developmental state and the genotype, etc. In one aspect of the methods of the invention, after the on-line MFA calculation, the dynamic behavior of the cells, their phenotype and other properties are analyzed by investigating the pathway utilization. For example, if the glucose supply is increased and the oxygen decreased during the yeast fermentation, the utilization of respiratory pathways will be reduced and/or stopped, and the utilization of the fermentative pathways will dominate. Control of physiological state of cell cultures will become possible after the pathway analysis. The methods of the invention can help determine how to manipulate the fermentation by determining how to change the substrate supply, temperature, use of inducers, etc. to control the physiological state of cells to move along desirable direction. In practicing the methods of the invention, the

MFA results can also be compared with transcriptome and proteome data to design experiments and protocols for metabolic engineering or gene shuffling, etc.

In practicing the methods of the invention, any modified or new phenotype can be conferred and detected, including new or improved characteristics in the cell. Any aspect of metabolism or growth can be monitored.

Monitoring expression of an mRNA transcript

In one aspect of the invention, the engineered phenotype comprises increasing or decreasing the expression of an mRNA transcript (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, message) or generating new (e.g., polypeptide, enzyme, protein, e.g. structural or binding protein) transcripts in a cell. This increased or decreased expression can be traced by testing for the presence of a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention or by a polypeptide, enzyme, protein, e.g. structural or binding protein, activity assays. Such assays are well known in the art. mRNA transcripts, or messages, also can be detected and quantified by any method known in the art, including, e.g., Northern blots, quantitative amplification reactions, hybridization to arrays, and the like. Quantitative amplification reactions include, e.g., quantitative PCR, including, e.g., quantitative reverse transcription polymerase chain reaction, or RT-PCR; quantitative real time RT-PCR, or "real-time kinetic RT-PCR" (see, e.g., Kreuzer (2001) *Br. J. Haematol.* 114:313-318; Xia (2001) *Transplantation* 72:907-914).

In one aspect of the invention, the engineered phenotype is generated by knocking out expression of a homologous gene. The gene's coding sequence or one or more transcriptional control elements can be knocked out, e.g., promoters or enhancers. Thus, the expression of a transcript can be completely ablated or only decreased.

In one aspect of the invention, the engineered phenotype comprises increasing the expression of a homologous gene. This can be effected by knocking out of a negative control element, including a transcriptional regulatory element acting in cis- or trans-, or, mutagenizing a positive control element. One or more, or, all the transcripts of a cell can be measured by hybridization of a sample comprising transcripts of the cell, or, nucleic acids representative of or complementary to transcripts of a cell, by hybridization to immobilized nucleic acids on an array.

Monitoring expression of a polypeptides, peptides and amino acids

In one aspect of the invention, the engineered phenotype comprises increasing or decreasing the expression of a polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,) or generating new polypeptides in a cell. This increased or decreased expression can be traced by determining the amount of a polypeptide, enzyme, protein, e.g. structural or binding protein, present or by a polypeptide, enzyme, protein, e.g. structural or binding protein, activity assays.

Polypeptides, peptides and amino acids also can be detected and quantified by any method known in the art, including, e.g., nuclear magnetic resonance (NMR), spectrophotometry, radiography (protein radiolabeling), electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, various immunological methods, e.g. immunoprecipitation, immunodiffusion, immuno-electrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, gel electrophoresis (e.g., SDS-PAGE), staining with antibodies, fluorescent activated cell sorter (FACS), pyrolysis mass spectrometry, Fourier-Transform Infrared Spectrometry, Raman spectrometry, GC-MS, and LC-Electrospray and cap-LC-tandem-electrospray mass spectrometries, and the like. Novel bioactivities can also be screened using methods, or variations thereof, described in U.S. Patent No. 6,057,103. Furthermore, as discussed below in detail, one or more, or, all the polypeptides of a cell can be measured using a protein array.

Pharmaceutical Compositions and Dietary Supplements

The invention provides pharmaceutical compositions, e.g., formulations, comprising a composition (including polypeptide, nucleic acid, or antibody) of the invention and a pharmaceutically acceptable excipient. The invention provides enteral and parenteral formulations comprising compositions of the invention. For example, the invention provides oral formulations (including or dietary supplements) comprising a composition of the invention. The invention provides formulations and methods for treating, ameliorating, diagnosing or preventing disease of condition of interest; e.g., in one aspect the invention provides methods comprising providing a pharmaceutical composition or dietary supplement comprising a composition of the invention; and administering an effective amount of the pharmaceutical composition or dietary supplement to a subject in need thereof.

The compositions and methods of the invention can also be practiced *ex vivo* or *in vitro*, or on a non-biological fluid or substance. In one aspect, the compositions and methods comprise providing a pharmaceutical composition or dietary supplement comprising a formulation of the invention; and administering an effective amount of the pharmaceutical composition or dietary supplement to a subject in need thereof.

The pharmaceutical compositions and dietary supplements used in the methods of the invention can be administered by any means known in the art, e.g., parenterally, topically, orally, or by local administration, such as by aerosol or transdermally. The compositions and dietary supplements of the invention can be formulated as a tablet, gel, gellab, pill, implant, liquid, spray, powder, food, feed pellet, as an injectable formulation or as an encapsulated formulation. The pharmaceutical compositions and dietary supplements can be formulated in any way and can be administered in a variety of unit dosage forms depending upon the condition or disease and the degree of illness, the general medical condition of each patient, the resulting preferred method of administration and the like. Details on techniques for formulation and administration are well described in the scientific and patent literature, see, e.g., the latest edition of Remington's Pharmaceutical Sciences, Maack Publishing Co, Easton PA ("Remington's") (e.g., Remington, The Science and Practice of Pharmacy, 21st Edition, by University of the Sciences in Philadelphia, Editor).

Pharmaceutical formulations and dietary supplements can be prepared according to any method known to the art for the manufacture of pharmaceuticals and dietary supplements. Such drugs and dietary supplements can contain sweetening agents, flavoring agents, coloring agents and preserving agents. A formulation (which includes "dietary supplements") can be admixed with nontoxic pharmaceutically or orally acceptable excipients which are suitable for manufacture. Formulations may comprise one or more diluents, emulsifiers, preservatives, buffers, excipients, etc. and may be provided in such forms as liquids, powders, emulsions, lyophilized powders, sprays, creams, lotions, controlled release formulations, tablets, pills, gels, on patches, in implants, etc.

Pharmaceutical formulations and dietary supplements for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in appropriate and suitable dosages. Such carriers enable the pharmaceuticals and dietary supplements to be formulated in unit dosage forms as tablets, pills, powder, dragees, capsules, liquids, lozenges, gels, syrups, slurries, suspensions, etc., suitable for ingestion

by the patient. Pharmaceutical preparations and dietary supplements for oral use can be formulated as a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable additional compounds, if desired, to obtain tablets or dragee cores. Suitable solid excipients are carbohydrate or protein fillers include, e.g., sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxy-methylcellulose; and gums including arabic and tragacanth; and proteins, e.g., gelatin and collagen. Disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores are provided with suitable coatings such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound (i.e., dosage). Pharmaceutical preparations and dietary supplements of the invention can also be used orally using, e.g., push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating such as glycerol or sorbitol. Push-fit capsules can contain active agents mixed with a filler or binders such as lactose or starches, lubricants such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active agents can be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycol with or without stabilizers.

Aqueous suspensions can contain an active agent (e.g., an enzyme or peptidomimetic of the invention) in admixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients include a suspending agent, such as sodium carboxymethylcellulose, methylcellulose, hydroxypropylmethylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia, and dispersing or wetting agents such as a naturally occurring phosphatide (e.g., lecithin), a condensation product of an alkylene oxide with a fatty acid (e.g., polyoxyethylene stearate), a condensation product of ethylene oxide with a long chain aliphatic alcohol (e.g., heptadecaethylene oxycetanol), a condensation product of ethylene oxide with a partial ester derived from a fatty acid and a hexitol (e.g., polyoxyethylene sorbitol mono-oleate), or a condensation product of ethylene oxide with a partial ester derived from fatty acid and a hexitol anhydride (e.g., polyoxyethylene sorbitan mono-oleate). The aqueous

suspension can also contain one or more preservatives such as ethyl or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents and one or more sweetening agents, such as sucrose, aspartame or saccharin. Formulations can be adjusted for osmolarity.

Oil-based pharmaceuticals are particularly useful for administration of hydrophobic formulations or active agents of the invention. Oil-based suspensions can be formulated by suspending an active agent (e.g., a composition of the invention) in a vegetable oil, such as arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin; or a mixture of these. See e.g., U.S. Patent No. 5,716,928 describing using essential oils or essential oil components for increasing bioavailability and reducing inter- and intra-individual variability of orally administered hydrophobic pharmaceutical compounds (see also U.S. Patent No. 5,858,401). The oil suspensions can contain a thickening agent, such as beeswax, hard paraffin or cetyl alcohol. Sweetening agents can be added to provide a palatable oral preparation, such as glycerol, sorbitol or sucrose. These formulations and dietary supplements can be preserved by the addition of an antioxidant such as ascorbic acid. As an example of an injectable oil vehicle, see Minto (1997) *J. Pharmacol. Exp. Ther.* 281:93-102.

The pharmaceutical formulations and dietary supplements of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil, described above, or a mixture of these. Suitable emulsifying agents include naturally-occurring gums, such as gum acacia and gum tragacanth, naturally occurring phosphatides, such as soybean lecithin, esters or partial esters derived from fatty acids and hexitol anhydrides, such as sorbitan mono-oleate, and condensation products of these partial esters with ethylene oxide, such as polyoxyethylene sorbitan mono-oleate. The emulsion can also contain sweetening agents and flavoring agents, as in the formulation of syrups and elixirs. Such formulations can also contain a demulcent, a preservative, or a coloring agent.

In the methods of the invention, the pharmaceutical compounds and dietary supplements can also be administered by intranasal, intraocular and intravaginal routes including suppositories, insufflation, powders and aerosol formulations (for examples of steroid inhalants, see Rohatagi (1995) *J. Clin. Pharmacol.* 35:1187-1193; Tjwa (1995) *Ann. Allergy Asthma Immunol.* 75:107-111). Suppositories formulations can be prepared by mixing the drug with a suitable non-irritating excipient which is solid at ordinary temperatures but liquid at body temperatures and will therefore melt in the body

to release the drug. Such materials are cocoa butter and polyethylene glycols.

In the methods of the invention, the pharmaceutical compounds and dietary supplements can be delivered by transdermally, by a topical route, formulated as applicator sticks, solutions, suspensions, emulsions, gels, creams, ointments, pastes, jellies, paints, powders, and aerosols.

In the methods of the invention, the pharmaceutical compounds and dietary supplements can also be delivered as microspheres for slow release in the body. For example, microspheres can be administered via intradermal injection of drug which slowly release subcutaneously; see Rao (1995) *J. Biomater Sci. Polym. Ed.* 7:623-645; as biodegradable and injectable gel formulations, see, e.g., Gao (1995) *Pharm. Res.* 12:857-863 (1995); or, as microspheres for oral administration, see, e.g., Eyles (1997) *J. Pharm. Pharmacol.* 49:669-674.

In the methods of the invention, the pharmaceutical compounds can be parenterally administered, such as by intravenous (IV) administration or administration into a body cavity or lumen of an organ. These formulations can comprise a solution of active agent dissolved in a pharmaceutically acceptable carrier. Acceptable vehicles and solvents that can be employed are water and Ringer's solution, an isotonic sodium chloride. In addition, sterile fixed oils can be employed as a solvent or suspending medium. For this purpose any bland fixed oil can be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid can likewise be used in the preparation of injectables. These solutions are sterile and generally free of undesirable matter. These formulations may be sterilized by conventional, well known sterilization techniques. The formulations may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like, in accordance with the particular mode of administration selected and the patient's needs. For IV administration, the formulation can be a sterile injectable preparation, such as a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated using those suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation can also be a suspension in a nontoxic parenterally-acceptable diluent or solvent, such as a solution of 1,3-butanediol. The administration can be by bolus or continuous infusion (e.g.,

substantially uninterrupted introduction into a blood vessel for a specified period of time).

The pharmaceutical compounds, formulations and dietary supplements of the invention can be lyophilized. The invention provides a stable lyophilized formulation comprising a composition of the invention, which can be made by lyophilizing a solution comprising a pharmaceutical of the invention and a bulking agent, e.g., mannitol, trehalose, raffinose, and sucrose or mixtures thereof. A process for preparing a stable lyophilized formulation can include the equivalent of lyophilizing a solution about 2.5 mg/mL protein, about 15 mg/mL sucrose, about 19 mg/mL NaCl, and a sodium citrate buffer having a pH greater than 5.5 but less than 6.5. See, e.g., U.S. patent app. no. 20040028670.

The compositions (e.g., formulations, including dietary supplements) of the invention can be delivered by the use of liposomes. By using liposomes, particularly where the liposome surface carries ligands specific for target cells, or are otherwise preferentially directed to a specific organ, one can focus the delivery of the active agent into target cells *in vivo*. See, e.g., U.S. Patent Nos. 6,063,400; 6,007,839; Al-Muhammed (1996) *J. Microencapsul.* 13:293-306; Chonn (1995) *Curr. Opin. Biotechnol.* 6:698-708; Ostro (1989) *Am. J. Hosp. Pharm.* 46:1576-1587.

The compositions (e.g., formulations, including dietary supplements) of the invention can be administered for prophylactic and/or therapeutic treatments. In therapeutic applications, compositions are administered to a subject already suffering from a condition, infection or disease of interest in an amount sufficient to cure, alleviate or partially arrest the clinical manifestations of the condition, infection or disease and its complications (a "therapeutically effective amount"). In the methods of the invention, a pharmaceutical composition is administered in an amount sufficient to treat (e.g., ameliorate) or prevent a disease-related condition, a diseases or a symptoms, or to decrease or increase the amount of substance in a body fluid such as blood, serum, CSF and the like. The amount of composition (e.g., pharmaceutical compositions, formulations, including dietary supplements) adequate to accomplish this is defined as a "therapeutically effective dose." The dosage schedule and amounts effective for this use, i.e., the "dosing regimen," will depend upon a variety of factors, including the stage of the disease or condition, the severity of the disease or condition, the general state of the patient's health, the patient's physical status, age and the like. In calculating the dosage regimen for a patient, the mode of administration also is taken into consideration.

The dosage regimen also takes into consideration pharmacokinetics parameters

well known in the art, i.e., the active agents' rate of absorption, bioavailability, metabolism, clearance, and the like (see, e.g., Hidalgo-Aragones (1996) *J. Steroid Biochem. Mol. Biol.* 58:611-617; Groning (1996) *Pharmazie* 51:337-341; Fotherby (1996) *Contraception* 54:59-69; Johnson (1995) *J. Pharm. Sci.* 84:1144-1146; Rohatagi (1995) *Pharmazie* 50:610-613; Brophy (1983) *Eur. J. Clin. Pharmacol.* 24:103-108; the latest Remington's, *supra*). The state of the art allows the clinician to determine the dosage regimen for each individual patient, active agent and disease or condition treated. Guidelines provided for similar compositions used as pharmaceuticals can be used as guidance to determine the dosage regiment, i.e., dose schedule and dosage levels, administered practicing the methods of the invention are correct and appropriate.

Single or multiple administrations of compositions (e.g., pharmaceutical compositions, formulations, including dietary supplements) of the invention can be given depending on the dosage and frequency as required and tolerated by the patient. The compositions should provide a sufficient quantity of active agent to effectively treat, ameliorate or prevent PKU or other PKU-related conditions, diseases or symptoms. For example, an exemplary pharmaceutical formulation for oral administration of a protein of the invention is in a daily amount of between about 0.1 to 0.5 to about 20, 50, 100 or 1000 or more μg per kilogram of body weight per day. In an alternative embodiment, dosages are from about 1 mg to about 4 mg per kg of body weight per patient per day are used. Lower dosages can be used, in contrast to administration orally, into the blood stream, into a body cavity or into a lumen of an organ. Substantially higher dosages can be used in topical or oral administration or administering by powders, spray or inhalation. Actual methods for preparing parenterally or non-parenterally administrable formulations will be known or apparent to those skilled in the art and are described in more detail in such publications as Remington's, *supra*.

The compositions (e.g., pharmaceutical compositions, formulations, including dietary supplements) of the invention can further comprise other drugs or pharmaceuticals, e.g., compositions for treating a disease of interest and related symptoms or conditions. The methods of the invention can further comprise co-administration with other drugs or pharmaceuticals, e.g., compositions for treating septic shock, infection, fever, pain and related symptoms or conditions. For example, the methods and/or compositions and formulations of the invention can be co-formulated with and/or co-administered with antibiotics (e.g., antibacterial or bacteriostatic peptides or proteins), particularly those effective against bacteria or toxins, e.g., germ warfare

agents, gram negative bacteria, fluids, cytokines, immunoregulatory agents, anti-inflammatory agents, complement activating agents, such as peptides or proteins comprising collagen-like domains or fibrinogen-like domains (e.g., a ficolin), carbohydrate-binding domains, and the like and combinations thereof.

In one aspect, the polypeptide (e.g., including a pharmaceutical composition or dietary supplement) of the invention is chemically modified. For example, the polypeptide can be chemically modified to produce a protected form that possesses better specific activity, prolonged half-life, and/or reduced immunogenicity *in vivo*. A polypeptide of the invention can be modified by any means known in the art, for example, by glycosylation, pegylation or a combination thereof.

In one aspect, the polypeptide (e.g., including a pharmaceutical composition or dietary supplement) of the invention is formulated by encapsulation in a liposome, or a micro- or nano-structure, such as a nanotubule or a nano- or microcapsule.

In one aspect, the polypeptide is formulated in a matrix stabilized enzyme crystal. The invention also provides matrix stabilized enzyme crystals comprising a polypeptide of the invention for use as pharmaceutical composition or dietary supplement, e.g., to treat or ameliorate a disease or condition of interest, e.g., as described in U.S. Patent App. No. 20020182201; for example, the formulation can be a cross-linked crystalline enzyme and a polymer with a reactive moiety effective to adhere to the crystal layer of the crystalline enzyme. The invention also provides polypeptides of the invention as polymers in the form of multimerized (e.g., multi-functional) cross-linking forms; which in one aspect comprise a matrix stabilized enzyme crystal, e.g., a form resistant to degradation by proteolytic enzymes; and in alternative aspects, the cross-linking reagents comprise a dialdehyde cross-linking reagent, such as a linear or branched dialdehyde, or a substituted or unsubstituted glutaraldehyde (1,5-pentanedial), malonaldehyde (1,3-propanedial), succinaldehyde (1,4-butanedial), adipaldehyde (1,6-hexanedial), pimelaldehyde (1,7-heptanedial), or, glutaraldehyde; in other alternative aspects, the cross-linking reagents comprise carbodiimides, isoxazolium derivatives, chloroformates, carbonyldiimidazole, bis-imidoesters, bis-succinimidyl derivatives, di-isocyanates, di-isothiocyanates, di-sulfonyl halides, bis-nitrophenyl esters, dialdehydes, diacylazides, bis-maleimides, bis-haloacetyl derivatives, di-alkyl halides and bis-oxiranes (e.g., as described in U.S. Pat. No. 5,753,487).

The compositions of the invention can also be manufactured into biocompatible matrices, e.g., sol-gels, for encapsulating a polypeptide of the invention for use as

pharmaceutical composition or dietary supplement, e.g., to treat or ameliorate a disease or condition of interest. In one aspect, compositions of the invention are manufactured as silica-based (e.g., oxysilane) sol-gel matrices, e.g., as described in U.S. Pat. No. 6,395,299, Pat. App. No. 20040241205. The invention also provides nano- or microcapsules comprising a composition of the invention for use as pharmaceutical composition or dietary supplement, e.g., to treat or ameliorate a disease or condition of interest, e.g., as described in U.S. Patent App. No. 20030157181.

The pharmaceutical compositions of the invention can be manufactured using any conventional method, e.g., mixing, dissolving, granulating, dragée-making, levigating, emulsifying, encapsulating, entrapping, melt-spinning, spray-drying, or lyophilizing processes. Alternative pharmaceutical formulations can be determined depending on the patient (e.g., adult or pediatric), condition, route of administration (e.g., oral) and the desired dosage.

Applications – Industrial, Medical, Experimental, Food and Feed Processing

Polypeptides (including enzymes and antibodies) and nucleic acids of the invention can be used for a variety of industrial, experimental, food and feed processing, nutritional and pharmaceutical applications, e.g., for food and feed supplements, colorants, nutraceuticals, cosmetic and pharmaceutical needs.

Polypeptides of the invention (e.g., having enzyme, structural or binding activity) can be highly selective catalysts. The invention provides methods using enzymes of the invention in the food and feed industries, e.g., in methods for making food and feed products and food and feed additives. In one aspect, the invention provides processes using enzymes of the invention in the medical industry, e.g., to make pharmaceuticals.

The enzymes of the invention can catalyze reactions with exquisite stereo-, regio- and chemo- selectivities. The polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention can be engineered to function in various solvents, operate at extreme pHs (for example, high pHs and low pHs) extreme temperatures (for example, high temperatures and low temperatures), extreme salinity levels (for example, high salinity and low salinity) and catalyze reactions with compounds that are structurally unrelated to their natural, physiological substrates.

Animal feeds and food or feed additives

The invention provides compositions (e.g., enzymes of the invention, as those described in Tables 1, 2, and 3) methods for treating animal feeds and foods and food or

feed additives using a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, and/or the antibodies of the invention. The invention provides animal feeds, foods, and additives comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, antibodies of the invention. The animal can be any farm animal or any animal raised for its meat, e.g., a pig, goat, cattle, sheep, horse and the like.

The animal feed additive of the invention may be a granulated enzyme product that may readily be mixed with feed components. Alternatively, feed additives of the invention can form a component of a pre-mix. The granulated enzyme product of the invention may be coated or uncoated. The particle size of the enzyme granulates can be compatible with that of feed and pre-mix components. This provides a safe and convenient mean of incorporating enzymes into feeds. Alternatively, the animal feed additive of the invention may be a stabilized liquid composition. This may be an aqueous or oil-based slurry. See, e.g., U.S. Patent No. 6,245,546.

A polypeptide, enzyme, protein, e.g. structural or binding protein, of the present invention, in the modification of animal feed or a food, can process the food or feed either *in vitro* (by modifying components of the feed or food) or *in vivo*. Polypeptides of the invention can be added to animal feed or food compositions.

In one aspect, an enzyme of the invention has any of the following enzyme activities, or is added in combination with another enzyme, e.g., beta-galactosidases, catalases, laccases, cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylo-laccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, cellobiohydrolases and/or transglutaminases. These enzyme digestion products are more digestible by the animal. Thus, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can contribute to the available energy of the feed or food. Also, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can improve the digestibility and uptake of carbohydrate and non-carbohydrate feed or food constituents such as protein, fat and minerals.

In another aspect, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can be supplied by expressing the enzymes directly in transgenic feed crops (as, e.g., transgenic plants, seeds and the like), such as grains, cereals, corn, soy bean, rape seed, lupin and the like. As discussed above, the invention provides transgenic plants, plant parts and plant cells comprising a nucleic acid sequence encoding a polypeptide of the invention. In one aspect, the nucleic acid is expressed such that the polypeptide, enzyme, protein, e.g. structural or binding protein of the invention is produced in recoverable quantities. The polypeptide, enzyme, protein, e.g. structural or binding protein can be recovered from any plant or plant part. Alternatively, the plant or plant part containing the recombinant polypeptide can be used as such for improving the quality of a food or feed, e.g., improving nutritional value, palatability, etc.

The enzyme delivery matrix of the invention is in the form of discrete plural particles, pellets or granules. By "granules" is meant particles that are compressed or compacted, such as by a pelletizing, extrusion, or similar compacting to remove water from the matrix. Such compression or compacting of the particles also promotes intraparticle cohesion of the particles. For example, the granules can be prepared by pelletizing the grain-based substrate in a pellet mill. The pellets prepared thereby are ground or crumbled to a granule size suitable for use as an adjuvant in animal feed. Since the matrix is itself approved for use in animal feed, it can be used as a diluent for delivery of enzymes in animal feed.

The polypeptide, enzyme, protein, e.g. structural or binding protein contained in the invention enzyme delivery matrix and methods is in one aspect thermostable polypeptide, enzyme, protein, e.g. structural or binding protein, as described herein, so as to resist inactivation of the polypeptide, enzyme, protein, e.g. structural or binding protein during manufacture where elevated temperatures and/or steam may be employed to prepare the palletized enzyme delivery matrix. During digestion of feed containing the invention enzyme delivery matrix, aqueous digestive fluids will cause release of the active enzyme. Other types of thermostable enzymes and nutritional supplements that are thermostable can also be incorporated in the delivery matrix for release under any type of aqueous conditions.

A coating can be applied to the invention enzyme matrix particles for many different purposes, such as to add a flavor or nutrition supplement to animal feed, to delay release of animal feed supplements and enzymes in gastric conditions, and the like. Or, the coating may be applied to achieve a functional goal, for example, whenever it is

desirable to slow release of the enzyme from the matrix particles or to control the conditions under which the enzyme will be released. The composition of the coating material can be such that it is selectively broken down by an agent to which it is susceptible (such as heat, acid or base, enzymes or other chemicals). Alternatively, two or more coatings susceptible to different such breakdown agents may be consecutively applied to the matrix particles.

The invention is also directed towards a process for preparing an enzyme-releasing matrix. In accordance with the invention, the process comprises providing discrete plural particles of a grain-based substrate in a particle size suitable for use as an enzyme-releasing matrix, wherein the particles comprise a polypeptide, enzyme, protein, e.g. structural or binding protein, encoded by an amino acid sequence of the invention. In one aspect, the process includes compacting or compressing the particles of enzyme-releasing matrix into granules, which most in one aspect is accomplished by pelletizing. The mold inhibitor and cohesiveness agent, when used, can be added at any suitable time, and in one aspect are mixed with the grain-based substrate in the desired proportions prior to pelletizing of the grain-based substrate. Moisture content in the pellet mill feed in one aspect is in the ranges set forth above with respect to the moisture content in the finished product, and in one aspect is about 14-15%. In one aspect, moisture is added to the feedstock in the form of an aqueous preparation of the enzyme to bring the feedstock to this moisture content. The temperature in the pellet mill in one aspect is brought to about 82°C with steam. The pellet mill may be operated under any conditions that impart sufficient work to the feedstock to provide pellets. The pelleting process itself is a cost-effective process for removing water from the enzyme-containing composition.

The compositions and methods of the invention can be practiced in conjunction with various nutritional and environmental factors including, e.g., (1) manipulation of gut microflora by supplementing feed with prebiotics and/or antibiotics, (2) low fiber diet (low energy and low purine diet), (3) restricting feed for 48 hours and withholding feed for 12 hours before slaughter, (4) increasing consumption of water, and/or (5) keeping animals clean.

The compositions and methods of the invention can be practiced in conjunction with administration of prebiotics, which are high molecular weight sugars, e.g., fructo-oligosaccharides (FOS); galacto-oligosaccharides (GOS), GRAS (Generally Recognized As Safe) material. These prebiotics can be metabolized by some probiotic lactic acid bacteria (LAB). They are non-digestible by the majority of intestinal microbes.

Treating foods and food processing

The polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention, e.g., as described in Tables 1, 2, and 3, have numerous applications in food processing industry. The invention provides treatment compositions, including, e.g., a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell, or any plant or plant part, or any food or feed, a waste product and the like.

The invention provides feeds or foods comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, the invention, e.g., a feed, a liquid, e.g., a beverage (such as a fruit juice or a beer), a bread or a dough or a bread product, or a beverage precursor (e.g., a wort).

The food treatment processes of the invention can comprise use of any enzyme of the invention, which can have the following enzymatic activities, and also include the use of any combination of any enzyme, including lyases, laccases, catalases, laccases, cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, cellobiohydrolases and/or transglutaminases.

Confectionaries, cacao butter and foods

In one aspect, the compositions and methods of the invention can be used to make and process hard butters, such as cacao butter (cocoa butter). The compositions and methods of the invention can be used to make cocoa butter alternatives by "structured" synthetic techniques using the enzymes of the invention, e.g., as described in Tables 1, 2, and 3, including esterases, acylases, lipases, phospholipases or proteases of the invention. For example, in one aspect, the methods of the invention process or synthesize triacylglycerides, diacylglycerides and/or monoacylglycerides for use as, e.g., cocoa butter alternatives. In one aspect, the methods of the invention generate a hard butter with a defined "plastic region" to maintain sufficient hardness below or at room temperature. In one aspect, the processed or synthesized lipid is designed to have a very narrow "plastic region," e.g., in one aspect, where it rapidly melts at about body temperature. Natural cacao butter begins to soften at approximately 30°C to 32°C, and

completely melts at approximately 36⁰C. Natural cacao butter can contain 70 wt % or more of three 1,3-disaturated -2-oleoyl glycerols, which are 1,3-dipalmitoyl-2-oleoyl glycerol (POP), 1-palmitoyl-2-oleoyl glycerol (POSt) and 1,3-distearoyl-2-oleoyl glycerol (StOSt). These three glycerols show a similar melting behavior to each other and are responsible for melting properties of the cacao butter, exhibiting a very narrow plastic region. The invention provides synthetic cacao butters or processed cacao butters (synthesized or processed using a hydrolase of the invention, all possible composition are referred to as cocoa-butter alternatives) with varying percentages of ,3-dipalmitoyl-2-oleoyl glycerol (POP), 1-palmitoyl-2-oleoyl glycerol (POSt) and 1,3-distearoyl-2-oleoyl glycerol (StOSt), depending on the desired properties of the synthetic cacao butter, and, synthetic cacao butters with more or less than 70 wt % of the three 1,3-disaturated -2-oleoyl glycerols. The synthetic cacao butters of the invention can partially or completely replace natural or unprocessed cacao butters and can maintain or improve essential hard butter properties.

The invention provides synthetic cacao butters or processed cacao butters (synthesized or processed using a hydrolase of the invention) with desired properties for use in confectionary, bakery and pharmaceutical products. In one aspect, the invention provides confectionary, bakery and pharmaceutical products comprising a hydrolase of the invention. In one aspect, the methods of the invention make or process a lipid (a fat) from a confection (e.g., a chocolate) or to be used in a confection. In one aspect, a lipid is made or processed such that the chocolate shows less finger-imprinting than chocolate made from natural cocoa butter, while still having sharp melting characteristics in the mouth. In one aspect, a lipid is made or processed such that a confection (e.g., chocolate) can be made at a comparatively high ambient temperature, or, be made using a cooling water at a comparatively high temperature. In one aspect, the lipid is made or processed such that a confection (e.g., chocolate) can be stored under relatively warmer conditions, e.g., tropical or semi-tropical conditions or in centrally heated buildings. In one aspect, the lipids are made or processed such that a confection (e.g., chocolate) will have a lipid (fat) content of consistent composition and quality. The enzymes of the invention can be used to provide a substitute composition for cacao butter which can significantly improve its thermal stability and replace it in a wide range of applications.

Margarine and shortening production

The invention provides synthetic or processed fats, e.g., margarine and shortening synthesized or processed using an enzyme of the invention, e.g., as described in Tables 1,

2, and 3, such as a hydrolase of the invention. In one aspect, the invention provides processed fats comprising a vegetable oil, such as soybean oil, corn oil, rapeseed oil, palm oil or lauric type oils synthesized or processed using a hydrolase of the invention. The synthetic or processed fats, e.g., margarine and shortening, are designed to have a desired "plasticity." Many of the plastic fat products, such as margarine and shortening, are produced from hard stocks and liquid oils as raw materials. For example, liquid oils such as soybean oil, corn oil, palm oil and rapeseed oil, are blended with their hardened oils (hard stocks), and the blend is adjusted to have an appropriate consistency (plasticity). The plastic fat products such as margarine and shortening so produced tend to cause the formation of relatively coarse crystallines because fats and oils used as the raw materials are composed of fatty acids having almost the same carbon chain length. In other words, they have a highly-unified composition of fatty acids. For this reason, the plasticity of these products can be maintained at an appropriate degree only within a narrow temperature range, so that the liquid oils contained therein have a tendency to exude. In one aspect, the invention provides methods of making or processing fats designed such that they have a varied (and defined) composition of fatty acids. The resultant oil, e.g., margarine or shortening, can have a broader range of plasticity.

In one aspect, the methods and compositions of the invention are used to make or process vegetable oils, such as soybean oil, corn oil, rapeseed oil, palm oil or lauric type oils using the hydrolases of the invention, including inter-esterification and enzymatic transesterification, see e.g., U.S. Patent No. 5,288,619. The methods and compositions of the invention can be used in place of random inter-esterification as described in, e.g., U.S. Patent No. 3,949,105. In one aspect, the methods and compositions of the invention are used to in enzymatic transesterification for preparing an oil, e.g., a margarine oil, having both low trans- acid and low intermediate chain fatty acid content.

In one aspect, the symmetric structure of an oil, e.g., a palm or lauric type oils is modified, e.g., into a random structure. Thus, the methods of the invention can be used to modify the properties of plastic fat products. In one aspect, the modification of oils by the methods of the invention can be designed to prevent or slow gradually hardening of the oil with time, particularly when the products are being stored.

In one aspect, the methods and compositions of the invention in a trans-esterification reaction mixture comprising a stearic acid source material and an edible liquid vegetable oil, trans-esterifying the stearic acid source material and the vegetable oil using a 1-, 3-positionally specific lipase of the invention, and then hydrogenating the fatty

acid mixture to provide a recycle stearic acid source material for a recyclic reaction with the vegetable oil. See e.g., U.S. Patent No. 5,288,619.

In one aspect, an inter-esterification reaction is conducted with a lipase of the invention. In one aspect, the lipase of the invention has a selectivity for the 1- and 3-positions of triglyceride to slow or inhibit an increase in the amount of tri-saturated triglycerides in the oil. In this reaction of the invention, deficiencies of conventional random inter-esterification and the difficulty of inter-esterification with a non-specific lipase can be overcome because the inter-esterification is conducted by an enzyme of the invention having a specificity for the 1- and 3-positions of triglycerides. In one aspect, the exudation of liquid oils contained in the products is slowed or prevented with a temperature increase in the reaction to inhibit a rise in the melting point caused by an increase in the amount of tri-saturated triglycerides. This addresses the problem of hardening of products during long-term storage.

Brewing and fermenting

The invention provides methods of brewing (e.g., fermenting) beer comprising hydrolases of the invention. In one exemplary process, starch-containing raw materials are disintegrated and processed to form a malt. A hydrolase of the invention is used at any point in the fermentation process. For example, hydrolases (e.g., proteases) of the invention can be used in the processing of barley malt. The major raw material of beer brewing is barley malt. This can be a three stage process. First, the barley grain can be steeped to increase water content, e.g., to around about 40%. Second, the grain can be germinated by incubation at 15 to 25°C for 3 to 6 days when enzyme synthesis is stimulated under the control of gibberellins. In one aspect, hydrolases of the invention are added at this (or any other) stage of the process. The action of hydrolases results in an increase in fermentable reducing sugars. This can be expressed as the diastatic power, DP, which can rise from around 80 to 190 in 5 days at 12°C. Hydrolases (e.g., proteases) of the invention can be used in any beer or alcoholic beverage producing process, as described, e.g., in U.S. Patent No. 5,762,991; 5,536,650; 5,405,624; 5,021,246; 4,788,066.

Waste treatment

The polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention, e.g., as described in Tables 1, 2, and 3, can be used in a variety of other industrial applications, e.g., in waste treatment (in addition to, e.g., biomass conversion to

fuels). For example, in one aspect, the invention provides a solid waste digestion process using a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention. The methods can comprise reducing the mass and volume of substantially untreated solid waste. Solid waste can be treated with an enzymatic digestive process in the presence of an enzymatic solution (including a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention) at a controlled temperature. This results in a reaction without appreciable bacterial fermentation from added microorganisms. The solid waste is converted into a liquefied waste and any residual solid waste. The resulting liquefied waste can be separated from said any residual solidified waste. See e.g., U.S. Patent No. 5,709,796.

In one aspect, the compositions and methods of the invention are used for odor removal or odor reduction in animal waste lagoons, e.g., on swine farms, and other animal waste management systems.

The waste treatment processes of the invention can comprise use of any enzyme of the invention, which can have the following enzymatic activities, and also include the use of any combination of any enzyme or protein, including e.g. structural or binding protein, catalases, lyases, laccases, cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, phytases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, cellobiohydrolases and/or transglutaminases.

Increasing the flow of production fluids from a subterranean formation

The invention also includes a method using an enzyme of the invention, e.g., as described in Tables 1, 2, and 3, wherein the method increases the flow of production fluids from a subterranean formation by removing viscous (e.g., starch-containing) damaging fluids formed during production operations; these fluids can be found within the subterranean formation which surrounds a completed well bore. Thus, this method of the invention results in production fluids being able to flow from the well bore. This method of the invention also addresses the problem of damaging fluids reducing the flow of production fluids from a formation below expected flow rates. In one aspect, the

invention provides for formulating an enzyme treatment (using an enzyme of the invention) by blending together an aqueous fluid and a polypeptide of the invention; pumping the enzyme treatment to a desired location within the well bore; allowing the enzyme treatment to degrade the viscous (e.g., starch-containing) damaging fluid, whereby the fluid can be removed from the subterranean formation to the well surface; and wherein the enzyme treatment is effective to attack linkages in the viscous (e.g., starch-containing) fluid.

The subterranean formation enzyme treatment processes of the invention can comprise use of any enzyme of the invention, which can have the following enzymatic activities, and also include the use of any combination of any enzyme, including tryptophanases or tyrosine decarboxylases, laccases, catalases, lyases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Latex processing

The methods and compositions (e.g., enzymes of the invention, e.g., as described in Tables 1, 2, and 3, including esterases, acylases, lipases, phospholipases or proteases of the invention) of the invention can be used to selectively hydrolyze saturated esters over unsaturated esters into acids or alcohols. In one aspect, the invention provides for the selective hydrolysis of ethyl propionate over ethyl acrylate. In one aspect, these methods are used to remove undesired esters from monomer feeds used in latex polymerization and from the latexes after polymerization. The methods and compositions (hydrolases) of the invention can be used to treat latexes for a variety of purposes, e.g., to treat latexes used in hair fixative compositions to remove unpleasant odors. Latexes treated by the methods and compositions of the invention include, e.g., polymers containing acrylic, vinyl and unsaturated acid monomers, including alkyl acrylate monomers such as methyl acrylate, ethyl acrylate, propyl acrylate and butyl acrylate, and acrylate acids such as acrylic acid, methacrylic acid, crotonic acid, itaconic acid and mixtures thereof. See, e.g.,

U.S. Patent No. 5,856,150.

Biomass conversion and production of clean bio fuels

The invention provides enzymes, e.g., as described in Tables 1, 2, and 3 (including mixtures, or "cocktails" of enzymes) and methods for the conversion of a biomass or any lignocellulosic material (e.g., any composition comprising cellulose, hemicellulose and lignin), to fuels (e.g., bioethanol, biodiesel), in addition to feeds, foods and chemicals. Thus, the compositions and methods of the invention provide effective and sustainable alternatives or adjuncts to use of petroleum-based products, e.g., as a mixture of bioethanol and gasoline. The invention provides organisms expressing enzymes of the invention for participation in chemical cycles involving natural biomass conversion. In one aspect, enzymes and methods for the conversion are used in enzyme ensembles for the efficient depolymerization of cellulosic and hemicellulosic polymers to metabolizeable carbon moieties. The invention provides methods for discovering and implementing the most effective of enzymes to enable these important new "biomass conversion" and alternative energy industrial processes.

The methods of the invention also include taking the converted lignocellulosic material (processed by enzymes of the invention) and making it into a fuel (e.g. a bioethanol, a biodiesel) by fermentation and/or by chemical synthesis. In one aspect, the produced sugars are fermented and/or the non-fermentable products are gasified.

The enzymes of the invention (including, for example, organisms, such as microorganisms, e.g., fungi, yeast or bacteria, making and in some aspects secreting recombinant enzymes of the invention) can be used in or included/ integrated at any stage of any biomass conversion process, e.g., at any one step, several steps, or included in all of the steps, or all of the following methods of biomass conversion processes, or all of these biofuel alternatives:

- Direct combustion: the burning of material by direct heat and is the simplest biomass technology; can be very economical if a biomass source is nearby.
- Pyrolysis: is the thermal degradation of biomass by heat in the absence of oxygen. In one aspect, biomass is heated to a temperature between about 800 and 1400 degrees Fahrenheit, but no oxygen is introduced to support combustion resulting in the creation of gas, fuel oil and charcoal.
- Gasification: biomass can be used to produce methane through heating or anaerobic digestion. Syngas, a mixture of carbon monoxide and hydrogen, can be derived from biomass.
 - Landfill Gas: is generated by the decay (anaerobic digestion) of buried garbage in landfills. When the organic waste decomposes, it generates gas consisting of approximately 50% methane, the major component of natural gas.

- **Anaerobic digestion:** converts organic matter to a mixture of methane, the major component of natural gas, and carbon dioxide. In one aspect, biomass such as wastewater (sewage), manure, or food processing waste, is mixed with water and fed into a digester tank without air.
- **Fermentation**
 - **Alcohol Fermentation:** fuel alcohol is produced by converting starch to sugar, fermenting the sugar to alcohol, then separating the alcohol water mixture by distillation. Feedstocks such as wheat, barley, potatoes, and waste paper, sawdust, and straw containing sugar, starch, or cellulose can be converted to alcohol by fermentation with yeast.
- **Transesterification:** An exemplary reaction for converting oil to biodiesel is called transesterification. The transesterification process reacts an alcohol (like methanol) with the triglyceride oils contained in vegetable oils, animal fats, or recycled greases, forming fatty acid alkyl esters (biodiesel) and glycerin. The reaction requires heat and a strong base catalyst, such as sodium hydroxide or potassium hydroxide.
 - **Biodiesel:** Biodiesel is a mixture of fatty acid alkyl esters made from vegetable oils, animal fats or recycled greases. Biodiesel can be used as a fuel for vehicles in its pure form, but it is usually used as a petroleum diesel additive to reduce levels of particulates, carbon monoxide, hydrocarbons and air toxics from diesel-powered vehicles.
- **Hydrolysis:** includes hydrolysis of a compound, e.g., a biomass, such as a lignocellulosic material, catalyzed using an enzyme of the instant invention.
- **Cogeneration:** is the simultaneous production of more than one form of energy using a single fuel and facility. In one aspect, biomass cogeneration has more potential growth than biomass generation alone because cogeneration produces both heat and electricity.

In one aspect, the polypeptides of the invention have cellulolytic activity, e.g., cellulases activity, such as endoglucanase, cellobiohydrolase and/or β -glucosidase (beta-glucosidase) activity, or other enzymatic activity for generating biodiesel or bioethanol from an organic material, e.g., a biomass, such as compositions derived from plants and animals, including any agricultural crop or other renewable feedstock, an agricultural residue or an animal waste, or the organic components of municipal and industrial wastes, or microorganisms such as algae or yeast. In one aspect, polypeptides of the invention are used in processes for converting lignocellulosic biomass to ethanol, or otherwise are used in processes for hydrolyzing or digesting biomaterials such that they can be used as a biofuel (including biodiesel or bioethanol), or for making it easier for the biomass to be processed into a fuel. In an alternative aspect, polypeptides of the invention are used in processes for a transesterification process reacting an alcohol (like methanol) with a triglyceride oil contained in a vegetable oil, animal fat or recycled greases, forming fatty acid alkyl esters (biodiesel) and glycerin. In one aspect, biodiesel is made from soybean

oil or recycled cooking oils. Animal's fats, other vegetable oils, and other recycled oils can also be used to produce biodiesel, depending on their costs and availability. In another aspect, blends of all kinds of fats and oils are used to produce a biodiesel fuel of the invention.

Enzymes of the invention can also be used in glycerin refining. The glycerin by-product contains unreacted catalyst and soaps that are neutralized with an acid. Water and alcohol are removed to produce 50% to 80% crude glycerin. The remaining contaminants include unreacted fats and oils, which can be processed using the polypeptides of the invention. In a large biodiesel plant of the invention, the glycerin can be further purified, e.g., to 99% or higher purity, for the pharmaceutical and cosmetic industries.

Both bioethanol and biodiesel made using the polypeptides of the invention can be used with fuel oxygenates to improve combustion characteristics. Adding oxygen results in more complete combustion, which reduces carbon monoxide emissions. This is another environmental benefit of replacing petroleum fuels with biofuels (e.g., a fuel of the invention). A bioethanol made using the compositions and/or methods of this invention can be blended with gasoline to form an E10 blend (about 5% to 10% ethanol and about 90% to 95% gasoline), but it can be used in higher concentrations such as E85 or in its pure form. A bioethanol made using the compositions and/or methods of this invention can be blended with petroleum diesel to form a B20 blend (20% biodiesel and 80% petroleum diesel), although other blend levels can be used up to B100 (pure biodiesel).

The invention also provides processes for making ethanol ("bioethanol") from compositions comprising lignocellulosic biomass. The lignocellulose biomass material can be obtained from agricultural crops, as a byproduct of food or feed production, or as lignocellulosic waste products, such as plant residues and waste paper. Examples of suitable plant sources or plant residues for treatment with polypeptides of the invention include kelp, algae, grains, seeds, stems, leaves, hulls, husks, corn cobs, corn stover, straw, grasses (e.g., Indian grass, such as *Sorghastrum nutans*; or, switch grass, e.g., *Panicum* species, such as *Panicum virgatum*), and the like, as well as wood, wood chips, wood pulp, and sawdust. Examples of paper waste suitable for treatment with polypeptides of the invention include discard photocopy paper, computer printer paper, notebook paper, notepad paper, typewriter paper, and the like, as well as newspapers, magazines, cardboard, and paper-based packaging materials.

In one aspect, the enzymes and methods of the invention can be used in conjunction with more "traditional" means of making ethanol from biomass, e.g., as methods comprising hydrolyzing lignocellulosic materials by subjecting dried lignocellulosic material in a reactor to a catalyst comprised of a dilute solution of a strong acid and a metal salt; this can lower the activation energy, or the temperature, of cellulose hydrolysis to obtain higher sugar yields; see, e.g., U.S. Patent Nos. 6,660,506; 6,423,145.

Another exemplary method that incorporated use of enzymes of the invention comprises hydrolyzing lignocellulosic material containing hemicellulose, cellulose and lignin by subjecting the material to a first stage hydrolysis step in an aqueous medium at a temperature and a pressure chosen to effect primarily depolymerization of hemicellulose without major depolymerization of cellulose to glucose. This step results in a slurry in which the liquid aqueous phase contains dissolved monosaccharides resulting from depolymerization of hemicellulose and a solid phase containing cellulose and lignin. A second stage hydrolysis step can comprise conditions such that at least a major portion of the cellulose is depolymerized, such step resulting in a liquid aqueous phase containing dissolved/ soluble depolymerization products of cellulose. See, e.g., U.S. Patent No. 5,536,325. Enzymes of the invention can be added at any stage of this exemplary process.

Another exemplary method that incorporated use of enzymes of the invention comprises processing a lignocellulose-containing biomass material by one or more stages of dilute acid hydrolysis with about 0.4% to 2% strong acid; and treating an unreacted solid lignocellulosic component of the acid hydrolyzed biomass material by alkaline delignification to produce precursors for biodegradable thermoplastics and derivatives. See, e.g., U.S. Patent No. 6,409,841. Enzymes of the invention can be added at any stage of this exemplary process.

Another exemplary method that incorporated use of enzymes of the invention comprises prehydrolyzing lignocellulosic material in a prehydrolysis reactor; adding an acidic liquid to the solid lignocellulosic material to make a mixture; heating the mixture to reaction temperature; maintaining reaction temperature for time sufficient to fractionate the lignocellulosic material into a solubilized portion containing at least about 20% of the lignin from the lignocellulosic material and a solid fraction containing cellulose; removing a solubilized portion from the solid fraction while at or near reaction temperature wherein the cellulose in the solid fraction is rendered more amenable to enzymatic digestion; and recovering a solubilized portion. See, e.g., U.S. Patent No.

5,705,369. Enzymes of the invention can be added at any stage of this exemplary process.

The invention provides methods for making motor fuel compositions (e.g., for spark ignition motors) based on liquid hydrocarbons blended with a fuel grade alcohol made by using an enzyme or a method of the invention. In one aspect, the fuels made by use of an enzyme of the invention comprise, e.g., coal gas liquid- or natural gas liquid-ethanol blends. In one aspect, a co-solvent is biomass-derived 2-methyltetrahydrofuran (MTHF). See, e.g., U.S. Patent No. 6,712,866.

In one aspect, methods of the invention for the enzymatic degradation of lignocellulose, e.g., for production of ethanol from lignocellulosic material, can also comprise use of ultrasonic treatment of the biomass material; see, e.g., U.S. Patent No. 6,333,181.

In another aspect, methods of the invention for producing bioethanol from a cellulosic substrate comprise providing a reaction mixture in the form of a slurry comprising cellulosic substrate, an enzyme of this invention and a fermentation agent (e.g., within a reaction vessel, such as a semi-continuously solids-fed bioreactor), and the reaction mixture is reacted under conditions sufficient to initiate and maintain a fermentation reaction (as described, e.g., in U.S. Pat. App. No. 20060014260). In one aspect, experiment or theoretical calculations can determine an optimum feeding frequency. In one aspect, additional quantities of the cellulosic substrate and the enzyme are provided into the reaction vessel at an interval(s) according to the optimized feeding frequency.

One exemplary process for making a biofuels and biodiesels of the invention is described in U.S. Pat. App. Pub. Nos. 20050069998; 20020164730; and in one aspect comprises stages of grinding the lignocellulosic biomass (e.g., to a size of 15-30 mm), subjecting the product obtained to steam explosion pre-treatment (e.g., at a temperature of 190-230°C) for between 1 and 10 minutes in a reactor; collecting the pre-treated material in a cyclone or related product of manufacture; and separating the liquid and solid fractions by filtration in a filter press, introducing the solid fraction in a fermentation deposit and adding one or more enzymes of the invention, e.g., a cellulase and/or beta-glucosidase enzyme (e.g., dissolved in citrate buffer pH 4.8).

Another exemplary process for making a biofuels and biodiesels of the invention comprising ethanol using enzymes of the invention comprises pretreating a starting material comprising a lignocellulosic feedstock comprising at least hemicellulose and

cellulose. In one aspect, the starting material comprises potatoes, soybean (rapeseed), barley, rye, corn, oats, wheat, beets or sugar cane or a component or waste or food or feed production byproduct. The starting material ("feedstock") is reacted at conditions which disrupt the plant's fiber structure to effect at least a partial hydrolysis of the hemicellulose and cellulose. Disruptive conditions can comprise, e.g., subjecting the starting material to an average temperature of 180°C to 270°C at pH 0.5 to 2.5 for a period of about 5 seconds to 60 minutes; or, temperature of 220°C to 270°C, at pH 0.5 to 2.5 for a period of 5 seconds to 120 seconds, or equivalent. This generates a feedstock with increased accessibility to being digested by an enzyme, e.g., a cellulase enzyme of the invention. U.S. Patent No. 6,090,595.

Exemplary conditions for cellulase hydrolysis of lignocellulosic material include reactions at temperatures between about 30°C and 48°C, and/or a pH between about 4.0 and 6.0. Other exemplary conditions include a temperature between about 30°C and 60°C and a pH between about 4.0 and 8.0.

Detergent Compositions

The invention provides detergent compositions comprising one or more polypeptides of the invention (e.g., enzymes as described in Tables 1, 2, and 3, e.g., having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) and methods of making and using these compositions. The invention incorporates all methods of making and using detergent compositions, see, e.g., U.S. Patent No. 6,413,928; 6,399,561; 6,365,561; 6,380,147. The detergent compositions can be a one and two part aqueous composition, a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel and/or a paste and a slurry form. The invention also provides methods capable of a rapid removal of gross food soils, films of food residue and other minor food compositions using these detergent compositions. Enzymes of the invention can facilitate the removal of starchy stains by means of catalytic hydrolysis of the starch polysaccharide. Enzymes of the invention can be used in dishwashing detergents in textile laundering detergents.

The actual active enzyme content depends upon the method of manufacture of a detergent composition and is not critical, assuming the detergent solution has the desired enzymatic activity. In one aspect, the amount of glucosidase present in the final solution ranges from about 0.001 mg to 0.5 mg per gram of the detergent composition. The particular enzyme chosen for use in the process and products of this invention depends upon the conditions of final utility, including the physical product form, use pH, use

temperature, and soil types to be degraded or altered. The enzyme can be chosen to provide optimum activity and stability for any given set of utility conditions. In one aspect, the polypeptides of the present invention are active in the pH ranges of from about 4 to about 12 and in the temperature range of from about 20°C to about 95°C. The detergents of the invention can comprise cationic, semi-polar nonionic or zwitterionic surfactants; or, mixtures thereof.

Enzymes of the present invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be formulated into powdered and liquid detergents having pH between 4.0 and 12.0 at levels of about 0.01 to about 5% (preferably 0.1% to 0.5%) by weight. These detergent compositions can also include other enzymes such as known proteases, cellulases, lipases or endoglycosidases, as well as builders and stabilizers. The addition of enzymes of the invention to conventional cleaning compositions does not create any special use limitation. In other words, any temperature and pH suitable for the detergent is also suitable for the present compositions as long as the pH is within the above range, and the temperature is below the described enzyme's denaturing temperature. In addition, the polypeptides of the invention can be used in a cleaning composition without detergents, again either alone or in combination with builders and stabilizers.

The present invention provides cleaning compositions including detergent compositions for cleaning hard surfaces, detergent compositions for cleaning fabrics, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, and contact lens cleaning solutions.

In one aspect, the invention provides a method for washing an object comprising contacting the object with a polypeptide of the invention under conditions sufficient for washing. A polypeptide of the invention may be included as a detergent additive. The detergent composition of the invention may, for example, be formulated as a hand or machine laundry detergent composition comprising a polypeptide of the invention. A laundry additive suitable for pre-treatment of stained fabrics can comprise a polypeptide of the invention. A fabric softener composition can comprise a polypeptide of the invention. Alternatively, a polypeptide of the invention can be formulated as a detergent composition for use in general household hard surface cleaning operations. In alternative aspects, detergent additives and detergent compositions of the invention may comprise one or more other enzymes such as a protease, a lipase, a cutinase, another glucosidase, a carbohydrase, another cellulase, a pectinase, a mannanase, an arabinase, a galactanase, a

xylanase, an oxidase, e.g., a lactase, and/or a peroxidase. The properties of the enzyme(s) of the invention are chosen to be compatible with the selected detergent (i.e. pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.) and the enzyme(s) is present in effective amounts. In one aspect, enzymes of the invention are used to remove malodorous materials from fabrics. Various detergent compositions and methods for making them that can be used in practicing the invention are described in, e.g., U.S. Patent Nos. 6,333,301; 6,329,333; 6,326,341; 6,297,038; 6,309,871; 6,204,232; 6,197,070; 5,856,164.

The detergents and related processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylo-laccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Treating fabrics and textiles

The invention provides compositions and methods of treating fabrics and textiles using one or more polypeptides of the invention, e.g., enzymes as described in Tables 1, 2, and 3, including enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity. The polypeptides of the invention can be used in any fabric-treating method, which are well known in the art, see, e.g., U.S. Patent No. 6,077,316. For example, in one aspect, the feel and appearance of a fabric is improved by a method comprising contacting the fabric with an enzyme of the invention in a solution. In one aspect, the fabric is treated with the solution under pressure.

In one aspect, the enzymes of the invention are applied during or after the weaving of textiles, or during the desizing stage, or one or more additional fabric processing steps. During the weaving of textiles, the threads are exposed to considerable mechanical strain. Prior to weaving on mechanical looms, warp yarns are often coated with sizing starch or starch derivatives in order to increase their tensile strength and to prevent breaking. The enzymes of the invention can be applied to remove these sizing

starch or starch derivatives. After the textiles have been woven, a fabric can proceed to a desizing stage. This can be followed by one or more additional fabric processing steps. Desizing is the act of removing size from textiles. After weaving, the size coating must be removed before further processing the fabric in order to ensure a homogeneous and wash-proof result. The invention provides a method of desizing comprising enzymatic hydrolysis of the size by the action of an enzyme of the invention.

The enzymes of the invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be used to desize fabrics, including cotton-containing fabrics, as detergent additives, e.g., in aqueous compositions. The invention provides methods for producing a stonewashed look on indigo-dyed denim fabric and garments. For the manufacture of clothes, the fabric can be cut and sewn into clothes or garments, which is afterwards finished. In particular, for the manufacture of denim jeans, different enzymatic finishing methods have been developed. The finishing of denim garment normally is initiated with an enzymatic desizing step, during which garments are subjected to the action of amylolytic enzymes in order to provide softness to the fabric and make the cotton more accessible to the subsequent enzymatic finishing steps. The invention provides methods of finishing denim garments (e.g., a "bio-stoning process"), enzymatic desizing and providing softness to fabrics using the Enzymes of the invention. The invention provides methods for quickly softening denim garments in a desizing and/or finishing process.

The invention also provides disinfectants comprising enzymes of the invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity).

The fabric or textile treatment processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylo-laccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Paper or pulp treatment

The enzymes of the invention e.g., enzymes as described in Tables 1, 2, and 3, including enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be in paper or pulp treatment or paper deinking. For example, in one aspect, the invention provides a paper treatment process using enzymes of the invention. In one aspect, the enzymes of the invention can be used to modify starch in the paper thereby converting it into a liquefied form. In another aspect, paper components of recycled photocopied paper during chemical and enzymatic deinking processes. In one aspect, Enzymes of the invention can be used in combination with other enzymes, including other cellulases (including other endoglucanases, cellobiohydrolases and/or beta-glucosidases). The wood, paper, paper product or pulp can be treated by the following three processes: 1) disintegration in the presence of an enzyme of the invention, 2) disintegration with a deinking chemical and an enzyme of the invention, and/or 3) disintegration after soaking with an enzyme of the invention. The recycled paper treated with an enzyme of the invention can have a higher brightness due to removal of toner particles as compared to the paper treated with just cellulase. While the invention is not limited by any particular mechanism, the effect of an enzyme of the invention may be due to its behavior as surface-active agents in pulp suspension.

The invention provides methods of treating paper and paper pulp using one or more polypeptides of the invention. The polypeptides of the invention can be used in any paper- or pulp-treating method, which are well known in the art, see, e.g., U.S. Patent No. 6,241,849; 6,066,233; 5,582,681. For example, in one aspect, the invention provides a method for deinking and decolorizing a printed paper containing a dye, comprising pulping a printed paper to obtain a pulp slurry, and dislodging an ink from the pulp slurry in the presence of an enzyme of the invention (other enzymes can also be added). In another aspect, the invention provides a method for enhancing the freeness of pulp, e.g., pulp made from secondary fiber, by adding an enzymatic mixture comprising an enzyme of the invention (can also include other enzymes, e.g., pectinase enzymes) to the pulp and treating under conditions to cause a reaction to produce an enzymatically treated pulp. The freeness of the enzymatically treated pulp is increased from the initial freeness of the secondary fiber pulp without a loss in brightness.

The paper, wood or pulp treatment or recycling processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-

beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipoxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Repulping: treatment of lignocellulosic materials

The invention also provides a method for the treatment of lignocellulosic fibers, wherein the fibers are treated with a polypeptide of the invention e.g., enzymes as described in Tables 1, 2, and 3, including enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity), in an amount which is efficient for improving the fiber properties. The enzymes of the invention may also be used in the production or recycling of lignocellulosic materials such as pulp, paper and cardboard, from starch reinforced waste paper and cardboard, especially where repulping or recycling occurs at pH above 7 and where the enzymes of the invention can facilitate the disintegration of the waste material through degradation of the reinforcing starch. The enzymes of the invention can be useful in a process for producing a papermaking pulp from starch-coated printed paper. The process may be performed as described in, e.g., WO 95/14807. An exemplary process comprises disintegrating the paper to produce a pulp, treating with a starch-degrading enzyme before, during or after the disintegrating, and separating ink particles from the pulp after disintegrating and enzyme treatment. See also U.S. Patent No. 6,309,871 and other US patents cited herein. Thus, the invention includes a method for enzymatic deinking of recycled paper pulp, wherein the polypeptide is applied in an amount which is efficient for effective de-inking of the fiber surface.

Brewing and fermenting

The invention provides compositions for and methods of brewing (e.g., fermenting) beer comprising an enzyme of the invention, e.g., enzymes as described in Tables 1, 2, and 3, including enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity. In one exemplary process, starch-containing

raw materials are disintegrated and processed to form a malt. An enzyme of the invention is used at any point in the fermentation process. For example, enzymes of the invention can be used in the processing of barley malt. The major raw material of beer brewing is barley malt. This can be a three stage process. First, the barley grain can be steeped to increase water content, e.g., to around about 40%. Second, the grain can be germinated by incubation at 15-25°C for 3 to 6 days when enzyme synthesis is stimulated under the control of gibberellins. During this time enzyme levels rise significantly. In one aspect, enzymes of the invention are added at this (or any other) stage of the process. The action of the enzyme results in an increase in fermentable reducing sugars. This can be expressed as the diastatic power, DP, which can rise from around 80 to 190 in 5 days at 12°C.

Enzymes of the invention can be used in any beer producing process, as described, e.g., in U.S. Patent No. 5,762,991; 5,536,650; 5,405,624; 5,021,246; 4,788,066.

Pharmaceutical compositions and dietary supplements

The invention also provides pharmaceutical compositions and dietary supplements (e.g., dietary aids) comprising an enzyme of the invention (e.g., an exemplary enzyme of the invention, including those described in Tables 1, 2, and 3). In one aspect, the pharmaceutical compositions and dietary supplements (e.g., dietary aids) are formulated for oral ingestion, e.g., to improve the digestibility of foods and feeds having a high cellulose or lignocellulosic component. See also discussion, above.

Periodontal treatment compounds can comprise an enzyme of the invention, e.g., as described in U.S. patent no. 6,776,979. Compositions and methods for the treatment or prophylaxis of acidic gut syndrome can comprise an enzyme of the invention, e.g., as described in U.S. patent no. 6,468,964.

In another aspect, wound dressings, implants and the like comprise antimicrobial (e.g., antibiotic-acting) enzymes, including an enzyme of the invention (including, e.g., exemplary sequences of the invention). Enzymes of the invention can also be used in alginate dressings, antimicrobial barrier dressings, burn dressings, compression bandages, diagnostic tools, gel dressings, hydro-selective dressings, hydrocellular (foam) dressings, hydrocolloid dressings, I.V dressings, incise drapes, low adherent dressings, odor absorbing dressings, paste bandages, post operative dressings, scar management, skin care, transparent film dressings and/or wound closure. Enzymes of the invention can be used in wound cleansing, wound bed preparation, to treat pressure ulcers, leg ulcers, burns, diabetic foot ulcers, scars, IV fixation, surgical wounds and minor wounds.

Enzymes of the invention can be used to in sterile enzymatic debriding compositions, e.g., ointments. In various aspects, the cellulase is formulated as a tablet, gel, pill, implant, liquid, spray, powder, food, feed pellet or as an encapsulated formulation.

The polypeptides of the invention, such as those having hydrolases activity (e.g., lipases, esterase, protease and/or phospholipases) of the invention can be used in detoxification processes, e.g., for the detoxification of endotoxins, e.g., compositions comprising lipopolysaccharides (LPS), and, the invention provides detoxification processes using at least one enzyme of the invention. In one aspect, a lipase and/or an esterase of the invention is used to detoxify a lipopolysaccharide (LPS). In one aspect, this detoxification is by deacylation of 2' and/or 3' fatty acid chains from lipid A. In one aspect, a hydrolase (e.g., a lipase and/or an esterase) of the invention is used to hydrolyze a 2'-lauroyl and/or a 3'-myristoyl chain from a lipid, e.g., a lipid A (e.g., from a bacterial endotoxin). In one aspect, the process of the invention is used to destroy an endotoxin, e.g., a toxin from a gram negative bacteria, as from *E. coli*. In one aspect, a hydrolase (e.g., a lipase and/or an esterase) of the invention is used to ameliorate the effects of toxin poisoning (e.g., from an on-going gram negative infection), or, to prophylactically to prevent the effects of endotoxin during an infection (e.g., an infection in an animal or a human). Accordingly, the invention provides a pharmaceutical composition comprising a hydrolase (e.g., a lipase and/or an esterase) of the invention, and method using a hydrolase of the invention, for the amelioration or prevention of lipopolysaccharide (LPS) toxic effects, e.g., during sepsis.

Biodefense applications

In other aspects, an enzyme of the invention (e.g., an exemplary enzyme of the invention, including those described in Tables 1, 2, and 3) can be used in biodefense (e.g., destruction of spores or bacteria comprising a lignocellulosic material). Use of enzymes of the invention in biodefense applications offer a significant benefit, in that they can be very rapidly developed against any currently unknown or biological warfare agents of the future. In addition, enzymes of the invention can be used for decontamination of affected environments. In aspect, the invention provides a biodefense or bio-detoxifying agent comprising a polypeptide of the invention (including, e.g., exemplary sequences of the invention), or a polypeptide encoded by a nucleic acid of the invention (including, e.g., exemplary sequences of the invention).

Nutraceuticals

In one aspect, the compositions, e.g., an exemplary enzyme of the invention, including those described in Tables 1, 2, and 3, and methods of the invention can be used to make nutraceuticals by processing or synthesizing lipids and oils using the enzymes of the invention, e.g., esterases, acylases, lipases, phospholipases or proteases of the invention. In one aspect, the processed or synthesized lipids or oils include polyunsaturated fatty acids (PUFAs), diacylglycerides, e.g., 1,3-diacyl glycerides (DAGs), monoacylglycerides, e.g., 2-monoacylglycerides (MAGs) and triacylglycerides (TAGs). In one aspect, the nutraceuticals is made by processing diacylglycerides, e.g., 1,3-diacyl glycerides (DAGs), monoacylglycerides, e.g., 2-monoacylglycerides (MAGs) and/or triacylglycerides (TAGs) from plant (e.g., oilseed) sources or from animal (e.g., fish oil) sources.

In one aspect, the compositions and methods of the invention can be used to fortify dietary compositions, especially cow's milk based products, e.g., cow's milk-based infant formulas, with bile salt-activated hydrolases. The compositions made by the methods and compositions of the invention can be used to feed newborn and premature infants, including administration of a bile salt-activated hydrolase of the invention to increase fat digestion and therefore growth rate. Similarly, the invention provides compositions and methods for treating subjects for inadequate pancreatic enzyme production by administration of bile salt-activated hydrolase in conjunction with ingestion of fats; see also discussion, below.

In one aspect, the invention provides a dietary composition comprising a hydrolase of the invention, e.g., bile salt-activated hydrolase of the invention. In one aspect, the invention provides a dietary composition comprising a nutritional base comprising a fat and an effective amount of bile salt-activated hydrolase of the invention. In one aspect, the invention provides a cow's milk-based infant formula comprising a hydrolase of the invention, e.g., bile salt-activated hydrolase of the invention. In one aspect, the hydrolase of the invention is active in the digestion of long chain fatty acids, e.g., C₁₂ to C₂₂, which make up a very high percentage of most milks, e.g., 99% of human breast milk. See, e.g., U.S. Patent No. 5,000,975.

In one aspect, the invention provides a dietary composition comprising a vegetable oil fat and a hydrolase of the invention. The invention provides methods of processing milk based products and/or vegetable oil-comprising compositions to make dietary compositions. In one aspect, the processed compositions comprise a lauric acid oil, an oleic acid oil, a palmitic acid oil and/or a linoleic acid oil. In one aspect, a rice

bran oil, sunflower oleic oil and/or canola oil may be used as oleic acids oils. In one aspect, fats and oils, e.g., oilseeds, from plants, including, e.g., rice, canola, sunflower, olive, palm, soy or lauric type oils for use in the nutraceuticals and dietary compositions are processed or made using a hydrolase of the invention. See, e.g., U.S. Patent No. 4,944,944.

In one aspect, the enzymes of the invention are provided in a form that is stable to storage in the formula and/or the stomach, but active when the formulation reaches the portion of the gastrointestinal tract where the formula would normally be digested. Formulations (e.g., microcapsules) for release in the intestine are well known in the art, e.g., biodegradable polymers such as polylactide and polyglycolide, as described, e.g., in U.S. Patent. Nos. 4,767,628; 4,897,268; 4,925,673; 5,902,617.

A number of aspects of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other aspects are within the scope of the following claims.

| SEQ ID NO: | NR or Geneseq Protein Accession Code | % Id | Evalue | Organism | Genbank Definition | Geneseq Definition | % Id | Evalue | EC No. |
|--------------|--------------------------------------|------|----------|---|---|--|------|----------|----------|
| 1, 2 | 15794814 | 60 | 2.00E-34 | Neisseria meningitidis Z2491 | DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] emb CAB85151.1 DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] pir A81821 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) NMA1931 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) | | | 3.2.2.20 | |
| 10001, 10002 | 48855446 | 36 | 7.00E-10 | Cytophaga hutchinsonii | COG1173: ABC-type dipeptide/oligopeptide/nickel transport systems, permease components [Cytophaga hutchinsonii] | | | | |
| 10003, 10004 | 34557261 | 45 | 5.00E-34 | Wolinella succinogenes DSM 1740 | GLUCOSE INHIBITED DIVISION PROTEIN B [Wolinella succinogenes DSM 1740] emb CAE09976.1 GLUCOSE INHIBITED DIVISION PROTEIN B [Wolinella succinogenes] sp Q7M9J8 GIDB_WOLSU Methyltransferase gidB (Glucose inhibited division protein B) | | | | |
| 10005, 10006 | 17936493 | 44 | 5.00E-30 | Agrobacterium tumefaciens str. C58 | methyl-accepting chemotaxis protein [Agrobacterium tumefaciens str. C58] gb AAL43599.1 methyl-accepting chemotaxis protein [Agrobacterium tumefaciens str. C58] pir A12897 methyl-accepting chemotaxis protein cheD [imported] - Agrobacterium tumefaciens (strain C58, Dupont) | | | 2.7.3.- | |
| 10007, 10008 | 21229884 | 24 | 3.00E-07 | Xanthomonas campestris pv. campestris str. ATCC 33913 | hypothetical protein XCC0407 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39725.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | | |
| 10009, 10010 | 34557182 | 49 | 4.00E-58 | Wolinella succinogenes DSM 1740 | PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09897.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] | | | | |
| 1001, 1002 | 29348342 | 36 | 4.00E-27 | Bacteroides thetaiotaomicron VPI-5482 | Methionyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78039.1 Methionyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] | Mus musculus cDNA clone IMAGE:30025832 | 82 | 9.00E-09 | 6.1.1.10 |
| 10011, 10012 | 34557182 | 39 | 6.00E-41 | Wolinella succinogenes DSM 1740 | PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09897.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] | | | | |
| 10015, 10016 | 53713997 | 40 | 1.00E-44 | Bacteroides fragilis YCH46 | two-component system sensor histidine kinase [Bacteroides fragilis YCH46] dbj BAD49455.1 two-component system sensor histidine kinase [Bacteroides fragilis YCH46] | | | 2.7.3.- | |
| 10019, 10020 | 34558361 | 32 | 4.00E-48 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-PREDICTED PEMEASE [Wolinella succinogenes DSM 1740] emb CAE11076.1 conserved hypothetical protein-PREDICTED PEMEASE [Wolinella succinogenes] | | | | |

| | | | | | | | | |
|--------|----------|----|-----------|---------------------------------|---|--|----|----------|
| 10021, | 48831352 | 31 | 2.00E-27 | Magnetococcus sp. MC-1 | COG0842: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | |
| 10022, | | | | | | | | |
| 10023, | | | | Cytophaga hutchinsonii | hypothetical protein Chit02001797 [Cytophaga hutchinsonii] | | | |
| 10024 | 48855460 | 26 | 3.00E-20 | hutchinsonii | putative transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 10025, | | | | Bacteroides fragilis | dbj BAD48817.1 putative transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 10026 | 53713359 | 38 | 4.00E-13 | YCH46 | | Wolinella succinogenes, complete genome; segment 4/7 | 89 | 5.00E-07 |
| 10027, | | | | Wolinella succinogenes DSM 1740 | hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] | | | |
| 10028 | 34557509 | 60 | 1.00E-68 | 1740 | emb CAE10224.1 hypothetical protein [Wolinella succinogenes DSM 1740] | | | |
| 10029, | | | | Wolinella succinogenes DSM 1740 | REPLICATIVE DNA HELICASE EC 3.6.1. [Wolinella succinogenes DSM 1740] | | | |
| 10030 | 34556788 | 58 | 7.00E-21 | 1740 | emb CAE09503.1 REPLICATIVE DNA HELICASE EC 3.6.1. [Wolinella succinogenes] | | | 3.6.1.- |
| 10031, | | | | Wolinella succinogenes DSM 1740 | DNA TRANSFER PROTEIN [Wolinella succinogenes DSM 1740] | | | |
| 10032 | 34556789 | 36 | 1.00E-15 | 1740 | emb CAE09504.1 DNA TRANSFER PROTEIN [Wolinella succinogenes] | | | |
| 10033, | | | | Wolinella succinogenes DSM 1740 | HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME | Wolinella succinogenes, complete genome; segment 4/7 | | |
| 10034 | 34557504 | 77 | 1.00E-120 | 1740 | emb CAE10219.1 HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella succinogenes] | | 80 | 2.00E-19 |
| 10035, | | | | Bacteroides fragilis | putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46] | | | 3.1.21.3 |
| 10036 | 53713554 | 53 | 9.00E-89 | YCH46 | dbj BAD49012.1 putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46] | | | |
| 10037, | | | | Leptospira borgpetersenii | transposase [Leptospira borgpetersenii] pir S43117 transposase - | | | |
| 10038 | 467673 | 26 | 5.00E-08 | borgpetersenii | Leptospira borgpetersenii | | | |
| 10039, | | | | Porphyromonas gingivalis W83 | PhoH family protein [Porphyromonas gingivalis W83] ref NP_905494.1 | | | |
| 10040 | 34397330 | 69 | 1.00E-92 | gingivalis W83 | PhoH family protein [Porphyromonas gingivalis W83] | | | |
| 10041, | | | | Wolinella succinogenes DSM 1740 | POTASSIUM CHANNEL PROTEIN [Wolinella succinogenes DSM 1740] | | | |
| 10042 | 34556764 | 49 | 2.00E-74 | 1740 | emb CAE09479.1 POTASSIUM CHANNEL PROTEIN [Wolinella succinogenes] | | | |
| 10043, | | | | uncultured archaeon | hypothetical protein sensory transduction histidine kinase [uncultured archaeon GZfos26B2] | | | 2.7.3.- |
| 10044 | 52549174 | 31 | 6.00E-23 | GZfos26B2 | hypothetical protein CPE1884 [Clostridium perfringens str. 13] | | | |
| 10051, | | | | Clostridium perfringens str. 13 | dbj BAB81590.1 hypothetical protein [Clostridium perfringens str. 13] | | | 3.1.11.- |
| 10052 | 18310866 | 26 | 1.00E-11 | perfringens str. 13 | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii] | | | |
| 10055, | | | | Cytophaga hutchinsonii | hydrogenase expression/formation protein HypA [Shewanella oneidensis MR-1] | | | 2.7.3.- |
| 10056 | 48855091 | 42 | 6.00E-47 | hutchinsonii | 1 gb AA55136.1 hydrogenase expression/formation protein HypA [Shewanella oneidensis MR-1] | | | |
| 10057, | | | | Shewanella oneidensis MR-1 | | | | |
| 10058 | 24373649 | 57 | 4.00E-31 | oneidensis MR-1 | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|--|---|---------|--|--|
| 10059, 10060 | 48844993 | 31 | 4.00E-20 | 15 | Geobacter metallireducens GS-15 | COG2068: Uncharacterized MobA-related protein [Geobacter metallireducens GS-15] | | | |
| 10061, 10062 | 39998151 | 29 | 2.00E-14 | PCA | Geobacter sulfurreducens PCA | transcriptional regulator, TetR family [Geobacter sulfurreducens PCA] gb AAR36452.1 transcriptional regulator, TetR family [Geobacter sulfurreducens PCA] | | | |
| 10063, 10064 | 50122251 | 50 | 5.00E-37 | SCR11043 | Erwinia carotovora subsp. atroseptica SCR11043 | putative acetyltransferase [Erwinia carotovora subsp. atroseptica SCR11043] emb CAG76227.1 putative acetyltransferase [Erwinia carotovora subsp. atroseptica SCR11043] | 2.3.1.- | | |
| 10065, 10066 | 56460369 | 40 | 3.00E-26 | Idiomarina loihlensis L2TR | Idiomarina loihlensis L2TR | Response regulator of the LytR/AIgR family [Idiomarina loihlensis L2TR] gb AAV82101.1 Response regulator of the LytR/AIgR family [Idiomarina loihlensis L2TR] | | | |
| 10067, 10068 | 15611919 | 46 | 2.00E-26 | Helicobacter pylori J99 | Helicobacter pylori J99 | hypothetical protein jhp0852 [Helicobacter pylori J99] gb AAD06430.1 putative [Helicobacter pylori J99] pir G71880 hypothetical protein jhp0852 - Helicobacter pylori (strain J99) | | | |
| 10069, 10070 | 34558359 | 55 | 1.00E-51 | Wolinella succinogenes DSM 1740 | Wolinella succinogenes DSM 1740 | PUTATIVE RIBOFLAVIN SYNTHASE ALPHA CHAIN [Wolinella succinogenes DSM 1740] emb CAE11074.1 PUTATIVE RIBOFLAVIN SYNTHASE ALPHA CHAIN [Wolinella succinogenes] | 2.5.1.9 | | |
| 1007, 1008 | ABB8477 1 | 45 | 9.00E-57 | | | Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org:Cytophaga hutchinsonii | 2.7.7.7 | | |
| 10071, 10072 | 56461220 | 47 | 9.00E-28 | Idiomarina loihlensis L2TR | Idiomarina loihlensis L2TR | Signal transduction histidine kinase [Idiomarina loihlensis L2TR] gb AAV82952.1 Signal transduction histidine kinase [Idiomarina loihlensis L2TR] | 2.7.3.- | | |
| 10075, 10076 | 53759861 | 49 | 7.00E-31 | Methylobacillus flagellatus KT | Methylobacillus flagellatus KT | COG0582: Integrase [Methylobacillus flagellatus KT] | | | |
| 10077, 10078 | 48832286 | 38 | 4.00E-36 | Magnetococcus sp. MC-1 | Magnetococcus sp. MC-1 | COG0470: ATPase Involved in DNA replication [Magnetococcus sp. MC-1] hypothetical protein PG2214 [Porphyromonas gingivalis W83] | 2.7.7.7 | | |
| 10079, 10080 | 34398094 | 38 | 2.00E-18 | Porphyromonas gingivalis W83 | Porphyromonas gingivalis W83 | ref NP_906255.1 hypothetical protein PG2214 [Porphyromonas gingivalis W83] | | | |
| 10081, 10082 | 29347582 | 32 | 2.00E-33 | Bacteroides thetaiotaomicron VPI-5482 | Bacteroides thetaiotaomicron VPI-5482 | putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO77279.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 10087, 10088 | 53713780 | 38 | 2.00E-42 | Bacteroides fragilis YCH46 | Bacteroides fragilis YCH46 | cobalamin biosynthesis protein CobD [Bacteroides fragilis YCH46] dbj BAD49238.1 cobalamin biosynthesis protein CobD [Bacteroides fragilis YCH46] | | | |
| 10089, 10090 | 34557782 | 43 | 9.00E-32 | Wolinella succinogenes DSM 1740 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | 2.7.3.- | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|----------------------------------|--|--|--|--|----------|
| 1009, 1010 | ABP6072 2 | 48 | 1.00E-21 | | | Desc: Cyanidium caldarium thioresdoxin SEQ ID NO:71. Org: Cyanidium caldarium | | | 1.6.4.5 |
| 10095, 10096 | 57167613 | 50 | 2.00E-21 | Campylobacter coli RM2228 | | probable periplasmic protein Cj1275c [Campylobacter coli RM2228] gb EAL57399.1 probable periplasmic protein Cj1275c [Campylobacter coli RM2228] | | | |
| 10097, 10098 | 21668035 | 38 | 6.00E-30 | Bacteroides fragilis uncultured | | hypothetical transposase [Bacteroides fragilis] | | | |
| 10099, 10100 | 31790367 | 32 | 5.00E-25 | Acidobacteria bacterium | | hypothetical protein [uncultured Acidobacteria bacterium] | | | |
| 10101, 10102 | 57240514 | 40 | 7.00E-35 | Campylobacter lari RM2100 | | DNA-binding response regulator CiaR [Campylobacter lari RM2100] gb EAL55628.1 DNA-binding response regulator CiaR [Campylobacter lari RM2100] | | | 2.7.3.- |
| 10103, 10104 | 57240513 | 33 | 3.00E-27 | Campylobacter lari RM2100 | | signal-transducing protein, histidine kinase, putative [Campylobacter lari RM2100] gb EAL55627.1 signal-transducing protein, histidine kinase, putative [Campylobacter lari RM2100] | | | 2.7.3.- |
| 10105, 10106 | 17549582 | 28 | 6.00E-07 | Ralstonia solanacearum GMI1000 | | PROBABLE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GMI1000] emb CAD18514.1 PROBABLE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] | | | |
| 10107, 10108 | 42628871 | 43 | 5.00E-57 | Haemophilus influenzae R2846 | | COG0147: Anthranilate/para-aminobenzoate synthases component I [Haemophilus influenzae R2846] | | | 4.1.3.- |
| 10109, 10110 | 34557081 | 59 | 3.00E-63 | Wolfinella succinogenes DSM 1740 | | hypothetical protein WS0668 [Wolfinella succinogenes DSM 1740] emb CAE09796.1 conserved hypothetical protein [Wolfinella succinogenes] | | | 2.1.1.64 |
| 1011, 10112 | 16802005 | 37 | 3.00E-22 | Listeria innocua Clp11262 | | hypothetical protein lin2946 [Listeria innocua Clp11262] emb CAC98171.1 lin2946 [Listeria innocua] pir AC1800 hypothetical protein lin2946 [Imported] [Listeria innocua (strain Clp11262)] | | | |
| 10111, 10112 | 42628859 | 44 | 5.00E-30 | Haemophilus influenzae R2846 | | COG1793: ATP-dependent DNA ligase [Haemophilus influenzae R2846] | | | 6.5.1.1 |
| 10113, 10114 | 21226270 | 30 | 3.00E-09 | Methanosarcina mazei Go1 | | hypothetical sensory transduction histidine kinase [Methanosarcina mazei Go1] gb AAM29864.1 hypothetical sensory transduction histidine kinase [Methanosarcina mazei Go1] | | | 2.7.3.- |
| 10115, 10116 | 39997412 | 45 | 8.00E-73 | Geobacter sulfurreducens PCA | | sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gb AAR35690.1 sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] | | | 2.7.3.- |
| 10117, 10118 | 54309594 | 27 | 4.00E-16 | Photobacterium profundum SS9 | | Hypothetical enzyme of sugar metabolism [Photobacterium profundum SS9] emb CAG20812.1 Hypothetical enzyme of sugar metabolism [Photobacterium profundum] | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|--|---|----|-------------------|
| 10119, 10120 | 20090576 | 40 | 3.00E-43 | Methanosarcina acetivorans C2A | hypothetical protein MA1724 [Methanosarcina acetivorans C2A] gb AAM05131.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | |
| 10123, 10124 | 56420550 | 30 | 9.00E-20 | Geobacillus kaustophilus HTA426 | transcriptional regulator [Geobacillus kaustophilus HTA426] dbj BAD76300.1 transcriptional regulator [Geobacillus kaustophilus HTA426] | | | |
| 10125, 10126 | 34763623 | 33 | 5.00E-21 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | Autolysin sensor kinase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23843.1 Autolysin sensor kinase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | 2.7.3.- |
| 10127, 10128 | 48855074 | 30 | 8.00E-15 | Cytophaga hutchinsonii | COG4276: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 10139, 10140 | 46201277 | 27 | 2.00E-18 | Magnetospirillum magnetotacticum MS-1 | COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1] | | | |
| 10141, 10142 | 45656100 | 46 | 1.00E-66 | Leptospira interrogans serovar Copenhageni str. Floeruz L1-130 | photoproduct lyase [Leptospira interrogans serovar Copenhageni str. Floeruz L1-130] gb AAS68823.1 photoproduct lyase [Leptospira interrogans serovar Copenhageni str. Floeruz L1-130] | | | 4.1.99.- |
| 10143, 10144 | 20095132 | 79 | 1.00E-122 | Providencia rettgeri | putative ATPase [Providencia rettgeri] | | | |
| 10149, 10150 | 6939919 | 68 | 1.00E-87 | Cytophaga fermentans | DNA gyrase subunit B [Cytophaga fermentans] | Polaribacter filamentus gyrB gene for DNA gyrase B subunit, partial cds | 89 | 1.00E-17 5.99.1.3 |
| 1015, 1016 | AAE1852 | 29 | 4.00E-28 | | Desc: Melon constitutive triple response (CTR) homologue. Org: Cucumis melo | | | 2.7.1.37 |
| 10151, 10152 | 57169090 | 35 | 1.00E-12 | Campylobacter coli RM2228 | N-terminal HTH domain of molybdenum-binding protein family [Campylobacter coli RM2228] gb EAL56239.1 N-terminal HTH domain of molybdenum-binding protein family [Campylobacter coli RM2228] | | | |
| 10153, 10154 | 15678768 | 42 | 7.00E-49 | Methanothermobacter thermautotrophicus str. Delta H | phenylalanyl-tRNA synthetase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85246.1 phenylalanyl-tRNA synthetase [Methanothermobacter thermautotrophicus str. Delta H] sp O26837 SYFA_METTH Phenylalanyl-tRNA synthetase alpha chain (Phenylalanine--tRNA ligase alpha chain) (PheRS) pif C69199 phenylalanyl-tRNA ligase (EC 6.1.1.20) - Methanobacterium thermautotrophicum (strain Delta H) | | | 6.1.1.20 |

| | | | | | | |
|-----------------|--------------|----|----------|--|---|----------|
| 10155, 10156 | 17229117 | 26 | 1.00E-18 | Nostoc sp. PCC 7120 | serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120] pir AC2009 serine/threonine kinase with two-component sensor domain ali1625 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB77991.1 serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120] | 2.7.3.- |
| 10159, 10160 | 34557161 | 54 | 2.00E-27 | Wollinella succinogenes DSM 1740 | PUTATIVE ARSENATE REDUCTASE [Wollinella succinogenes DSM 1740] emb CAE09876.1 PUTATIVE ARSENATE REDUCTASE [Wollinella succinogenes] | 1.97.1.5 |
| 10161, 10162 | 48855564 | 54 | 7.00E-35 | Cytophaga hutchinsonii | COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | |
| 10163, 10164 | 53715139 | 42 | 5.00E-30 | Bacteroides fragilis YCH46 | putative acetyltransferase [Bacteroides fragilis YCH46] dbj BAD50597.1 putative acetyltransferase [Bacteroides fragilis YCH46] | 2.3.1.- |
| 10167, 10168 | ABU0070 0 | 31 | 3.00E-26 | | Desc:S. pneumoniae type 4 strain protein from coding region #267. Org:Streptococcus pneumoniae type 4 strain | 2.4.1.- |
| 10169, 10170 | 421666 | 50 | 3.00E-58 | Acholeplasma laidlawii | probable nucleotide-binding protein - Acholeplasma laidlawii emb CAA80494.1 hypothetical nucleotide binding protein [Acholeplasma laidlawii] | 5.1.3.13 |
| 1017, 1018 | 1076839 | 34 | 9.00E-18 | Dictyostellum discoideum | protein kinase - slime mold [Dictyostellum discoideum] emb CAA86053.1 protein kinase [Dictyostellum discoideum] | 2.7.1.- |
| 10171, 10172 | 56461419 | 35 | 3.00E-21 | Idiomarina loihensis L2TR | Predicted glycosyltransferase [Idiomarina loihensis L2TR] gb AAV83151.1 Predicted glycosyltransferase [Idiomarina loihensis L2TR] | |
| 10173, 10174 | 34557616 | 29 | 4.00E-20 | Wollinella succinogenes DSM 1740 | HELICASE [Wollinella succinogenes DSM 1740] emb CAE10331.1 HELICASE [Wollinella succinogenes] | |
| 10175, 10176 | 57238505 | 31 | 2.00E-44 | Campylobacter jejuni RM1221 | hypothetical protein CJE1655 [Campylobacter jejuni RM1221] gb AAW36088.1 conserved hypothetical protein [Campylobacter jejuni RM1221] | |
| 10177, 10178 | 34557335 | 38 | 4.00E-18 | Wollinella succinogenes DSM 1740 | PHOSPHATE TRANSPORT PERMEASE [Wollinella succinogenes DSM 1740] emb CAE10050.1 PHOSPHATE TRANSPORT PERMEASE [Wollinella succinogenes] | |
| 10179, 10180 | 34556892 | 59 | 8.00E-72 | Wollinella succinogenes DSM 1740 | DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes] sp Q7MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [Includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)] | 2.7.7.6 |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|---------------|--|
| 10181, | 46202599 | 33 | 5.00E-27 | Magnetospirillum magnetotacticum MS-1 | hypothetical protein Magn03007449 [Magnetospirillum magnetotacticum MS-1] | | | | |
| 10182 | | | | | | | | | |
| 10185, | | | | | | | | | |
| 10186 | 40062812 | 44 | 1.00E-50 | uncultured bacterium 440 | amino transferase, DegT/DntJ/ErYc1/StrS family [uncultured bacterium 440] | | | | |
| 10189, | | | | | | | | | |
| 10190 | 29347915 | 38 | 1.00E-51 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2505 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77612.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 1019, | | | | | | | | | |
| 1020 | 29348728 | 44 | 3.00E-53 | Bacteroides thetaiotaomicron VPI-5482 | signal peptidase I [Bacteroides thetaiotaomicron VPI-5482] gb AAO78425.1 signal peptidase I [Bacteroides thetaiotaomicron VPI-5482] | | | 3.4.21.8 9 | |
| 10193, | | | | | | | | | |
| 10194 | 34556614 | 56 | 2.00E-66 | Wolinella succinogenes DSM 1740 | CARBOXYNORSPERMIDINE DECARBOXYLASE (NSPC) [Wolinella succinogenes DSM 1740] emb CAE09329.1 CARBOXYNORSPERMIDINE DECARBOXYLASE (NSPC) [Wolinella succinogenes] | | | 4.1.1.- | |
| 10195, | | | | | | | | | |
| 10196 | 6968098 | 31 | 2.00E-08 | Campylobacter jejuni subsp. jejuni NCTC 11168 | putative ribonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281814.1 putative ribonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] pir F81411 probable ribonuclease C 0631c [imported] - Campylobacter jejuni (strain NCTC 11168) | | | | |
| 10197, | | | | | | | | | |
| 10198 | 48856713 | 34 | 1.00E-17 | Cytophaga hutchinsonii | COG3210: Large exoproteins involved in heme utilization or adhesion [Cytophaga hutchinsonii] | | | | |
| 10207, | | | | | | | | | |
| 10208 | 24372121 | 39 | 9.00E-16 | Shewanella oneidensis MR-1 | hypothetical protein SO0527 [Shewanella oneidensis MR-1] gb AAN53608.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | | |
| 10209, | | | | | | | | | |
| 10210 | 23130207 | 33 | 1.00E-18 | Nostoc punctiforme PCC 73102 | COG0732: Restriction endonuclease S subunits [Nostoc punctiforme PCC 73102] | | | 3.1.21.3 | |
| 1021, | | | | | | | | | |
| 1022 | 51894182 | 52 | 1.00E-72 | Symbiobacterium thermophilum IAM 14863 | RNA polymerase alpha subunit [Symbiobacterium thermophilum IAM 14863] dbj BAD42029.1 RNA polymerase alpha subunit [Symbiobacterium thermophilum IAM 14863] | | | 2.7.7.6 | |
| 10217, | | | | | | | | | |
| 10218 | 2654483 | 30 | 2.00E-20 | Bacillus pseudofirmus | putative 32.7 kDa rhodanese-like thiosulfate sulfurtransferase [Bacillus pseudofirmus] pir T52549 probable thiosulfate sulfurtransferase (EC 2.8.1.1) [imported] - Bacillus firmus | | | 2.8.1.1 | |
| 10219, | | | | | | | | | |
| 10220 | 54310587 | 33 | 1.00E-24 | Photobacterium profundum SS9 | hypothetical sensory box/GGDEF family protein [Photobacterium profundum SS9] emb CAG21805.1 hypothetical sensory box/GGDEF family protein [Photobacterium profundum] | | | | |
| 10223, | | | | | | | | | |
| 10224 | 48856499 | 71 | 4.00E-81 | Cytophaga hutchinsonii | COG0152: Phosphoribosylaminoimidazole succinocarboxamide (SAICAR) synthase [Cytophaga hutchinsonii] | | | 6.3.2.6 | |
| 10225, | | | | | | | | | |
| 10226 | 21668035 | 38 | 2.00E-21 | Bacteroides fragilis | hypothetical transposase [Bacteroides fragilis] | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|---|--|--|---------|
| 10227, 10228 | 16945757 | 26 | 4.00E-14 | Photobacterium damselae subsp. placidia | capsular polysaccharide [Photobacterium damsela subsp. placida] | | | |
| 10229, 10230 | 15898433 | 35 | 6.00E-09 | Sulfolobus solfataricus P2 | hypothetical protein SSO1613 [Sulfolobus solfataricus P2] gb AAK41828.1 Hypothetical protein SSO1613 [Sulfolobus solfataricus P2] pir E90321 hypothetical protein SSO1613 [imported] - Sulfolobus solfataricus | | | |
| 10231, 10232 | 4234793 | 37 | 2.00E-24 | Leptospira borgpetersenii | unknown [Leptospira borgpetersenii] | | | |
| 10235, 10236 | 57504674 | 46 | 1.00E-31 | Campylobacter coli RM2228 | citrate synthase I [Campylobacter coli RM2228] gb EAL56138.1 citrate synthase I [Campylobacter coli RM2228] | | | 4.1.3.7 |
| 10237, 10238 | 34557509 | 62 | 1.00E-60 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wolinella succinogenes] | | | |
| 10239, 10240 | 57242574 | 30 | 2.00E-14 | Campylobacter upsallensis RM3195 | probable membrane protein Cj1484c [Campylobacter upsallensis RM3195] gb EAL53642.1 probable membrane protein Cj1484c [Campylobacter upsallensis RM3195] | | | |
| 10241, 10242 | 48730607 | 47 | 4.00E-30 | Pseudomonas fluorescens PfO-1 | COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Pseudomonas fluorescens PfO-1] | | | 6.2.1.3 |
| 10243, 10244 | 15668217 | 35 | 1.00E-23 | Methanocaldococ- cus jannaschii DSM 2661 | putative mRNA 3'-end processing factor 1 [Methanocaldococcus jannaschii DSM 2661] gb AAB98027.1 putative mRNA 3'-end processing factor 1 [Methanocaldococcus jannaschii DSM 2661] sp Q60355 Y047_METJA | | | |
| 10245, 10246 | 29350111 | 62 | 8.00E-53 | Bacteroides thetaiotaomicron VPI-5482 | Hypothetical protein MJ0047 chloromuconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79808.1 chloromuconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482] | | | 4.2.1.- |
| 10249, 10250 | 48846045 | 42 | 3.00E-46 | Geobacter metallireducens GS- 15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 1025, 1026 | 20089441 | 35 | 3.00E-29 | Methanosarcina acetivorans C2A | sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AAM03996.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A] | | | 2.7.3.- |
| 10251, 10252 | 57237341 | 44 | 5.00E-15 | Campylobacter jejuni RM1221 | hypothetical protein CJE0334 [Campylobacter jejuni RM1221] gb AAW34924.1 conserved hypothetical protein [Campylobacter jejuni RM1221] | | | |
| 10253, 10254 | 34556562 | 56 | 2.00E-46 | Wolinella succinogenes DSM 1740 | PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes DSM 1740] emb CAE09277.1 PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes] | | | |
| 10255, 10256 | 34556562 | 80 | 1.00E-108 | Wolinella succinogenes DSM 1740 | PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes DSM 1740] emb CAE09277.1 PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes] | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|--|--|----|----------|---------------|
| 10259, 10260 | 37719606 | 59 | 3.00E-73 | Campylobacter jejuni | putative GDP-fucose synthase [Campylobacter jejuni] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 5/6 | 86 | 8.00E-09 | 5.1.3.- |
| 10261, 10262 | 57167870 | 50 | 5.00E-29 | Campylobacter coli RM2228 | thioesterase family protein, putative [Campylobacter coli RM2228] gb EAL57656.1 thioesterase family protein, putative [Campylobacter coli RM2228] | | | | |
| 10263, 10264 | 34557419 | 31 | 4.00E-17 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | |
| 10265, 10266 | 34556810 | 38 | 4.00E-32 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09525.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | 2.7.3.- |
| 10267, 10268 | 29349340 | 61 | 1.00E-101 | Bacteroides thetaiotaomicron VPI-5482 | DNA primase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79037.1 DNA primase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.7.- |
| 10269, 10270 | 48854613 | 32 | 6.00E-35 | Cytophaga hutchinsonii | COG0842: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 1027, 1028 | 30249488 | 37 | 2.00E-19 | Nitrosomonas europaea ATCC 19718 | 6-pyruvoyl tetrahydropterin synthase [Nitrosomonas europaea ATCC 19718] emb CAD85428.1 6-pyruvoyl tetrahydropterin synthase [Nitrosomonas europaea ATCC 19718] | | | | 4.6.1.10 |
| 10273, 10274 | 34396339 | 63 | 6.00E-65 | Porphyromonas gingivalis W83 | peptidyl-tRNA hydrolase [Porphyromonas gingivalis W83] ref NP_904507.1 peptidyl-tRNA hydrolase [Porphyromonas gingivalis W83] sp Q7MXK9 PTH_PORGI Peptidyl-tRNA hydrolase (PTH) | | | | 3.1.1.29 |
| 10275, 10276 | 45358149 | 51 | 6.00E-55 | Methanococcus maripaludis S2 | uncharacterized endonuclease III related protein [Methanococcus maripaludis S2] emb CAF30142.1 uncharacterized endonuclease III related protein [Methanococcus maripaludis S2] | | | | 4.2.99.1 8 |
| 10279, 10280 | 57169064 | 41 | 4.00E-26 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 10281, 10282 | 57241406 | 54 | 3.00E-43 | Campylobacter lari RM2100 | ATP-dependent Clp protease, ATP-binding subunit ClpX [Campylobacter lari RM2100] gb EAL54518.1 ATP-dependent Clp protease, ATP-binding subunit ClpX [Campylobacter lari RM2100] | | | | |
| 10283, 10284 | 34558260 | 57 | 1.00E-93 | Wolinella succinogenes DSM 1740 | PUTATIVE ATP-DEPENDENT PROTEASE LA PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10975.1 PUTATIVE ATP-DEPENDENT PROTEASE LA PROTEIN [Wolinella succinogenes] | | | | 3.4.21.5 3 |
| 10285, 10286 | 57167957 | 65 | 2.00E-99 | Campylobacter coli RM2228 | ATP-dependent protease La [Campylobacter coli RM2228] gb EAL57000.1 ATP-dependent protease La [Campylobacter coli RM2228] | | | | 3.4.21.5 3 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|---------|----------|
| 10287, 10288 | 39997199 | 60 | 1.00E-70 | Geobacter sulfurreducens PCA | formate acetyltransferase [Geobacter sulfurreducens PCA] gb AAR35477.1 formate acetyltransferase [Geobacter sulfurreducens PCA] | | | | 2.3.1.54 |
| 10289, 10290 | 29346832 | 32 | 3.00E-12 | Bacteroides thetaitotaomicron VPI-5482 | hypothetical protein BT1422 [Bacteroides thetaitotaomicron VPI-5482] gb AAO76529.1 conserved hypothetical protein [Bacteroides thetaitotaomicron VPI-5482] | | | | |
| 10291, 10292 | 57241378 | 50 | 8.00E-25 | Campylobacter lari RM2100 | molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100] gb EAL54490.1 molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100] | | | | |
| 10293, 10294 | 48846592 | 31 | 5.00E-15 | Geobacter metallireducens GS-15 | COG4753: Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain [Geobacter metallireducens GS-15] Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] gb AAK81185.1 Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] pir F97299 sensory transduction protein containing HD_GYP domain [Imported] - Clostridium acetobutylicum | | | 2.7.3.- | |
| 10295, 10296 | 15896496 | 37 | 1.00E-40 | Clostridium acetobutylicum ATCC 824 | phosphoenolpyruvate synthase [Pyrococcus horikoshii OT3] dbj BAA29161.1 821aa long hypothetical phosphoenolpyruvate synthase [Pyrococcus horikoshii OT3] pir B71229 pyruvate, water dikinase (EC 2.7.9.2) - Pyrococcus horikoshii sp O57830 PPSA_PYRHO Probable phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase) Phosphoenolpyruvate synthase/pyruvate phosphate dikinase [Methanopyrus kandleri AV19] gb AAM01469.1 Phosphoenolpyruvate synthase/pyruvate phosphate dikinase [Methanopyrus kandleri AV19] | | | 2.7.9.2 | |
| 10297, 10298 | 14590043 | 33 | 4.00E-31 | Pyrococcus horikoshii OT3 | hypothetical protein [Encephalitozoon cuniculi] emb CAD25326.1 hypothetical protein [Encephalitozoon cuniculi] GB-M1] peptidase, M42 family [Enterococcus faecalis V583] gb AAO82426.1 peptidase, M42 family [Enterococcus faecalis V583] COG0847: DNA polymerase II, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] | | | 2.7.9.2 | |
| 10299, 10300 | 20093692 | 31 | 1.00E-32 | Methanopyrus kandleri AV19 | two-component response regulator [Synecococcus elongatus PCC 6301] dbj BAD78390.1 two-component response regulator [Synecococcus elongatus PCC 6301] ref ZP_00202158.1 COG2200: FOG: EAL domain [Synecococcus elongatus PCC 7942] | | | | |
| 10301, 10302 | 29377202 | 45 | 4.00E-57 | Enterococcus faecalis V583 | hypothetical protein aq_988 [Aquifex aeolicus VF5] gb AAC07080.1 hypothetical protein [Aquifex aeolicus VF5] pir F70385 conserved hypothetical protein aq_988 - Aquifex aeolicus | | | 3.2.1.4 | |
| 10303, 10304 | 48853783 | 34 | 2.00E-30 | Cytophaga hutchinsonii | | | | | |
| 10307, 10308 | 56750209 | 43 | 9.00E-57 | Synechococcus elongatus PCC 6301 | | | | | |
| 10309, 10310 | 15606297 | 27 | 7.00E-07 | Aquifex aeolicus VF5 | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|----|------------------|
| 10311, 10312 | 29348867 | 49 | 1.00E-43 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3458 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78564.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 10313, 10314 | 48862374 | 37 | 7.00E-20 | Microbulbifer degradans 2-40 | COG0501: Zn-dependent protease with chaperone function [Microbulbifer degradans 2-40] | | | |
| 10317, 10318 | 48832341 | 33 | 4.00E-11 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | |
| 10321, 10322 | 48863739 | 32 | 7.00E-26 | Microbulbifer degradans 2-40 | COG2202: FOG: PAS/PAC domain [Microbulbifer degradans 2-40] | | | 2.7.3.- |
| 10323, 10324 | 15611181 | 61 | 4.00E-98 | Helicobacter pylori J99 | PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] gb AAD05690.1 PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] pir E71972 pyruvate, water dikinase (EC 2.7.9.2) - Helicobacter pylori (strain J99) sp Q9ZMV4 PPSA_HELP J Phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase) | | | 2.7.9.2 |
| 10325, 10326 | 21233748 | 39 | 2.00E-54 | Proteus vulgaris | transposase [Proteus vulgaris] dbj BAB93648.1 transposase [Proteus vulgaris] | | | |
| 10327, 10328 | 32261558 | 35 | 4.00E-25 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859542.1 hypothetical protein HH0011 [Helicobacter hepaticus ATCC 51449] | | | |
| 10335, 10336 | 48832337 | 37 | 2.00E-29 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 10339, 10340 | 48890583 | 32 | 1.00E-15 | Trichodesmium erythraeum IMS101 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] | | | |
| 10341, 10342 | 4234794 | 38 | 5.00E-09 | Leptospira borgpetersenii | unknown [Leptospira borgpetersenii] | | | |
| 10343, 10344 | 45657980 | 38 | 9.00E-25 | Leptospira interrogans serovar Copenhagen I str. Flocruz L1-130 | glycosyltransferase [Leptospira interrogans serovar Copenhagen I str. Flocruz L1-130] gb AAK19901.1 unknown [Leptospira interrogans] gb AAD52180.1 unknown [Leptospira interrogans] gb AAS70703.1 glycosyltransferase [Leptospira interrogans serovar Copenhagen I str. Flocruz L1-130] | | | |
| 10345, 10346 | 48853652 | 52 | 1.00E-69 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | Nostoc sp. PCC 7120 DNA, complete genome | 95 | 1.00E-08 2.7.3.- |
| 10347, 10348 | 48853652 | 47 | 6.00E-55 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 10349, 10350 | 48895677 | 50 | 4.00E-33 | Trichodesmium erythraeum IMS101 | COG0778: Nitroreductase [Trichodesmium erythraeum IMS101] | | | 1.-.-.- |

| | | | | | | | | | |
|-----------------|----------|----|-----------|--|--|---|----|----------|----------|
| 10351, 10352 | 19704257 | 29 | 4.00E-11 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Homoserine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95118.1 Homoserine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] transcriptional regulator, AraC/XylS family [Bacillus clausii dbj BAD63749.1 transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16] | | | | 2.7.1.39 |
| 10353, 10354 | 56962983 | 24 | 2.00E-11 | Bacillus clausii KSM-K16 | transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16] transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16] | | | | |
| 10355, 10356 | 48858010 | 33 | 3.00E-09 | Clostridium thermocellum ATCC 27405 | COG0367: Asparagine synthase (glutamine-hydrolyzing) [Clostridium thermocellum ATCC 27405] | | | | |
| 10357, 10358 | 48855327 | 82 | 1.00E-119 | Cytophaga hutchinsonii | COG0086: DNA-directed RNA polymerase, beta' subunit/160 kD subunit [Cytophaga hutchinsonii] | Cyanophora paradoxa cyanelle, complete genome | 83 | 4.00E-20 | 2.7.7.6 |
| 10359, 10360 | 57240881 | 41 | 3.00E-32 | Campylobacter lari RM2100 | molybdenum cofactor biosynthesis protein [Campylobacter lari RM2100] gb EAL55274.1 molybdenum cofactor biosynthesis protein [Campylobacter lari RM2100] | | | | |
| 10361, 10362 | 34558237 | 40 | 1.00E-43 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1946 [Wolinella succinogenes DSM 1740] emb CAE10952.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 10363, 10364 | 18309906 | 54 | 6.00E-32 | Clostridium perfringens str. 13 | hypothetical protein CPE0924 [Clostridium perfringens str. 13] dbj BAB80630.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | | |
| 10365, 10366 | 56750582 | 21 | 4.00E-12 | Synechococcus elongatus PCC 6301 | similar to phytoene dehydrogenase [Synechococcus elongatus PCC 6301] dbj BAD78763.1 similar to phytoene dehydrogenase [Synechococcus elongatus PCC 6301] ref ZP_00164110.1 COG1233: Phytoene dehydrogenase and related proteins [Synechococcus elongatus PCC 7942] | | | | |
| 10369, 10370 | 46135061 | 31 | 2.00E-26 | Anabaena variabilis ATCC 29413 | COG0438: Glycosyltransferase [Anabaena variabilis ATCC 29413] related to transcription regulator [Desulfotalea psychrophila LSV54] emb CAG36428.1 related to transcription regulator [Desulfotalea psychrophila LSV54] | | | | |
| 10371, 10372 | 51245551 | 24 | 1.00E-09 | Desulfotalea psychrophila LSV54 | related to transcription regulator [Desulfotalea psychrophila LSV54] emb CAG36428.1 related to transcription regulator [Desulfotalea psychrophila LSV54] | | | | |
| 10375, 10376 | 41722683 | 41 | 1.00E-16 | Dechloromonas aromatica RCB | hypothetical protein Daro03003755 [Dechloromonas aromatica RCB] | | | | |
| 10379, 10380 | 33602582 | 42 | 1.00E-18 | Bordetella bronchiseptica RB50 | modification methylase [Bordetella bronchiseptica RB50] emb CAE35580.1 modification methylase [Bordetella bronchiseptica RB50] | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|----|----------|----------|
| 10381, 10382 | 34557728 | 38 | 3.00E-34 | Wollinella succinogenes DSM 1740 | CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wollinella succinogenes DSM 1740] emb CAE10443.1 CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wollinella succinogenes] | | | |
| 10383, 10384 | 34557728 | 34 | 2.00E-15 | Wollinella succinogenes DSM 1740 | CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wollinella succinogenes DSM 1740] emb CAE10443.1 CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wollinella succinogenes] | | | |
| 10385, 10386 | 29608580 | 31 | 3.00E-18 | Streptomyces avermitilis MA-4680 | hypothetical protein [Streptomyces avermitilis MA-4680] ref NP_826099.1 hypothetical protein SAV4922 [Streptomyces avermitilis MA-4680] | | | |
| 10389, 10390 | 57242734 | 44 | 9.00E-44 | Campylobacter upsaliensis RM3195 | response regulator, putative [Campylobacter upsaliensis RM3195] gb EAL53447.1 response regulator, putative [Campylobacter upsaliensis RM3195] | 87 | 7.00E-12 | 2.7.3.- |
| 1039, 1040 | 48839656 | 88 | 2.00E-99 | Methanosarcina barkeri str. fusaro | COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro] | 80 | 8.00E-58 | |
| 10391, 10392 | 57238514 | 28 | 4.00E-23 | Campylobacter jejuni RM1221 | DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221] | | | 2.7.3.- |
| 10399, 10400 | 9656845 | 44 | 1.00E-54 | Vibrio cholerae O1 biovar eltor str. N16961 | conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231913.1 hypothetical protein VC2282 [Vibrio cholerae O1 biovar eltor str. N16961] pir F82096 conserved hypothetical protein VC2282 [Imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | |
| 10401, 10402 | 34558071 | 68 | 1.00E-121 | Wollinella succinogenes DSM 1740 | RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN [Wollinella succinogenes DSM 1740] emb CAE10786.1 RIBONUCLEOSIDE- DIPHOSPHATE REDUCTASE LARGE CHAIN [Wollinella succinogenes] | | | 1.17.4.1 |
| 10403, 10404 | 34556560 | 35 | 3.00E-51 | Wollinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes] | | | |
| 10405, 10406 | 32262256 | 66 | 5.00E-35 | Helicobacter hepaticus ATCC 51449 | guanylate kinase [Helicobacter hepaticus ATCC 51449] ref NP_860238.1 guanylate kinase [Helicobacter hepaticus ATCC 51449] sp Q7VIA1 KGUA_HELP Guanylate kinase (GMP kinase) | | | 2.7.4.8 |
| 10407, 10408 | 58461322 | 33 | 1.00E-22 | Idiomarina lohiensis L2TR | Predicted PhoH-related ATPase [Idiomarina lohiensis L2TR] gb AAV83054.1 Predicted PhoH-related ATPase [Idiomarina lohiensis L2TR] | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|--|--|----|----------|
| 10409, 10410 | 34557146 | 45 | 2.00E-58 | Wollinella succinogenes DSM 1740 | A/G-SPECIFIC ADENINE GLYCOSYLASE EC 3.2.2. [Wollinella succinogenes DSM 1740] emb CAE09861.1 A/G-SPECIFIC ADENINE GLYCOSYLASE EC 3.2.2. [Wollinella succinogenes] putative adenylate cyclase [Burkholderia pseudomallei K96243] ref YP_104436.1 adenylate cyclase, putative [Burkholderia mallei ATCC 23344] gb AAU48007.1 adenylate cyclase, putative [Burkholderia mallei ATCC 23344] emb CAH37434.1 putative adenylate cyclase [Burkholderia pseudomallei K96243] | | | 3.2.2.- |
| 1041, 1042 | 53721029 | 37 | 3.00E-16 | Burkholderia pseudomallei K96243 | thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790] gb AAT43873.1 thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790] | | | 4.6.1.1 |
| 10411, 10412 | 48478360 | 30 | 4.00E-12 | Picrophilus torridus DSM 9790 | dehydrogenase, putative [Cryptococcus neoformans var. neoformans JEC21] gb EAL21937.1 hypothetical protein CNBC0770 [Cryptococcus neoformans var. neoformans B-3501A] | | | 2.5.1.3 |
| 10415, 10416 | 57226131 | 50 | 1.00E-66 | Cryptococcus neoformans var. neoformans JEC21 | COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301665.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301374.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300257.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300170.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298468.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298384.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] | Geobacter metallireducens putative ferredoxin gene, partial cds; hypothetical protein gene, complete cds; and putative transposase gene, partial cds | 81 | 5.00E-41 |
| 10419, 10420 | 48847450 | 79 | 1.00E-107 | Francisella tularensis subsp. tularensis Schu 4 | Integrase/recombinase XerC [Francisella tularensis subsp. tularensis Schu 4] emb CAG46136.1 Integrase/recombinase XerC [Francisella tularensis subsp. tularensis] | | | |
| 10423, 10424 | 56708541 | 33 | 6.00E-14 | Bacillus cereus ZK | acetyltransferase, GNAT family [Bacillus cereus ZK] gb AAU18574.1 | | | |
| 10425, 10426 | 52143555 | 35 | 1.00E-18 | Campylobacter lari RM2100 | acetyltransferase, GNAT family [Bacillus cereus ZK] methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100] gb EAL54712.1 methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100] | | | |
| 10427, 10428 | 57241016 | 33 | 3.00E-28 | Haemophilus sommus 129PT | hypothetical protein Hsom02000323 [Haemophilus sommus 129PT] | | | |
| 10429, 10430 | 53692808 | 33 | 6.00E-19 | Pseudomonas syringae pv. tomato str. DC3000 | ISPsy11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794264.1 ISPsy11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000] | | | |
| 1043, 1044 | 28854897 | 36 | 1.00E-22 | | | | | |

| | | | | | | | | |
|--------------|----------|----|----------|--|---|--|--|-----------|
| 10431, 10432 | 46120923 | 34 | 9.00E-32 | Methylobacillus flagellatus KT | COG0438: Glycosyltransferase [Methylobacillus flagellatus KT] | | | 2.4.1.- |
| 10433, 10434 | 93830 | 33 | 1.00E-22 | | regulatory protein cII - phage phi-R73 | | | |
| 10435, 10436 | 23003026 | 33 | 1.00E-15 | Lactobacillus gasseri | COG0553: Superfamily II DNA/RNA helicases, SNF2 family [Lactobacillus gasseri] | | | 3.6.1.3 |
| 10437, 10438 | AAG8151 | 26 | 6.00E-11 | | Desc:S. epidermidis open reading frame protein sequence SEQ ID NO:130. Org:Staphylococcus epidermidis | | | |
| 10445, 10446 | 34558393 | 45 | 7.00E-30 | Wolinnella succinogenes DSM 1740 | THREONINE SYNTHASE [Wolinnella succinogenes DSM 1740] emb CAE11108.1 THREONINE SYNTHASE [Wolinnella succinogenes] | | | 4.2.99.2 |
| 10447, 10448 | 42525591 | 33 | 6.00E-11 | Treponema denticola ATCC 35405 | methyI-accepting chemotaxis protein [Treponema denticola ATCC 35405] gblAAS10570.1 methyl-accepting chemotaxis protein [Treponema denticola ATCC 35405] | | | |
| 10449, 10450 | 56476606 | 21 | 9.00E-07 | Azoarcus sp. Ebn1 | hemin receptor precursor, TonB-dependent outer membrane uptake protein [Azoarcus sp. Ebn1] | | | |
| 1045, 1046 | 48833013 | 33 | 3.00E-35 | Magnetococcus sp. MC-1 | COG0842: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 10451, 10452 | 45657583 | 36 | 2.00E-46 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | nucleotide excision repair subunit A UVRABC [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_712393.1 Excinuclease ABC subunit A [Leptospira interrogans serovar Lai str. 56601] gblAAN4941.1 Excinuclease ABC subunit A [Leptospira interrogans serovar lai str. 56601] gblAAS70306.1 nucleotide excision repair subunit A UVRABC [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | |
| 10453, 10454 | 27380846 | 40 | 2.00E-17 | Bradyrhizobium japonicum USDA 110 | transcriptional regulatory protein [Bradyrhizobium japonicum USDA 110] dbj BAC51000.1 transcriptional regulatory protein [Bradyrhizobium japonicum USDA 110] | | | |
| 10455, 10456 | 15606172 | 45 | 3.00E-33 | Aquifex aeolicus VF5 | hydrogenase large subunit [Aquifex aeolicus VF5] gblAAC06945.1 hydrogenase large subunit [Aquifex aeolicus VF5] pfr A70370 hydrogenase large subunit - Aquifex aeolicus | | | 1.18.99.1 |
| 10459, 10460 | 48834391 | 24 | 1.00E-07 | Magnetococcus sp. MC-1 | COG0694: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Magnetococcus sp. MC-1] | | | |
| 10461, 10462 | 54302734 | 30 | 5.00E-23 | Photobacterium profundum SS9 | hypothetical dinitrification protein NorD [Photobacterium profundum] emb CAG22927.1 hypothetical dinitrification protein NorD [Photobacterium profundum] | | | 1.7.99.7 |

| | | | | | | | | | |
|-----------------|----------|----|----------|----------------|----------------------------------|--|--|--|----------|
| 10463, 10464 | 20808390 | 30 | 1.00E-12 | MB4 | Thermoanaerobacter tengcongensis | hypothetical protein TTE1987 [Thermoanaerobacter tengcongensis MB4] gb AAAM25165.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4] | | | |
| 10465, 10466 | 56418878 | 58 | 3.00E-47 | HTA426 | Geobacillus kaustophilus | type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426] dbj BAD74628.1 type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426] | | | 2.1.1.72 |
| 10467, 10468 | 34557088 | 43 | 2.00E-41 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS0675 [Wolinella succinogenes DSM 1740] emb CAE09803.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 10469, 10470 | 57240386 | 40 | 1.00E-46 | RM2100 | Campylobacter lari | tRNA pseudouridine synthase A [Campylobacter lari RM2100] gb EAL55500.1 tRNA pseudouridine synthase A [Campylobacter lari RM2100] | | | 4.2.1.70 |
| 1047, 1048 | 17231815 | 32 | 7.00E-27 | 7120 | Nostoc sp. PCC | hypothetical protein alr4323 [Nostoc sp. PCC 7120] pir AD2346 hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB76022.1 alr4323 [Nostoc sp. PCC 7120] | | | 2.4.2.26 |
| 10471, 10472 | 48864587 | 37 | 2.00E-34 | degradans 2-40 | Microbulbifer | COG0694: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Microbulbifer degradans 2-40] putative transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 10473, 10474 | 53713359 | 38 | 8.00E-34 | YCH46 | Bacteroides fragilis | dbj BAD48817.1 putative transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 10475, 10476 | 34557749 | 52 | 4.00E-61 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS1398 [Wolinella succinogenes DSM 1740] emb CAE10464.1 conserved hypothetical protein [Wolinella succinogenes] | | | 1.1.1.21 |
| 10477, 10478 | 45546445 | 28 | 7.00E-14 | 9941 | Rubrobacter xylanophilus DSM | COG4770: Acetyl/propionyl-CoA carboxylase, alpha subunit [Rubrobacter xylanophilus DSM 9941] | | | 4.1.1.3 |
| 10483, 10484 | 57242491 | 60 | 3.00E-52 | RM3195 | Campylobacter upsallensis | polypeptide deformylase [Campylobacter upsallensis RM3195] gb EAL53559.1 polypeptide deformylase [Campylobacter upsallensis RM3195] | | | 3.5.1.88 |
| 10485, 10486 | 52550565 | 32 | 7.00E-19 | GZfos9E5 | uncultured archaeon | mannosyl-3-phosphoglycerate phosphatase [uncultured archaeon GZfos9E5] | | | |
| 10489, 10490 | 39995815 | 38 | 8.00E-17 | PCA | Geobacter sulfurreducens | hypothetical protein GSU0709 [Geobacter sulfurreducens PCA] gb AAR34039.1 hypothetical protein GSU0709 [Geobacter sulfurreducens PCA] | | | |
| 1049, 1050 | 48855421 | 33 | 5.00E-43 | hutchinsonii | Cytophaga hutchinsonii | COG0210: Superfamily I DNA and RNA helicases [Cytophaga hutchinsonii] | | | 3.6.1.- |

| | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|----------|
| 10491, | 57242338 | 30 | 9.00E-23 | Campylobacter upsaliensis RM3195 | conserved hypothetical protein [Campylobacter upsaliensis RM3195] | | | |
| 10492 | | | | | gb EAL53800.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195] | | | |
| 10495, | 40062476 | 36 | 2.00E-41 | uncultured bacterium 105 | hypothetical protein EBAC750-01A01.2 [uncultured bacterium 105] | | | |
| 10496 | | | | | putative transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 105, | | | | | dbj BAD50718.1 putative transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 106 | 53715260 | 46 | 2.00E-32 | Bacteroides fragilis YCH46 | PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE11047.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes] | | | |
| 10501, | 34558332 | 30 | 7.00E-10 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-PREDICTED PEMEASE [Wolinella succinogenes DSM 1740] emb CAE11076.1 conserved hypothetical protein-PREDICTED PEMEASE [Wolinella succinogenes] | | | |
| 10503, | | | | | formyltetrahydrofolate deformylase VC1992 [Campylobacter lari RM2100] | | | 2.7.7.25 |
| 10504 | 34558361 | 32 | 2.00E-42 | Wolinella succinogenes DSM 1740 | gb EAL55533.1 formyltetrahydrofolate deformylase VC1992 [Campylobacter lari RM2100] | | | |
| 10507, | | | | | gb EAL55533.1 formyltetrahydrofolate deformylase VC1992 [Campylobacter lari RM2100] | | | 2.7.7.25 |
| 10508 | 57240419 | 41 | 1.00E-30 | Campylobacter lari RM2100 | tRNA nucleotidyltransferase [Campylobacter upsaliensis RM3195] | | | |
| 10509, | | | | | gb EAL53338.1 tRNA nucleotidyltransferase [Campylobacter upsaliensis RM3195] | | | 2.7.7.25 |
| 10510 | 57242625 | 41 | 3.00E-21 | Campylobacter upsaliensis RM3195 | COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Microbulifer degradans 2-40] | | | |
| 10511, | 48861334 | 48 | 4.00E-23 | Microbulifer degradans 2-40 | DIAMINOBTYRIC ACID AMINOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09865.1 DIAMINOBTYRIC ACID AMINOTRANSFERASE [Wolinella succinogenes] | | | 2.6.1.46 |
| 10513, | 34557250 | 38 | 1.00E-15 | Wolinella succinogenes DSM 1740 | hypothetical protein SAR0197 [Staphylococcus aureus subsp. aureus MRSA252] emb CAG39224.1 hypothetical protein [Staphylococcus aureus subsp. aureus MRSA252] | | | |
| 10515, | | | | | sensory transduction histidine kinase [Methanosarcina acetivorans C2A] | | | 2.7.3.- |
| 10516 | 49482438 | 26 | 7.00E-14 | Staphylococcus aureus subsp. aureus MRSA252 | gb AAM04570.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A] | | | |
| 10517, | | | | | ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes DSM 1740] emb CAE10562.1 ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes] | | | 3.4.24.- |
| 10518 | 20090015 | 36 | 9.00E-12 | Methanosarcina acetivorans C2A | bleomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306] | | | |
| 10519, | 34557847 | 35 | 2.00E-29 | Wolinella succinogenes DSM 1740 | gb AAM39068.1 bleomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306] | | | |
| 10520 | | | | | COG0445: NAD/FAD-utilizing enzyme apparently involved in cell division [Chloroflexus aurantiacus] | | | |
| 10521, | | | | | | | | |
| 10522 | 21244950 | 36 | 7.00E-12 | Xanthomonas axonopodis pv. citri str. 306 | | | | |
| 10523, | | | | | | | | |
| 10524 | 53795632 | 42 | 2.00E-18 | Chloroflexus aurantiacus | | | | |
| 10525, | AAB4639 | | | | | | | |
| 10526 | 8 | 26 | 1.00E-11 | | Desc:H. pylori HPC095 protein. Org:Helicobacter pylori | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|---------|
| 10527, 10528 | 46201536 | 50 | 4.00E-63 | Magnetospirillum magnetotacticum MS-1 | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Magnetospirillum magnetotacticum MS-1] | | | 2.7.3.- |
| 10529, 10530 | 34558265 | 46 | 2.00E-53 | Wolinella succinogenes DSM 1740 | PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes] | | | |
| 1053, 1054 | 53711426 | 42 | 3.00E-67 | Bacteroides fragilis YCH46 | hypothetical protein BF0135 [Bacteroides fragilis YCH46] dbj BAD46884.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 10531, 10532 | 57241759 | 41 | 2.00E-31 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54429.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 10533, 10534 | 34558271 | 68 | 5.00E-99 | Wolinella succinogenes DSM 1740 | DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10986.1 DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes] | | | 2.7.7.7 |
| 10535, 10536 | 19705092 | 37 | 2.00E-09 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Tetratricopeptide repeat family protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93886.1 Tetratricopeptide repeat family protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | |
| 10537, 10538 | 32262177 | 34 | 6.00E-13 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860160.1 hypothetical protein HH0629 [Helicobacter hepaticus ATCC 51449] | | | |
| 10539, 10540 | 34556616 | 37 | 3.00E-41 | Wolinella succinogenes DSM 1740 | CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes] | | | |
| 10541, 10542 | 34557806 | 37 | 4.00E-24 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10521.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes] | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|--|---------------------------------------|--|---|-------------|----------|---|
| 10543, 10544 | | | | | | | Zebrafish DNA sequence from clone CH211- 286J13 in linkage group 4 Contains the gene for a novel protein containing a T-complex protein 11 domain (zgc:73347) and the 5' end of a novel gene, complete sequence | ## 7.00E-15 | | |
| 10545, 10546 | 1230584 | 70 | 3.00E-84 | | Vibrio cholerae O139 | nucleotide sugar dehydrogenase [Vibrio cholerae O139] pir S70888 nucleotide sugar dehydrogenase homolog - Vibrio cholerae dbj BAA33612.1 probable nucleotide sugar dehydrogenase [Vibrio cholerae] prf 2209416H nucleotide sugar dehydrogenase | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 5/6 | 87 8.00E-09 | 1.1.1.22 | |
| 10547, 10548 | 57238687 | 39 | 1.00E-20 | | Campylobacter jejuni RM1221 | UDP-N-acetylenolpyruvoylglucosamine reductase [Campylobacter jejuni RM1221] gb AAW36270.1 UDP-N-acetylenolpyruvoylglucosamine reductase [Campylobacter jejuni RM1221] | | | 1.1.1.15 | 8 |
| 10549, 10550 | 48856129 | 37 | 3.00E-18 | | Cytophaga hutchinsonii | COG1011: Predicted hydrolase (HAD superfamily) [Cytophaga hutchinsonii] | | | | |
| 1055, 1056 | 48856079 | 66 | 1.00E-60 | | Cytophaga hutchinsonii | COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | 1.8.-.- | |
| 10551, 10552 | 41725960 | 47 | 6.00E-34 | | Dechloromonas aromatica RCB | COG4232: Thiol:disulfide interchange protein [Dechloromonas aromatica RCB] | | | 5.3.4.1 | |
| 10553, 10554 | 34557246 | 33 | 2.00E-22 | | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | | | 2.7.3.- | |
| 10555, 10556 | 15611164 | 50 | 2.00E-27 | | Helicobacter pylori J99 | hypothetical protein jhp0094 [Helicobacter pylori J99] gb AAD05675.1 putative [Helicobacter pylori J99] pir E71975 hypothetical protein jhp0094 - Helicobacter pylori (strain J99) | Bacteroides fragilis YCH46 DNA, complete genome | 95 2.00E-09 | 2.4.-.- | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 10559, 10560 | 9656923 | 55 | 3.00E-34 | Vibrio cholerae O1 biovar eltor str. N16961 | conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231985.1 hypothetical protein VC2355 [Vibrio cholerae O1 biovar eltor str. N16961] pit C82088 conserved hypothetical protein VC2355 [imported] - Vibrio cholerae (strain N16961 serogroup O1) sp Q9KPL2 YN55_VIBCH Hypothetical UPF0246 protein VC2355 | | | |
| 10561, 10562 | 34557623 | 60 | 3.00E-28 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1259 [Wolinella succinogenes DSM 1740] emb CAE10338.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 10565, 10566 | 20809022 | 26 | 5.00E-12 | Thermoanaerobact er tengcongensis MB4 | hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4] gb AAM25797.1 hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4] | | | 4.1.99.- |
| 10569, 10570 | 53715826 | 52 | 3.00E-57 | Bacteroides fragilis YCH46 | carboxy-terminal processing protease precursor [Bacteroides fragilis YCH46] db JBAD51284.1 carboxy-terminal processing protease precursor [Bacteroides fragilis YCH46] | | | 3.4.21.- |
| 1057, 1058 | 48855421 | 32 | 1.00E-34 | Cytophaga hutchinsonii | COG0210: Superfamily I DNA and RNA helicases [Cytophaga hutchinsonii] | | | 3.6.1.- |
| 10571, 10572 | 48855898 | 48 | 1.00E-26 | Cytophaga hutchinsonii | hypothetical protein Chut02001116 [Cytophaga hutchinsonii] | | | |
| 10581, 10582 | 48858979 | 43 | 4.00E-26 | Clostridium thermocellum ATCC 27405 | hypothetical protein Chte02001700 [Clostridium thermocellum ATCC 27405] | | | |
| 10583, 10584 | 23003026 | 34 | 8.00E-30 | Lactobacillus gasseri | COG0553: Superfamily II DNA/RNA helicases, SNF2 family [Lactobacillus gasseri] | | | 3.6.1.3 |
| 10585, 10586 | 34557291 | 47 | 2.00E-40 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 10587, 10588 | 46317983 | 60 | 7.00E-64 | Burkholderia cepacia R18194 | COG0720: 6-pyruvoyl-tetrahydropterin synthase [Burkholderia cepacia R18194] | | | |
| 1059, 1060 | 13491145 | 47 | 1.00E-34 | Aneurinibacillus thermoaerophilus | D-glycero-D-manno-heptose 1-phosphate guanosyltransferase [Aneurinibacillus thermoaerophilus] | | | 2.7.7.13 |
| 10593, 10594 | 34557314 | 38 | 3.00E-23 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0925 [Wolinella succinogenes DSM 1740] emb CAE10029.1 hypothetical protein [Wolinella succinogenes] | | | |
| 10599, 10600 | 51245638 | 55 | 7.00E-19 | Desulfotalea psychrophila Lsv54 | hypothetical protein DP1786 [Desulfotalea psychrophila Lsv54] emb CAG36515.1 unknown protein [Desulfotalea psychrophila Lsv54] | | | |
| 10601, 10602 | 52425046 | 31 | 1.00E-10 | Mannheimia succiniciproducens MBEL55E | hypothetical protein MS0991 [Mannheimia succiniciproducens MBEL55E] gb AAU37598.1 unknown [Mannheimia succiniciproducens MBEL55E] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|---------------|
| 10603, 10604 | 7592813 | 52 | 1.00E-68 | Actinobacillus actinomycetemcomitans | GDP-mannose pyrophosphorylase homolog [Actinobacillus actinomycetemcomitans] | | | 2.7.7.22 |
| 10605, 10606 | 32262161 | 64 | 9.00E-56 | Helicobacter hepaticus ATCC 51449 | phosphohexosemutase [Helicobacter hepaticus ATCC 51449] ref NP_860144.1 phosphohexosemutase [Helicobacter hepaticus ATCC 51449] | | | 5.4.2.8 |
| 10607, 10608 | 32263402 | 44 | 1.00E-46 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861381.1 hypothetical protein HH1850 [Helicobacter hepaticus ATCC 51449] | | | |
| 10609, 10610 | 34557341 | 45 | 7.00E-34 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0953 [Wolinella succinogenes DSM 1740] emb CAE10056.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 1061, 1062 | 29349972 | 61 | 1.00E-66 | Bacteroides thetaiotaomicron VPI-5482 | putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.4.1.83 |
| 10613, 10614 | 57506236 | 67 | 3.00E-13 | Campylobacter upsallensis RM3195 | malate:quinone oxidoreductase, putative [Campylobacter upsallensis RM3195] gb EAL52259.1 malate:quinone oxidoreductase, putative [Campylobacter upsallensis RM3195] | | | 1.1.99.1 6 |
| 10615, 10616 | 56459896 | 37 | 2.00E-15 | Idiomarina lolihensis L2TR | DSBH domain containing protein [Idiomarina lolihensis L2TR] gb AAV81628.1 DSBH domain containing protein [Idiomarina lolihensis L2TR] | | | |
| 10617, 10618 | 42526240 | 26 | 2.00E-25 | Treponema denticola ATCC 35405 | aldehyde oxidase and xanthine dehydrogenase family protein [Treponema denticola ATCC 35405] gb AAS11219.1 aldehyde oxidase and xanthine dehydrogenase family protein [Treponema denticola ATCC 35405] | | | 1.1.1.20 4 |
| 10619, 10620 | 32262126 | 66 | 1.00E-84 | Helicobacter hepaticus ATCC 51449 | UTP-glucose-1-phosphate uridylyltransferase [Helicobacter hepaticus ATCC 51449] ref NP_860109.1 UTP-glucose-1-phosphate uridylyltransferase [Helicobacter hepaticus ATCC 51449] | | | 2.7.7.9 |
| 10621, 10622 | 34556541 | 42 | 6.00E-30 | Wolinella succinogenes DSM 1740 | ANTHRANILATE SYNTHASE COMPONENT I [Wolinella succinogenes DSM 1740] emb CAE09256.1 ANTHRANILATE SYNTHASE COMPONENT I [Wolinella succinogenes] | | | |
| 10623, 10624 | 54302166 | 27 | 8.00E-14 | Photobacterium profundum SS9 | hypothetical protein PBPRB0486 [Photobacterium profundum SS9] emb CAG22359.1 hypothetical protein [Photobacterium profundum] | | | |
| 10625, 10626 | 45358586 | 30 | 1.00E-16 | Methanococcus maripaludis S2 | Transcriptional regulator, TetR Family Member S2 emb CAF30579.1 Transcriptional regulator, TetR Family Member [Methanococcus maripaludis S2] | | | |
| 10627, 10628 | 23130537 | 45 | 4.00E-17 | Nostoc punctiforme PCC 73102 | COG0778: Nitroreductase [Nostoc punctiforme PCC 73102] | | | |

| | | | | | | | | |
|--------|----------|----|----------|----------------------|---|--|--|----------|
| 1063, | 21674172 | 32 | 6.00E-19 | Chlorobium | ABC transporter efflux protein [Chlorobium tepidum TLS] gb AAM72579.1 | | | |
| 1064 | AAG8272 | | | tepidum TLS | ABC transporter efflux protein [Chlorobium tepidum TLS] | | | |
| 10633, | | | | | Desc:S. epidermidis open reading frame protein sequence SEQ ID NO:2538. | | | |
| 10634 | 2 | 23 | 2.00E-07 | | Org:Staphylococcus epidermidis | | | |
| 10635, | | | | Treponema | cytidylate kinase/ribosomal protein S1 [Treponema denticola ATCC 35405] | | | 2.7.7.8 |
| 10636 | 42527583 | 52 | 1.00E-38 | denticola ATCC 35405 | gb AAS12592.1 cytidylate kinase/ribosomal protein S1 [Treponema denticola ATCC 35405] | | | |
| 10637, | | | | Helicobacter | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] | | | |
| 10638 | 32262573 | 45 | 1.00E-31 | hepaticus ATCC 51449 | ref NP_860554.1 hypothetical protein HH1023 [Helicobacter hepaticus ATCC 51449] | | | |
| 10639, | | | | Campylobacter lari | conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 10640 | 57241759 | 38 | 2.00E-48 | RM2100 | gb EAL54429.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 10641, | | | | Bacteroides fragilis | aspartate carbamoyltransferase regulatory chain [Bacteroides fragilis YCH46] db BAD48954.1 aspartate carbamoyltransferase regulatory chain | | | 2.1.3.2 |
| 10642 | 53713496 | 53 | 2.00E-30 | YCH46 | [Bacteroides fragilis YCH46] | | | |
| 10643, | | | | Bacteroides fragilis | aspartate carbamoyltransferase regulatory chain [Bacteroides fragilis YCH46] db BAD48954.1 aspartate carbamoyltransferase regulatory chain | | | 2.1.3.2 |
| 10644 | 53713496 | 53 | 3.00E-29 | YCH46 | [Bacteroides fragilis YCH46] | | | |
| 1065, | | | | Nostoc sp. PCC 7120 | two-component system, regulatory protein [Nostoc sp. PCC 7120] | | | |
| 1066 | 17230650 | 40 | 4.00E-11 | | db BAB74857.1 two-component system, regulatory protein [Nostoc sp. PCC 7120] pir AG2200 two-component system, regulatory protein alr3158 [Imported] - Nostoc sp. (strain PCC 7120) | | | 2.7.3.- |
| 10651, | | | | Methanosarcina | hypothetical protein Meth02004168 [Methanosarcina barkeri str. fusaro] | | | |
| 10652 | 48837993 | 46 | 2.00E-39 | barkeri str. fusaro | | | | |
| 10653, | | | | Cytophaga | COG0277: FAD/FMN-containing dehydrogenases [Cytophaga hutchinsonii] | | | 1.1.99.5 |
| 10654 | 48853549 | 52 | 8.00E-42 | hutchinsonii | putative sulfatase yidJ [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 10655, | | | | Bacteroides | putative sulfatase yidJ [Bacteroides thetaiotaomicron VPI-5482] | | | 3.1.6.- |
| 10656 | 29349207 | 39 | 9.00E-37 | VPI-5482 | gb AAO78904.1 putative sulfatase yidJ [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 10659, | | | | Geobacter | COG1053: Succinate dehydrogenase/fumarate reductase, flavoprotein subunit [Geobacter metallireducens GS-15] | | | 1.3.99.1 |
| 10660 | 48845483 | 41 | 2.00E-31 | 15 | putative transport protein [Bacteroides fragilis YCH46] db BAD49430.1 | | | |
| 10661, | | | | Bacteroides fragilis | putative transport protein [Bacteroides fragilis YCH46] | | | |
| 10662 | 53713972 | 37 | 7.00E-36 | YCH46 | putative transport protein [Bacteroides fragilis YCH46] | | | |
| 10663, | | | | Methanosarcina | hypothetical protein MM0206 [Methanosarcina mazel Go1] gb AAM29502.1 | | | |
| 10664 | 21226308 | 47 | 1.00E-17 | mazel Go1 | conserved protein [Methanosarcina mazel Goe1] | | | |
| 10665, | | | | Bacteroides | exonuclease ABC subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 10666 | 29345988 | 51 | 1.00E-69 | VPI-5482 | gb AAO75685.1 exonuclease ABC subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|--|--|---|----|---------------|----------|
| 10667, 10668 | 53713904 | 75 | 9.00E-98 | Bacteroides fragilis YCH46 | excinuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46] | Haemophilus influenzae excinuclease ABC subunit A (uvrA) gene, complete cds | 82 | 3.00E-08 | |
| 10669, 10670 | 15605819 | 41 | 8.00E-20 | Aquifex aeolicus VF5 | endonuclease III [Aquifex aeolicus VF5] gb AAC06594.1 endonuclease III [Aquifex aeolicus VF5] pir H70325 endonuclease III - Aquifex aeolicus | | | 4.2.99.1 8 | |
| 1067, 1068 | 28211966 | 65 | 1.00E-111 | Clostridium tetani E88 | ATP-dependent clp protease ATP-binding subunit clpX [Clostridium tetani E88] gb AAO36847.1 ATP-dependent clp protease ATP-binding subunit clpX [Clostridium tetani E88] sp Q891.8 CLPX_CLOTE ATP-dependent Clp protease ATP-binding subunit clpX | Caulobacter crescentus CB15 section 195 of 359 of the complete genome | 85 | 1.00E-17 | 3.4.24.- |
| 10671, 10672 | 57241904 | 79 | 1.00E-117 | Campylobacter upsaliensis RM3195 | transcription termination factor Rho [Campylobacter upsaliensis RM3195] gb EAL53877.1 transcription termination factor Rho [Campylobacter upsaliensis RM3195] | Campylobacter jejuni HS:19 lipooligosaccharide biosynthesis locus, partial sequence | 80 | 1.00E-26 | 3.6.3.14 |
| 10677, 10678 | 29376809 | 40 | 8.00E-38 | Enterococcus faecalis V583 | hypothetical protein EF2307 [Enterococcus faecalis V583] gb AAO82033.1 conserved hypothetical protein [Enterococcus faecalis V583] | | | | |
| 10679, 10680 | 23099116 | 40 | 1.00E-23 | Oceanobacillus lheyensis HTE831 | adenylylsulfate kinase [Oceanobacillus lheyensis HTE831] dbj BAC13617.1 adenylylsulfate kinase [Oceanobacillus lheyensis HTE831] | | | | 2.7.1.25 |
| 10681, 10682 | 29346299 | 40 | 9.00E-40 | Bacteroides thetataoomicron VPI-5482 | hypothetical protein BT0889 [Bacteroides thetataoomicron VPI-5482] gb AAO75996.1 conserved hypothetical protein [Bacteroides thetataoomicron VPI-5482] | | | | |
| 10687, 10688 | 48854843 | 49 | 3.00E-34 | Cytophaga hutchinsonii | COG0196: FAD synthase [Cytophaga hutchinsonii] | | | | 2.7.1.26 |
| 10689, 10690 | 57241016 | 35 | 3.00E-27 | Campylobacter lari RM2100 | methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100] gb EAL54712.1 methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100] | | | | |
| 1069, 1070 | 31194577 | 43 | 9.00E-67 | Anopheles gambiae | ENSANGP00000000035 [Anopheles gambiae] | | | | 1.10.3.3 |
| 10691, 10692 | 32476967 | 29 | 4.00E-16 | Rhodopirellula baltica SH 1 | type I restriction enzyme EcoAI R protein [Rhodopirellula baltica SH 1] emb CAD79104.1 type I restriction enzyme EcoAI R protein [Pirellula sp.] | | | | 3.1.21.3 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 10697, 10698 | 15669884 | 39 | 1.00E-45 | Methanocaldococcus jannaschii DSM 2661 | Heterodisulfide reductase, subunit A [Methanocaldococcus jannaschii DSM 2661] | | | 1.6.4.- |
| 10699, 10700 | 32262118 | 57 | 2.00E-26 | Helicobacter hepaticus ATCC 51449 | competence protein ComM [Helicobacter hepaticus ATCC 51449] ref[NP_860101.1] competence protein ComM [Helicobacter hepaticus ATCC 51449] | | | |
| 107, 108 | 48855577 | 48 | 3.00E-26 | Cytophaga hutchinsonii | COG0858: Ribosome-binding factor A [Cytophaga hutchinsonii] | | | |
| 10701, 10702 | 19704078 | 46 | 8.00E-29 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | ATP-dependent helicase, DinG family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gblAAL94939.1] ATP-dependent helicase, DinG family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | 3.6.1.- |
| 10703, 10704 | 48894830 | 41 | 9.00E-28 | Trichodesmium erythraeum IMS101 | COG0235: Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases [Trichodesmium erythraeum IMS101] | | | |
| 10705, 10706 | 14518311 | 39 | 6.00E-24 | Microscilla sp. PRE1 | putative outer membrane protein [Microscilla sp. PRE1] gblAAK62828.1] IMS106, putative outer membrane protein [Microscilla sp. PRE1] | | | |
| 10709, 10710 | 57240752 | 43 | 2.00E-25 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gblEAL55145.1] conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 10711, 10712 | 24372039 | 40 | 3.00E-13 | Shewanella oneidensis MR-1 | hypothetical protein SO0444 [Shewanella oneidensis MR-1] gblAAN53526.1] hypothetical protein [Shewanella oneidensis MR-1] | | | |
| 10713, 10714 | 34558169 | 32 | 2.00E-17 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-DNA polymerase III delta subunit [Wolinella succinogenes DSM 1740] emb CAE10884.1] conserved hypothetical protein-DNA polymerase III delta subunit [Wolinella succinogenes] | | | |
| 10715, 10716 | 52007843 | 48 | 5.00E-32 | Thiobacillus denitrificans ATCC 25259 | COG0607: Rhodanese-related sulfurtransferase [Thiobacillus denitrificans ATCC 25259] | | | |
| 10721, 10722 | 29346070 | 26 | 1.00E-11 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0660 [Bacteroides thetaiotaomicron VPI-5482] gblAAO75767.1] conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 10723, 10724 | 19704806 | 31 | 2.00E-13 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | N-acetylmannosamine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gblAAL95667.1] N-acetylmannosamine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | 2.7.1.60 |
| 10725, 10726 | 51246738 | 68 | 6.00E-33 | Desulfotalea psychrophila LSv54 | probable pyruvate-flavodoxin oxidoreductase [Desulfotalea psychrophila LSv54] emb CAG37615.1] probable pyruvate-flavodoxin oxidoreductase [Desulfotalea psychrophila LSv54] | | | 1.2.7.1 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|--|----------|
| 10727, 10728 | 20089049 | 29 | 5.00E-12 | Methanosarcina acetivorans C2A | hypothetical protein MA0151 [Methanosarcina acetivorans C2A] gb AA03604.1 predicted protein [Methanosarcina acetivorans str. C2A] tRNA pseudouridine synthase A [Campylobacter lari RM2100] gb EAL55500.1 tRNA pseudouridine synthase A [Campylobacter lari RM2100] | | | | 4.2.1.70 |
| 10729, 10730 | 57240386 | 37 | 1.00E-42 | Campylobacter lari RM2100 | | | | | |
| 1073, 1074 | 31194811 | 42 | 2.00E-32 | Anopheles gambiae | ENSANGP00000002016 [Anopheles gambiae] related to 27kDa outer membrane protein [Desulfotalea psychrophila LSV54] emb CAG36336.1 related to 27kDa outer membrane protein [Desulfotalea psychrophila LSV54] | | | | 3.1.-.- |
| 10731, 10732 | 51245459 | 25 | 2.00E-07 | Desulfotalea psychrophila LSV54 | putative integrase/recombinase [Staphylococcus aureus subsp. aureus MRS252] emb CAG40230.1 putative integrase/recombinase [Staphylococcus aureus subsp. aureus MRS252] | | | | |
| 10733, 10734 | 49483415 | 32 | 6.00E-22 | Staphylococcus aureus subsp. aureus MRS252 | glucose inhibited division protein A [Campylobacter lari RM2100] gb EAL55623.1 glucose inhibited division protein A [Campylobacter lari RM2100] | | | | |
| 10735, 10736 | 57240509 | 56 | 3.00E-26 | Campylobacter lari RM2100 | COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Psychrobacter sp. 273-4] | | | | 2.3.1.51 |
| 10739, 10740 | 46141178 | 80 | 2.00E-98 | Psychrobacter sp. 273-4 | Desc:Herbicide active polypeptide SEQ ID NO 1547. Org:Arabidopsis thaliana | | | | |
| 10741, 10742 | ABB9233 | 6 | 7.00E-10 | | | | | | |
| 10743, 10744 | 15896258 | 34 | 5.00E-43 | Clostridium acetobutylicum ATCC 824 | Zn-dependent peptidase, insulinase family [Clostridium acetobutylicum ATCC 824] gb AAK80947.1 Zn-dependent peptidase, insulinase family [Clostridium acetobutylicum ATCC 824] pir H97269 Zn-dependent peptidase, insulinase family [imported] - Clostridium acetobutylicum | | | | |
| 10745, 10746 | 53712196 | 46 | 7.00E-63 | Bacteroides fragilis YCH46 | tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides fragilis YCH46] db BAD47654.1 tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides fragilis YCH46] | | | | 2.5.1.8 |
| 10747, 10748 | 13358424 | 30 | 2.00E-07 | Lymphocystis disease virus 1 | unknown [Lymphocystis disease virus 1] | | | | |
| 10749, 10750 | 23114483 | 45 | 6.00E-27 | Desulfotobacterium hafniense DCB-2 | COG2931: RTX toxins and related Ca2+-binding proteins [Desulfotobacterium hafniense DCB-2] | | | | |
| 1075, 1076 | 48853390 | 34 | 3.00E-31 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] co-chaperone-curved DNA binding protein A (CbpA) [Campylobacter upsaliensis RM3195] gb EAL53788.1 co-chaperone-curved DNA binding protein A (CbpA) [Campylobacter upsaliensis RM3195] | | | | 2.7.3.- |
| 10751, 10752 | 57242326 | 28 | 2.00E-11 | Campylobacter upsaliensis RM3195 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|--|---|---|--|----|----------|
| 10755, 10756 | 34557593 | 49 | 3.00E-54 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1227 [Wolinella succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wolinella succinogenes] sp P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridyate synthase) [Uracil hydrolyase] | | | | |
| 10759, 10760 | 32469350 | 53 | 4.00E-25 | Francisella tularensis subsp. novicida | unknown [Francisella tularensis subsp. novicida] TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10442.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolinella succinogenes] | | | 88 | 2.00E-07 |
| 10761, 10762 | 34557727 | 42 | 5.00E-18 | Wolinella succinogenes DSM 1740 | | Francisella tularensis subsp. novicida strain FSC040 region of difference 1 (RD1), complete sequence | | | 2.7.3.- |
| 10763, 10764 | 34558250 | 67 | 1.00E-112 | Wolinella succinogenes DSM 1740 | EXINUCLEASE ABC SUBUNIT B [Wolinella succinogenes DSM 1740] emb CAE10965.1 EXINUCLEASE ABC SUBUNIT B [Wolinella succinogenes] | Mycoplasma penetrans HF-2 DNA, complete genome | | 87 | 3.00E-12 |
| 10765, 10766 | 34557419 | 40 | 5.00E-21 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | 2.7.3.- |
| 10767, 10768 | 29347815 | 40 | 8.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2405 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77512.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 1077, 1078 | 48853455 | 28 | 2.00E-13 | Cytophaga hutchinsonii | COG0806: RimM protein, required for 16S rRNA processing [Cytophaga hutchinsonii] | | | | |
| 10773, 10774 | 53711380 | 28 | 2.00E-07 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] db BAD46838.1 two-component system response regulator [Bacteroides fragilis YCH46] | | | | |
| 10775, 10776 | 29347827 | 28 | 8.00E-19 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2417 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77524.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 10779, 10780 | 48834423 | 35 | 3.00E-27 | Magnetococcus sp. MC-1 | COG0535: Predicted Fe-S oxidoreductases [Magnetococcus sp. MC-1] dimethyladenosine transferase [Campylobacter jejuni RM1221] | | | | |
| 10781, 10782 | 57236897 | 50 | 7.00E-44 | Campylobacter jejuni RM1221 | gb AAW34480.1 dimethyladenosine transferase [Campylobacter jejuni RM1221] | | | | 2.1.1.- |
| 10783, 10784 | 53711848 | 32 | 3.00E-29 | Bacteroides fragilis YCH46 | putative outer membrane efflux protein [Bacteroides fragilis YCH46] db BAD47306.1 putative outer membrane efflux protein [Bacteroides fragilis YCH46] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|----|----------|----------|
| 10787, 10788 | 53795029 | 29 | 1.00E-17 | Chloroflexus aurantiacus | COG2202: FOG: PAS/PAC domain [Chloroflexus aurantiacus] | | | 2.7.3.- |
| 10789, 10790 | 34557494 | 69 | 4.00E-61 | Wolinella succinogenes DSM 1740 | PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes DSM 1740] emb CAE10209.1 PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes] | 84 | 3.00E-08 | 6.3.5.- |
| 10791, 10792 | 39996989 | 31 | 5.00E-29 | Geobacter sulfurreducens PCA | response regulator [Geobacter sulfurreducens PCA] gb AAR35267.1 response regulator [Geobacter sulfurreducens PCA] | | | 2.7.3.- |
| 10793, 10794 | 48853942 | 37 | 1.00E-18 | Cytophaga hutchinsonii | COG4206: Outer membrane cobalamin receptor protein [Cytophaga hutchinsonii] | | | |
| 10795, 10796 | 48853942 | 35 | 9.00E-30 | Cytophaga hutchinsonii | COG4206: Outer membrane cobalamin receptor protein [Cytophaga hutchinsonii] | | | |
| 10797, 10798 | 34557362 | 27 | 7.00E-19 | Wolinella succinogenes DSM 1740 | TWO-COMPONENT HYBRID PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10077.1 TWO-COMPONENT HYBRID PROTEIN [Wolinella succinogenes] | | | |
| 10799, 10800 | 47568045 | 48 | 1.00E-21 | Bacillus cereus G9241 | glycogen synthase [Bacillus cereus G9241] gb EAL13693.1 glycogen synthase [Bacillus cereus G9241] | | | 2.4.1.21 |
| 10801, 10802 | 20807518 | 43 | 9.00E-58 | Thermoanaerobact er tengcongensis MB4 | Chemotaxis protein histidine kinase and related kinases [Thermoanaerobacter tengcongensis MB4] gb AAM24293.1 Chemotaxis protein histidine kinase and related kinases [Thermoanaerobacter tengcongensis MB4] | | | 2.7.3.- |
| 10803, 10804 | 1197006 | 55 | 8.00E-32 | Bacteroides fragilis | unknown protein [Bacteroides fragilis] gb AAA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551) | 85 | 1.00E-09 | |
| 10805, 10806 | 34398065 | 28 | 8.00E-08 | Porphyrromonas gingivalis W83 | ISPg2, transposase [Porphyrromonas gingivalis W83] gb AAQ66749.1 ISPg2, transposase [Porphyrromonas gingivalis W83] gb AAQ66414.1 ISPg2, transposase [Porphyrromonas gingivalis W83] gb AAQ66012.1 ISPg2, transposase [Porphyrromonas gingivalis W83] gb AAQ65497.1 ISPg2, transposase [Porphyrromonas gingivalis W83] ref NP_906226.1 ISPg2, transposase [Porphyrromonas gingivalis W83] ref NP_905850.1 ISPg2, transposase [Porphyrromonas gingivalis W83] ref NP_905515.1 ISPg2, transposase [Porphyrromonas gingivalis W83] ref NP_905113.1 ISPg2, transposase [Porphyrromonas gingivalis W83] ref NP_904598.1 ISPg2, transposase [Porphyrromonas gingivalis W83] gb AAC45368.1 putative transposase [Porphyrromonas gingivalis] | | | |

| | | | | | | | | | |
|-----------------|--------------|----|-----------|--|---|--|----|----------|----------|
| 10809, 10810 | 34558040 | 45 | 1.00E-43 | Wollinella succinogenes DSM 1740 | hypothetical protein WS1730 [Wollinella succinogenes DSM 1740] emb CAE10755.1 conserved hypothetical protein [Wollinella succinogenes] | | | | |
| 1081, 1082 | 48860907 | 37 | 4.00E-40 | Microbulbifer degradans 2-40 | COG3279: Response regulator of the LytR/AigR family [Microbulbifer degradans 2-40] | | | | 3.1.1.61 |
| 10811, 10812 | 42561229 | 48 | 8.00E-22 | Mycoplasma mycoides subsp. mycoides SC str. PG1 | omithine carbamoyltransferase [Mycoplasma mycoides subsp. mycoides SC str. PG1] emb CAE77322.1 omithine carbamoyltransferase [Mycoplasma mycoides subsp. mycoides SC] | | | | 2.1.3.3 |
| 10815, 10816 | ABG9157 1 | 36 | 4.00E-33 | | Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus | | | | 2.7.7.13 |
| 10817, 10818 | 54298940 | 37 | 3.00E-33 | Legionella pneumophila str. Paris | hypothetical protein lpp3007 [Legionella pneumophila str. Paris] emb CAH14160.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | |
| 10819, 10820 | 39996002 | 42 | 2.00E-29 | Geobacter sulfurreducens PCA | hypothetical protein GSU0897 [Geobacter sulfurreducens PCA] gb AAR34226.1 conserved hypothetical protein [Geobacter sulfurreducens PCA] | | | | |
| 10821, 10822 | 48839054 | 25 | 8.00E-10 | Methanosarcina barkeri str. fusaro | COG0542: ATPases with chaperone activity, ATP-binding subunit [Methanosarcina barkeri str. fusaro] | | | | |
| 10823, 10824 | 48839054 | 29 | 2.00E-20 | Methanosarcina barkeri str. fusaro | COG0542: ATPases with chaperone activity, ATP-binding subunit [Methanosarcina barkeri str. fusaro] | | | | |
| 10827, 10828 | 34558244 | 35 | 2.00E-32 | Wollinella succinogenes DSM 1740 | SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wollinella succinogenes DSM 1740] emb CAE10959.1 SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wollinella succinogenes] | | | | 2.7.3.- |
| 10829, 10830 | 34557313 | 51 | 7.00E-31 | Wollinella succinogenes DSM 1740 | ABC TRANSPORTER, ATP-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10028.1 ABC TRANSPORTER, ATP-BINDING PROTEIN [Wollinella succinogenes] | | | | 1.8.- |
| 1083, 1084 | 48855328 | 79 | 1.00E-126 | Cytophaga hutchinsonii | COG0085: DNA-directed RNA polymerase, beta subunit/140 kD subunit [Cytophaga hutchinsonii] | Bacteroides thetaiotaomicron VPI-5482, section 12 of 21 of the complete genome | 90 | 2.00E-13 | 2.7.7.6 |
| 10831, 10832 | 34557317 | 35 | 3.00E-08 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0928 [Wollinella succinogenes DSM 1740] emb CAE10032.1 hypothetical protein [Wollinella succinogenes] | | | | |
| 10833, 10834 | 34557316 | 35 | 8.00E-21 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0927 [Wollinella succinogenes DSM 1740] emb CAE10031.1 hypothetical protein [Wollinella succinogenes] | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|--|---|--|----|----------|----------|
| 10837, 10838 | 32263347 | 48 | 1.00E-60 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861326.1 hypothetical protein HH1795 [Helicobacter hepaticus ATCC 51449] | | | | |
| 10841, 10842 | 34556857 | 48 | 2.00E-63 | Wolinella succinogenes DSM 1740 | DNA POLYMERASE I [Wolinella succinogenes DSM 1740] emb CAE09572.1 DNA POLYMERASE I [Wolinella succinogenes] | | | | 2.7.7.7 |
| 10843, 10844 | 34556857 | 60 | 4.00E-73 | Wolinella succinogenes DSM 1740 | DNA POLYMERASE I [Wolinella succinogenes DSM 1740] emb CAE09572.1 DNA POLYMERASE I [Wolinella succinogenes] | | | | 2.7.7.7 |
| 10845, 10846 | 29654150 | 46 | 2.00E-21 | Coxiella burnetii RSA 493 | hypothetical protein CBU0822 [Coxiella burnetii RSA 493] gb AAO90356.1 conserved hypothetical protein [Coxiella burnetii RSA 493] | | | | |
| 10847, 10848 | 48853408 | 46 | 2.00E-77 | Cytophaga hutchinsonii | COG0567: 2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes [Cytophaga hutchinsonii] | | | | 1.2.4.2 |
| 10849, 10850 | 34556786 | 37 | 2.00E-42 | Wolinella succinogenes DSM 1740 | PUTATIVE PROCESSING PROTEASE [Wolinella succinogenes DSM 1740] emb CAE09501.1 PUTATIVE PROCESSING PROTEASE [Wolinella succinogenes] | | | | 3.4.-.- |
| 1085, 1086 | 2281663 | 59 | 2.00E-76 | Flavobacterium johnsoniae | gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [imported] - Flavobacterium johnsoniae | | | | 1.8.-.- |
| 10851, 10852 | 46580033 | 44 | 3.00E-47 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | phosphoribosylformylglycinamide synthase I [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96100.1 phosphoribosylformylglycinamide synthase I [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | 6.3.5.3 |
| 10857, 10858 | 29347851 | 35 | 7.00E-22 | Bacteroides thetaiotaomicron VPI-5482 | putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77548.1 putative 5'-nucleotidase/2',3'- cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.1.4.16 |
| 10861, 10862 | 32262861 | 24 | 9.00E-10 | Helicobacter hepaticus ATCC 51449 | methyl-accepting chemotaxis protein [Helicobacter hepaticus ATCC 51449] ref NP_860841.1 methyl-accepting chemotaxis protein [Helicobacter hepaticus ATCC 51449] | | | | |
| 10863, 10864 | ABP6590 6 | 61 | 1.00E-75 | | Desc:Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:650. Org:Bifidobacterium longum | Streptococcus mutans UA159 section 3 of 185 of the complete genome | 86 | 1.00E-10 | 6.3.5.3 |
| 10865, 10866 | 29346742 | 52 | 2.00E-64 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1332 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76439.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |

| | | | | | | | | | |
|------------------------------------|----------------------|----------|----------------------|--|---|--|----|---------------|----------|
| 10867, 10868 10869, 10870 | 23002396 32473409 | 33 43 | 1.00E-31 4.00E-23 | Lactobacillus gasseri Rhodopirellula baltica SH 1 | COG2344: AT-rich DNA-binding protein [Lactobacillus gasseri] ref NP_964480.1 hypothetical protein LJO455 [Lactobacillus johnsonii] NCC 533 gb AAS08446.1 hypothetical protein LJO455 [Lactobacillus johnsonii] NCC 533] probable aminopeptidase [Rhodopirellula baltica SH 1] emb CAD78184.1 probable aminopeptidase [Pirellula sp.] | | | 3.4.17.2 1 | |
| 10873, 10874 | 32261675 | 44 | 5.00E-56 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859659.1 hypothetical protein HH0128 [Helicobacter hepaticus ATCC 51449] | Alvinella pompejana epibiont 6C6 fosmid clone 6C6, complete sequence | 87 | 2.00E-09 | 6.3.2.15 |
| 10875, 10876 | 32477370 | 31 | 5.00E-19 | Rhodopirellula baltica SH 1 | phosphoribosylaminimidazole-succinocarboxamide synthase [Rhodopirellula baltica SH 1] emb CAD77441.1 phosphoribosylaminimidazole-succinocarboxamide synthase [Pirellula sp.] | | | | 6.3.2.6 |
| 10877, 10878 | 20806994 | 32 | 2.00E-27 | Thermoanaerobact er tengcongensis MB4 | ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Thermoanaerobacter tengcongensis MB4] gb AAM23769.1 ATP-dependent exoDNase (exonuclease V), alpha subunit helicase superfamily I member [Thermoanaerobacter tengcongensis MB4] | | | | 3.1.11.5 |
| 10879, 10880 | 32263354 | 37 | 2.00E-24 | Helicobacter hepaticus ATCC 51449 | chemotaxis signal transduction protein CheV [Helicobacter hepaticus ATCC 51449] ref NP_861333.1 chemotaxis signal transduction protein CheV [Helicobacter hepaticus ATCC 51449] | | | | 2.7.3.- |
| 10881, 10882 | 57241192 | 38 | 2.00E-48 | Campylobacter lari RM2100 | fructose-1,6-bisphosphatase [Campylobacter lari RM2100] gb EAL54888.1 fructose-1,6-bisphosphatase [Campylobacter lari RM2100] | | | | 3.1.3.11 |
| 10883, 10884 | 53712231 | 38 | 2.00E-20 | Bacteroides fragilis YCH46 | transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD47689.1 transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 10885, 10886 | 15643941 | 57 | 3.00E-45 | Thermotoga maritima MSB8 | methylglyoxal synthase [Thermotoga maritima MSB8] gb AAD36260.1 methylglyoxal synthase [Thermotoga maritima MSB8] pir G72284 | | | | 4.2.3.3 |
| 10889, 10890 | 48856411 | 56 | 4.00E-21 | Cytophaga hutchinsonii | methylglyoxal synthase - Thermotoga maritima (strain MSB8) COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | | 1.8.- |
| 10891, 10892 | 54031326 | 37 | 8.00E-46 | Polaromonas sp. JS666 | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Polaromonas sp. JS666] | | | | |
| 10895, 10896 | 48856297 | 63 | 5.00E-42 | Cytophaga hutchinsonii | COG0735: Fe2+/Zn2+ uptake regulation proteins [Cytophaga hutchinsonii] | | | | |
| 10897, 10898 | 48833126 | 35 | 1.00E-26 | Magnetococcus sp. MC-1 | COG1355: Predicted dioxygenase [Magnetococcus sp. MC-1] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|-------|------------------------------------|---|---|----|------------------|
| 10899, 10900 | 32262440 | 21 | 4.00E-07 | 51449 | Helicobacter hepaticus ATCC | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860422.1 hypothetical protein HH0891 [Helicobacter hepaticus ATCC 51449] | | | |
| 109, 110 | 48854911 | 41 | 5.00E-35 | | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | |
| 10901, 10902 | AAU4054 | 34 | 7.00E-34 | | | Desc:Propionibacterium acnes immunogenic protein #1445. Org:Propionibacterium acnes | | | |
| 10903, 10904 | 48855091 | 40 | 4.00E-31 | | Cytophaga hutchinsonii | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 10907, 10908 | 558266 | 68 | 1.00E-29 | | Wolinella succinogenes | orf [Wolinella succinogenes] pil[S50154 hypothetical protein 2 - Wolinella succinogenes] | | | |
| 1091, 1092 | 21229419 | 43 | 2.00E-30 | | Methanosarcina mazel Go1 | hypothetical protein MM3317 [Methanosarcina mazel Go1] gb AAM33013.1 | | | |
| 10913, 10914 | 48866340 | 28 | 6.00E-19 | | Oenococcus oeni PSU-1 | hypothetical protein [Methanosarcina mazel Goe1] COG1252: NADH dehydrogenase, FAD-containing subunit [Oenococcus oeni PSU-1] | | | 1.6.99.3 |
| 10915, 10916 | 45516527 | 47 | 6.00E-37 | | Ralstonia eutropha JMP134 | COG0796: Glutamate racemase [Ralstonia eutropha JMP134] | | | 5.1.1.3 |
| 10917, 10918 | 34398066 | 50 | 3.00E-74 | | Porphyromonas gingivalis W83 | NADH:ubiquinone oxidoreductase, Na translocating, F subunit [Porphyromonas gingivalis W83] ref NP_906227.1 NADH:ubiquinone oxidoreductase, Na translocating, F subunit [Porphyromonas gingivalis W83] | | | 1.6.5.- |
| 10919, 10920 | 56418633 | 44 | 2.00E-52 | | Geobacillus kaustophilus HTA426 | DNA-directed RNA polymerase beta subunit [Geobacillus kaustophilus HTA426] dbj BAD74383.1 DNA-directed RNA polymerase beta subunit [Geobacillus kaustophilus HTA426] | Bosea sp. 7F RNA polymerase beta subunit (poB) gene, complete cds | 91 | 6.00E-07 2.7.7.6 |
| 10921, 10922 | 34558157 | 29 | 1.00E-16 | | Wolinella succinogenes DSM 1740 | SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes] DSM 1740 | | | 2.7.3.- |
| 10923, 10924 | 34557665 | 39 | 7.00E-46 | | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | 2.7.3.- |
| 10927, 10928 | 18653301 | 35 | 1.00E-08 | | Vibrio cholerae | putative Kdo transferase [Vibrio cholerae] | | | 2.4.99.- |
| 1093, 1094 | 15646208 | 39 | 3.00E-45 | | Helicobacter pylori 26695 | Adenine-specific DNA methylase [Helicobacter pylori 26695] | | | 2.1.1.72 |
| 10931, 10932 | 50085130 | 32 | 8.00E-16 | | Acinetobacter sp. ADP1 | hypothetical protein ACIAD1995 [Acinetobacter sp. ADP1] | | | |
| 10933, 10934 | 57167696 | 50 | 2.00E-82 | | Campylobacter coli RM2228 | emb CAG68818.1 hypothetical protein [Acinetobacter sp. ADP1] primosomal protein N' [Campylobacter coli RM2228] gb EAL57482.1 primosomal protein N' [Campylobacter coli RM2228] | | | 3.6.1.- |

| | | | | | | | | |
|--------------|----------|----|----------|-----------------------------------|---|--|--|----------|
| 10935, 10936 | 51244082 | 49 | 3.00E-28 | Desulfotalea psychrophila Lsv54 | hypothetical protein DP0230 [Desulfotalea psychrophila Lsv54] emb[CAG34959.1] hypothetical protein [Desulfotalea psychrophila Lsv54] Signal transduction histidine kinase [Idiomarina loihiensis L2TR] gb AAV82952.1 Signal transduction histidine kinase [Idiomarina loihiensis L2TR] | | | 2.7.3.- |
| 10937, 10938 | 56461220 | 30 | 3.00E-31 | Idiomarina loihiensis L2TR | hypothetical protein [Agrobacterium rhizogenes] ref NP_066673.1 hypothetical protein [Agrobacterium rhizogenes] dbj BAA97803.1 | | | |
| 10939, 10940 | 10567402 | 34 | 1.00E-07 | Agrobacterium rhizogenes | hypothetical protein [Rhizobium rhizogenes] | | | |
| 10943, 10944 | 15606018 | 40 | 2.00E-28 | Aquifex aeolicus VF5 | hypothetical protein ac_563 [Aquifex aeolicus VF5] gb AAC06808.1 | | | 2.7.3.- |
| 10945, 10946 | 48834077 | 46 | 2.00E-21 | Magnetococcus sp. MC-1 | hypothetical protein [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 10949, 10950 | 33596250 | 41 | 2.00E-24 | Bordetella parapertussis 12822 | putative membrane protein [Bordetella parapertussis 12822] emb CAE36915.1 putative membrane protein [Bordetella parapertussis] GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE | | | 2.7.3.- |
| 10953, 10954 | 34556480 | 49 | 4.00E-42 | Wolinella succinogenes DSM 1740 | ISOMERIZING [Wolinella succinogenes DSM 1740] emb CAE09195.1 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE | | | 2.6.1.16 |
| 10955, 10956 | 15643834 | 34 | 3.00E-08 | Thermotoga maritima MSB8 | hypothetical protein TM1076 [Thermotoga maritima MSB8] gb AAD36153.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir D72296 VPS29-like phosphoesterase-related protein TM1076 [similarity] - Thermotoga maritima (strain MSB8) | | | |
| 10957, 10958 | 42528087 | 26 | 2.00E-14 | Treponema denticola ATCC 35405 | endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405] gb AAS13104.1 | | | |
| 10959, 10960 | 48832245 | 49 | 7.00E-41 | Magnetococcus sp. MC-1 | endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405] | | | |
| 10963, 10964 | 57241714 | 36 | 4.00E-38 | Campylobacter lari RM2100 | COG0379: Quinolinate synthase [Magnetococcus sp. MC-1] fibronectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100] gb EAL54384.1 fibronectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100] | | | |
| 10965, 10966 | 39936981 | 50 | 5.00E-67 | Rhodopseudomonas palustris CGA009 | possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] emb CAE29361.1 possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] | | | 2.7.- |
| 10969, 10970 | 48853984 | 52 | 4.00E-74 | Cytophaga hutchinsonii | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | 3.6.1.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|---------------|
| 10971, 10972 | 15606287 | 34 | 5.00E-16 | Aquifex aeolicus VF5 | beta lactamase precursor [Aquifex aeolicus VF5] gb AAC07059.1 beta lactamase precursor [Aquifex aeolicus VF5] pir D70384 beta lactamase precursor - Aquifex aeolicus | | | | |
| 10973, 10974 | 24374636 | 33 | 4.00E-22 | Shewanella oneidensis MR-1 | thioredoxin, putative [Shewanella oneidensis MR-1] gb AAN56123.1 thioredoxin, putative [Shewanella oneidensis MR-1] | | | | 1.8.4.6 |
| 10975, 10976 | 53692808 | 33 | 6.00E-19 | Haemophilus sommus 129PT | hypothetical protein Hsom02000323 [Haemophilus sommus 129PT] | | | | |
| 10977, 10978 | 34557339 | 39 | 2.00E-41 | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10054.1 SENSORY TRANSDUCTION REGULATOR [Wolinella succinogenes] | | | | 2.7.3.- |
| 10979, 10980 | 9947383 | 29 | 1.00E-17 | Pseudomonas aeruginosa PAO1 | conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir [G83465 conserved hypothetical protein PA1433 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_250124.1 hypothetical protein PA1433 [Pseudomonas aeruginosa PAO1] | | | | 2.7.3.- |
| 10981, 10982 | 34558459 | 42 | 3.00E-50 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2183 [Wolinella succinogenes DSM 1740] emb CAE11174.1 hypothetical protein [Wolinella succinogenes] | | | | 2.1.1.- |
| 10983, 10984 | 24373682 | 42 | 1.00E-18 | Shewanella oneidensis MR-1 | purine-binding chemotaxis protein CheW [Shewanella oneidensis MR-1] gb AAN55169.1 purine-binding chemotaxis protein CheW [Shewanella oneidensis MR-1] | | | | 2.7.3.- |
| 10985, 10986 | 48856986 | 40 | 2.00E-10 | Cytophaga hutchinsonii | COG4753: Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain [Cytophaga hutchinsonii] | | | | |
| 10987, 10988 | 48845271 | 53 | 3.00E-17 | Geobacter metallireducens GS 15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | | 2.7.3.- |
| 10989, 10990 | 34557204 | 44 | 3.00E-28 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0806 [Wolinella succinogenes DSM 1740] emb CAE09919.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 1099, 1100 | 15893801 | 36 | 1.00E-22 | Clostridium acetobutylicum ATCC 824 | UDP-N-acetylenolpyruvoylglucosamine reductase (murB) [Clostridium acetobutylicum ATCC 824] gb AAK78490.1 UDP-N- acetylenolpyruvoylglucosamine reductase (murB) [Clostridium acetobutylicum ATCC 824] pir [G96962 UDP-N- acetylenolpyruvoylglucosamine reductase (murB) [imported] - Clostridium acetobutylicum sp Q97LP4 MURB_CLOAB UDP-N- acetylenolpyruvoylglucosamine reductase (UDP-N-acetylmuramate dehydrogenase) | | | | 1.1.1.15 8 |
| 10991, 10992 | 48833775 | 35 | 2.00E-21 | Magnetococcus sp. MC-1 | COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Magnetococcus sp. MC-1] | | | | 2.7.3.- |
| 10993, 10994 | 6460223 | 22 | 5.00E-12 | Deinococcus radiodurans | cobW protein, putative [Deinococcus radiodurans] pir [A75278 probable cobW protein - Deinococcus radiodurans (strain R1) ref NP_296129.1 cobW protein, putative [Deinococcus radiodurans R1] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|---------------|--|
| 10997, 10998 | 48864458 | 60 | 2.00E-39 | Microbubifer degradans 2-40 | COG2824: Uncharacterized Zn-ribbon-containing protein involved in phosphonate metabolism [Microbubifer degradans 2-40] | | | |
| 11, 12 | 29347043 | 42 | 4.00E-23 | Bacteroides thetaiotaomicron VPI-5482 | mannose-1-phosphate guanylyltransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76740.1 mannose-1-phosphate guanylyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | 2.7.7.13 | |
| 11001, 11002 | 15606171 | 35 | 2.00E-25 | Aquifex aeolicus VF5 | hydrogenase small subunit [Aquifex aeolicus VF5] gb AAC06946.1 hydrogenase small subunit [Aquifex aeolicus VF5] pir H70369 hydrogenase small subunit - Aquifex aeolicus | | 1.18.99. 1 | |
| 11003, 11004 | ABG1373 | 45 | 4.00E-21 | | Desc:Novel human diagnostic protein #13722. Org:Homo sapiens | | | |
| 11007, 11008 | 48856129 | 39 | 2.00E-43 | Cytophaga hutchinsonii | COG1011: Predicted hydrolase (HAD superfamily) [Cytophaga hutchinsonii] integrase:recombinase [Oceanobacillus ihayensis HTE831] dbj BAC13803.1 integrase : recombinase [Oceanobacillus ihayensis HTE831] sp Q7ZAM3 XERD_OCEIH Tyrosine recombinase xerD | | 3.8.1.2 | |
| 11009, 11010 | 23099302 | 34 | 7.00E-25 | Oceanobacillus ihayensis HTE831 | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 1101, 1102 | 48856112 | 35 | 1.00E-19 | Cytophaga hutchinsonii | | | | |
| 11011, 11012 | 48854182 | 33 | 2.00E-20 | Cytophaga hutchinsonii | COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii] biotin-protein ligase [Clostridium perfringens str. 13] dbj BAB80379.1 biotin- protein ligase [Clostridium perfringens str. 13] | | 3.2.1.52 | |
| 11013, 11014 | 18309655 | 38 | 4.00E-50 | Clostridium perfringens str. 13 | hypothetical protein CJE0015 [Campylobacter jejuni RM1221] gb AAW34510.1 conserved hypothetical protein [Campylobacter jejuni RM1221] | | 6.3.4.15 | |
| 11015, 11016 | 57236927 | 67 | 4.00E-80 | Campylobacter jejuni RM1221 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54399.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 11017, 11018 | 57241729 | 49 | 9.00E-25 | Campylobacter lari RM2100 | Methylenetetrahydrofolate cyclohydrolase; Methylenetetrahydrofolate dehydrogenase (NADP+) [Methanosarcina mazei Go1] gb AAM30137.1 Methylenetetrahydrofolate dehydrogenase (NADP+); Methylenetetrahydrofolate cyclohydrolase [Methanosarcina mazei Go1] transposase [Azoarcus sp. EbN1] emb CAI10611.1 transposase [Azoarcus sp. EbN1] | | 1.5.1.5 | |
| 11019, 11020 | 21226543 | 27 | 4.00E-17 | Methanosarcina mazei Go1 | | | | |
| 11021, 11022 | 56315983 | 48 | 2.00E-44 | Azoarcus sp. EbN1 | | | | |
| 11025, 11026 | | | | | Oryza sativa chromosome 11 BAC clone OSJNB0018N12, complete sequence | | 6.00E-10 | |
| 11027, 11028 | 18957982 | 50 | 2.00E-39 | Xenorhabdus nematophila | putative transposase [Xenorhabdus nematophila] | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|--|--|--|----|----------|----------|
| 11029, 11030 | 57238615 | 31 | 6.00E-07 | Campylobacter jejuni RM1221 | HrgA protein [Campylobacter jejuni RM1221] gb AAW36198.1 HrgA protein [Campylobacter jejuni RM1221] | | | | |
| 1103, 1104 | 53714652 | 40 | 6.00E-25 | Bacteroides fragilis YCH46 | putative two-component system sensor protein [Bacteroides fragilis YCH46] dbj BAD50110.1 putative two-component system sensor protein [Bacteroides fragilis YCH46] | | | 2.7.3.- | |
| 11031, 11032 | 52007199 | 26 | 8.00E-15 | Thiobacillus denitrificans ATCC 25259 | COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Thiobacillus denitrificans ATCC 25259] | | | | |
| 11033, 11034 | 29349224 | 48 | 6.00E-80 | Bacteroides thetaiotaomicron VPI-5482 | penicillin-binding protein 2 (PBP-2) [Bacteroides thetaiotaomicron VPI-5482] gb AAO7892.1 penicillin-binding protein 2 (PBP-2) [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 11035, 11036 | 50122190 | 47 | 3.00E-51 | Erwinia carotovora subsp. atroseptica SCR11043 | putative toxin secretion ATP-binding protein [Erwinia carotovora subsp. atroseptica SCR11043] emb CAG76166.1 putative toxin secretion ATP-binding protein [Erwinia carotovora subsp. atroseptica SCR11043] | | | 3.4.21.- | |
| 11037, 11038 | 21674374 | 39 | 4.00E-22 | Chlorobium tepidum TLS | hypothetical protein CT1556 [Chlorobium tepidum TLS] gb AAM72781.1 conserved hypothetical protein [Chlorobium tepidum TLS] | | | 3.4.21.- | |
| 11039, 11040 | 34557740 | 39 | 2.00E-55 | Wolinella succinogenes DSM 1740 | NIFEN2 [Wolinella succinogenes DSM 1740] emb CAE10455.1 NIFEN2 [Wolinella succinogenes] | | | 1.18.6.1 | |
| 11041, 11042 | 34556892 | 72 | 1.00E-114 | Wolinella succinogenes DSM 1740 | DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wolinella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wolinella succinogenes] sp Q7MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 82 | 4.00E-36 | 2.7.7.6 |
| 11043, 11044 | 28899070 | 32 | 2.00E-13 | Vibrio parahaemolyticus RIMD 2210633 | membrane-bound lytic murein transglycosylase D [Vibrio parahaemolyticus RIMD 2210633] dbj BAC60559.1 membrane-bound lytic murein transglycosylase D [Vibrio parahaemolyticus] | | | 3.2.1.- | |
| 11045, 11046 | 53715699 | 55 | 1.00E-75 | Bacteroides fragilis YCH46 | DNA topoisomerase I [Bacteroides fragilis YCH46] dbj BAD51157.1 DNA topoisomerase I [Bacteroides fragilis YCH46] | | | 5.99.1.2 | |
| 11047, 11048 | 46193085 | 30 | 2.00E-22 | Rhodobacter sphaeroides 2.4.1 | hypothetical protein RspH0300134.1 [Rhodobacter sphaeroides 2.4.1] | | | | |
| 11049, 11050 | 28897010 | 78 | 7.00E-83 | Vibrio parahaemolyticus RIMD 2210633 | nucleotide sugar dehydrogenase [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58499.1 nucleotide sugar dehydrogenase [Vibrio parahaemolyticus] | Vibrio vulnificus YJ016 DNA, chromosome I, complete sequence | 86 | 1.00E-13 | 1.1.1.22 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|----|----------|---------------|
| 1105, 1106 | 56750395 | 34 | 4.00E-07 | Synechococcus elongatus PCC 6301 | hypothetical protein syc0386_c [Synechococcus elongatus PCC 6301] dbj BAD78576.1 unknown protein [Synechococcus elongatus PCC 6301] | | | | |
| 11051, 11052 | 53765426 | 33 | 3.00E-26 | Anabaena variabilis ATCC 29413 | COG0642: Signal transduction histidine kinase [Anabaena variabilis ATCC 29413] | | | | 2.7.3.- |
| 11053, 11054 | 28900037 | 29 | 7.00E-19 | Vibrio parahaemolyticus RIMD 2210633 | putative C4-dicarboxylate transport sensor protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61525.1 putative C4-dicarboxylate transport sensor protein [Vibrio parahaemolyticus] | | | | 2.7.3.- |
| 11057, 11058 | 32469831 | 37 | 5.00E-21 | Campylobacter jejuni | VirD4 [Campylobacter jejuni] gb AA46901.1 VirD4 [Campylobacter jejuni] | | | | |
| 11059, 11060 | 53713904 | 73 | 1.00E-73 | Bacteroides fragilis YCH46 | exonuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46] | Haemophilus influenzae exonuclease ABC subunit A (uvrA) gene, complete cds | 82 | 3.00E-08 | |
| 11061, 11062 | 34557850 | 62 | 1.00E-84 | Wolinella succinogenes DSM 1740 | 3-DEHYDROQUINATE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE10565.1 3-DEHYDROQUINATE SYNTHASE [Wolinella succinogenes] sp Q7M8N9 AROB_WOLSU 3-dehydroquinase synthase | | | | 4.2.3.4 |
| 11065, 11066 | 48855885 | 61 | 5.00E-73 | Cytophaga hutchinsonii | COG0209: Ribonucleotide reductase, alpha subunit [Cytophaga hutchinsonii] | Onyza sativa (japonica cultivar- group), mRNA | 88 | 3.00E-08 | 1.17.4.1 |
| 11067, 11068 | 48860260 | 28 | 3.00E-26 | Clostridium thermocellum ATCC 27405 | COG0489: ATPases involved in chromosome partitioning [Clostridium thermocellum ATCC 27405] | | | | 2.7.1.11 2 |
| 11069, 11070 | 48857909 | 25 | 6.00E-08 | Clostridium thermocellum ATCC 27405 | COG1316: Transcriptional regulator [Clostridium thermocellum ATCC 27405] | | | | |
| 1107, 1108 | 42557777 | 53 | 2.00E-14 | uncultured crenarchaeote | hypothetical protein [uncultured crenarchaeote] | | | | |
| 11071, 11072 | 34557590 | 31 | 6.00E-20 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10305.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes] | | | | |
| 11073, 11074 | 53684488 | 25 | 3.00E-07 | Desulfotobacterium hafniense DCB-2 | COG0840: Methyl-accepting chemotaxis protein [Desulfotobacterium hafniense DCB-2] | | | | |
| 11075, 11076 | 48855450 | 60 | 6.00E-35 | Cytophaga hutchinsonii | COG0817: Holliday junction resolvase, endonuclease subunit [Cytophaga hutchinsonii] | | | | 3.1.22.4 |
| 11077, 11078 | 46425373 | 38 | 3.00E-32 | Xanthomonas albilineans | McbG-like protein [Xanthomonas albilineans] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|---------|
| 11079, 11080 | 53714706 | 60 | 9.00E-83 | Bacteroides fragilis YCH46 | adenylosuccinate synthetase [Bacteroides fragilis YCH46] dbj BAD50164.1 adenylosuccinate synthetase [Bacteroides fragilis YCH46] | | | 6.3.4.4 |
| 11081, 11082 | 29349257 | 37 | 1.00E-47 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3849 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78954.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 11083, 11084 | 23125110 | 28 | 3.00E-24 | Nostoc punctiforme PCC 73102 | COG0784: FOG: CheY-like receiver [Nostoc punctiforme PCC 73102] hypothetical protein aq_367 [Aquifex aeolicus VF5] gb AAC06656.1 | | | 2.7.3.- |
| 11085, 11086 | 15605874 | 32 | 1.00E-33 | Aquifex aeolicus VF5 | hypothetical protein [Aquifex aeolicus VF5] pir G70332 conserved hypothetical protein aq_367 - Aquifex aeolicus | | | |
| 11087, 11088 | 54302389 | 56 | 2.00E-69 | Photobacterium profundum SS9 | hypothetical protein PBPRB0710 [Photobacterium profundum SS9] emb CAG22582.1 hypothetical protein [Photobacterium profundum] | | | 6.3.2.3 |
| 11089, 11090 | 34557665 | 51 | 2.00E-24 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | 2.7.3.- |
| 11091, 11092 | 34556560 | 30 | 2.00E-27 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 11093, 11094 | 48858102 | 46 | 1.00E-36 | Clostridium thermocellum ATCC 27405 | COG1905: NADH:ubiquinone oxidoreductase 24 kD subunit [Clostridium thermocellum ATCC 27405] | | | 1.6.5.3 |
| 11095, 11096 | 53688150 | 26 | 9.00E-13 | Nostoc punctiforme PCC 73102 | COG0500: SAM-dependent methyltransferases [Nostoc punctiforme PCC 73102] | | | |
| 11099, 11100 | 53713110 | 56 | 5.00E-32 | Bacteroides fragilis YCH46 | putative long-chain-fatty-acid-CoA ligase [Bacteroides fragilis YCH46] dbj BAD48568.1 putative long-chain-fatty-acid-CoA ligase [Bacteroides fragilis YCH46] | | | 6.2.1.3 |
| 111, 112 | 29349624 | 54 | 5.00E-45 | Bacteroides thetaiotaomicron VPI-5482 | ubiquinone/menaquinone biosynthesis methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79321.1 ubiquinone/menaquinone biosynthesis methyltransferase [Bacteroides thetaiotaomicron VPI-5482] spiQ8A005 UBIE_BACTN Menaquinone biosynthesis methyltransferase ubiE | | | 2.1.1.- |
| 11103, 11104 | 57241252 | 41 | 2.00E-36 | Campylobacter lari RM2100 | signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54948.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100] | | | 2.7.3.- |
| 11105, 11106 | 51243987 | 26 | 2.00E-11 | Desulfotalea psychrophila LSV54 | hypothetical protein DP0135 [Desulfotalea psychrophila LSV54] emb CAG34864.1 hypothetical protein [Desulfotalea psychrophila LSV54] | | | 2.7.3.- |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|--|---|----|------------------|
| 11109, 11110 | 45507729 | 33 | 2.00E-47 | Anabaena variabilis ATCC 29413 | COG0479: Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit [Anabaena variabilis ATCC 29413] | | | 1.3.99.1 |
| 11111, 11112 | 53715477 | 81 | 1.00E-116 | Bacteroides fragilis YCH46 | DNA-directed RNA polymerase beta chain [Bacteroides fragilis YCH46] dbj BAD50935.1 DNA-directed RNA polymerase beta chain [Bacteroides fragilis YCH46] | Bacteroides thetataoimicron VPI-5482, section 12 of 21 of the complete genome | 78 | 3.00E-15 2.7.7.6 |
| 11113, 11114 | 34557844 | 34 | 1.00E-22 | Wolinella succinogenes DSM 1740 | MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10559.1 MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes] | | | |
| 11119, 11120 | 34558325 | 53 | 2.00E-69 | Wolinella succinogenes DSM 1740 | PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11040.1 PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes] sp Q7M7W8 ENGA_WOLSU GTP-binding protein engA putative UROPORPHYRINOGEN-III SYNTHASE [Helicobacter pylori J99] gb AAD06731.1 putative UROPORPHYRINOGEN-III SYNTHASE [Helicobacter pylori J99] pir C71843 probable uroporphyrinogen-III synthase - Helicobacter pylori (strain J99) | | | 4.2.1.75 |
| 11121, 11122 | 15612210 | 33 | 9.00E-11 | Helicobacter pylori J99 | COG0659: Sulfate permease and related transporters (MFS superfamily) [Anabaena variabilis ATCC 29413] | | | |
| 11123, 11124 | 46134647 | 29 | 4.00E-10 | Anabaena variabilis ATCC 29413 | DNA polymerase III alpha subunit [Bacteroides fragilis YCH46] dbj BAD47459.1 DNA polymerase III alpha subunit [Bacteroides fragilis YCH46] | | | 2.7.7.7 |
| 11125, 11126 | 53712001 | 62 | 6.00E-86 | Bacteroides fragilis YCH46 | transcriptional regulator, AraC family [Agrobacterium tumefaciens str. C58] gb AAL45674.1 transcriptional regulator, AraC family [Agrobacterium tumefaciens str. C58] pir AD3157 transcription regulator, AraC family Atu4880 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont) | | | |
| 11129, 11130 | 17938569 | 39 | 2.00E-08 | Agrobacterium tumefaciens str. C58 | COG1530: Ribonucleases G and E [Cytophaga hutchinsonii] | | | 3.1.4.- |
| 1113, 1114 | 48854348 | 55 | 4.00E-91 | Cytophaga hutchinsonii | COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii] | | | |
| 11131, 11132 | 48853591 | 55 | 2.00E-65 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Desulfovibrio desulfuricans G20] | | | |
| 11133, 11134 | 53691920 | 22 | 5.00E-07 | Desulfovibrio desulfuricans G20 | putative two-component system sensor protein, no kinase domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76902.1 putative two- component system sensor protein, no kinase domain [Bacteroides thetataoimicron VPI-5482] | | | 2.7.3.- |
| 11135, 11136 | 29347205 | 34 | 1.00E-30 | Bacteroides thetataoimicron VPI-5482 | | | | |

| | | | | | | | | |
|----------------|----------|----|----------|---------------------------------------|--|----------|----------|----------|
| 111143, 111144 | 48862944 | 32 | 4.00E-25 | Microbulifer degradans 2-40 | COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Microbulifer degradans 2-40] | | | |
| 111145, 111146 | 48890454 | 35 | 1.00E-38 | Trichodesmium erythraeum IMS101 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] probable formate dehydrogenase [Clostridium perfringens str. 13] dbj BAB81254.1 probable formate dehydrogenase [Clostridium perfringens str. 13] | 1.2.7.- | | |
| 111147, 111148 | 18310530 | 31 | 2.00E-27 | Clostridium perfringens str. 13 | probable formate dehydrogenase [Clostridium perfringens str. 13] dbj BAB81254.1 probable formate dehydrogenase [Clostridium perfringens str. 13] | 1.7.99.4 | | |
| 111149, 111150 | 18310530 | 29 | 8.00E-32 | Clostridium perfringens str. 13 | hypothetical protein-signal peptide and transmembrane prediction [Rhodopirellula ballica SH 1] emb CAD71383.1 hypothetical protein-signal peptide and transmembrane prediction [Pirellula sp.] | | | |
| 111151, 111152 | 32470719 | 29 | 2.00E-23 | Rhodopirellula ballica SH 1 | COG2143: Thiorodoxin-related protein [Magnetococcus sp. MC-1] hypothetical protein RS01112 [Ralstonia solanacearum GM1000] emb CAD16190.1 CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] | | | |
| 111153, 111154 | 48833189 | 31 | 9.00E-19 | Magnetococcus sp. MC-1 | COG2200: FOG: EAL domain [Magnetococcus sp. MC-1] | | | |
| 111155, 111156 | 17547202 | 27 | 6.00E-09 | Ralstonia solanacearum GM1000 | Desc:Orthosomycin biosynthetic polypeptide SEQ ID NO 197. Org:Micromonospora carbonacea africana | | | |
| 111159, 111160 | 48834030 | 37 | 1.00E-28 | Magnetococcus sp. MC-1 | aminoacyl-histidine dipeptidase [Campylobacter upsaliensis gb EAL53077.1 aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195] | 3.4.13.3 | | |
| 111161, 111162 | 57505466 | 39 | 2.00E-49 | Campylobacter upsaliensis RM3195 | DNA topoisomerase I [Bacteroides fragilis YCH46] dbj BAD51157.1 DNA topoisomerase I [Bacteroides fragilis YCH46] | 5.99.1.2 | | |
| 111163, 111164 | 53715699 | 45 | 2.00E-48 | Bacteroides fragilis YCH46 | COG1087: UDP-glucose 4-epimerase [Trichodesmium erythraeum IMS101] hypothetical protein GSU0680 [Geobacter sulfurreducens PCA] gb AAR34010.1 conserved hypothetical protein [Geobacter sulfurreducens PCA] | 5.1.3.2 | | |
| 111165, 111166 | 48891975 | 54 | 1.00E-44 | Trichodesmium erythraeum IMS101 | putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 111167, 111168 | 39995786 | 32 | 4.00E-18 | Geobacter sulfurreducens PCA | Bacteroides thetaiotaomicron VPI-5482 | | | |
| 11117, 11118 | 29349972 | 66 | 1.00E-89 | Bacteroides thetaiotaomicron VPI-5482 | complete genome | 85 | 2.00E-07 | 2.4.1.83 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 11173, 11174 | 51246493 | 35 | 1.00E-23 | Desulfotalea psychrophila LSv54 | related to peptidyl-prolyl cis-trans isomerase (FKBP-type) [Desulfotalea psychrophila LSv54] emb CAG37370.1 related to peptidyl-prolyl cis-trans isomerase (FKBP-type) [Desulfotalea psychrophila LSv54] | | | 5.2.1.8 |
| 11175, 11176 | 53712042 | 45 | 5.00E-13 | Bacteroides fragilis YCH46 | hypothetical protein BF0749 [Bacteroides fragilis YCH46] dbj BAD47500.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 11177, 11178 | 48856222 | 33 | 9.00E-31 | Cytophaga hutchinsonii | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | 2.4.1.21 |
| 11179, 11180 | 57242490 | 57 | 1.00E-74 | Campylobacter upsaliensis RM3195 | Mg chelatase-related protein [Campylobacter upsaliensis RM3195] gb EAL53558.1 Mg chelatase-related protein [Campylobacter upsaliensis RM3195] | | | |
| 11181, 11182 | 6967663 | 51 | 4.00E-38 | Campylobacter jejuni subsp. jejuni NCTC.11168 | hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281400.1 hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81437 hypothetical protein Cj0190c [imported] - Campylobacter jejuni (strain NCTC 11168) | | | |
| 11183, 11184 | 48892769 | 26 | 4.00E-22 | Trichodesmium erythraeum IMS101 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] | | | |
| 11185, 11186 | 53729414 | 33 | 1.00E-36 | Dechloromonas aromatica RCB | COG0515: Serine/threonine protein kinase [Dechloromonas aromatica RCB] | | | 2.7.1.37 |
| 11187, 11188 | 39996253 | 30 | 4.00E-11 | Geobacter sulfurreducens PCA | hypothetical protein GSU1151 [Geobacter sulfurreducens PCA] gb AAR34527.1 conserved hypothetical protein [Geobacter sulfurreducens PCA] | | | |
| 11189, 11190 | 53713588 | 45 | 5.00E-22 | Bacteroides fragilis YCH46 | ATP-dependent RNA helicase [Bacteroides fragilis YCH46] dbj BAD49046.1 ATP-dependent RNA helicase [Bacteroides fragilis YCH46] | | | 2.7.7.- |
| 11191, 11192 | 48854956 | 38 | 2.00E-16 | Cytophaga hutchinsonii | COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii] | | | 2.7.7.- |
| 11195, 11196 | 50085810 | 28 | 8.00E-13 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD2753 [Acinetobacter sp. ADP1] emb CAG69498.1 hypothetical protein [Acinetobacter sp. ADP1] | | | |
| 11199, 11200 | 23130207 | 34 | 7.00E-18 | Nostoc punctiforme PCC 73102 | COG0732: Restriction endonuclease S subunits [Nostoc punctiforme PCC 73102] | | | 3.1.21.3 |
| 11205, 11206 | 11499361 | 39 | 5.00E-27 | Archaeoglobus fulgidus DSM 4304 | long-chain-fatty-acid-CoA ligase (fadD-7) [Archaeoglobus fulgidus DSM 4304] gb AAB89478.1 long-chain-fatty-acid-CoA ligase (fadD-7) [Archaeoglobus fulgidus DSM 4304] pir C69471 probable fatty-acid-CoA ligase (EC 6.2.1.-) fadD7 - Archaeoglobus fulgidus | | | 6.2.1.3 |
| 11207, 11208 | 31195627 | 54 | 2.00E-70 | Anopheles gambiae | ENSANGP00000000430 [Anopheles gambiae] | | | 6.3.2.1 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|---|----|----------|---------|
| 1121, 1122 | 45441661 | 24 | 1.00E-06 | Yersinia pestis biovar Medievalis str. 91001 | Transposase [Yersinia pestis biovar Medievalis str. 91001] gb AAS62077.1 Transposase [Yersinia pestis biovar Medievalis str. 91001] | | | | |
| 11211, 11212 | 53690630 | 28 | 1.00E-16 | Desulfovibrio desulfuricans G20 | COG1309: Transcriptional regulator [Desulfovibrio desulfuricans G20] | | | | |
| 11213, 11214 | 19705384 | 25 | 7.00E-12 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | General secretion pathway protein F [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94178.1 General secretion pathway protein F [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | |
| 11217, 11218 | 54302389 | 49 | 4.00E-57 | Photobacterium profundum SS9 | hypothetical protein PBPRB0710 [Photobacterium profundum SS9] emb CAG22582.1 hypothetical protein [Photobacterium profundum] | | | | |
| 11221, 11222 | 24374072 | 40 | 3.00E-46 | Shewanella oneidensis MR-1 | hypothetical protein SO2529 [Shewanella oneidensis MR-1] gb AAN55559.1 hypothetical protein [Shewanella oneidensis MR-1] conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54746.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 11223, 11224 | 57241050 | 26 | 6.00E-13 | Campylobacter lari RM2100 | putative two-component system sensor protein [Bacteroides fragilis YCH46] dbj BAD51256.1 putative two-component system sensor protein [Bacteroides fragilis YCH46] | | | 2.7.3.- | |
| 11229, 11230 | 53715798 | 44 | 5.00E-34 | Bacteroides fragilis YCH46 | COG0857: BioD-like N-terminal domain of phosphotransacetylase | | | 2.3.1.8 | |
| 11231, 11232 | 23473597 | 33 | 5.00E-27 | Desulfovibrio desulfuricans G20 | [Desulfovibrio desulfuricans G20] | | | 1.4.1.2 | |
| 11233, 11234 | 48833808 | 41 | 6.00E-53 | Magnetococcus sp. MC-1 | COG2902: NAD-specific glutamate dehydrogenase [Magnetococcus sp. MC- 1] | | | 2.7.2.11 | |
| 11235, 11236 | 32261967 | 51 | 6.00E-51 | Helicobacter hepaticus ATCC 51449 | glutamate 5-kinase [Helicobacter hepaticus ATCC 51449] ref NP_859950.1 glutamate 5-kinase [Helicobacter hepaticus ATCC 51449] sp Q7VJ31 PROB_HELHP Glutamate 5-kinase (Gamma-glutamyl kinase) (GK) | | | | |
| 11237, 11238 | 48853332 | 35 | 1.00E-23 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | | |
| 11239, 11240 | 32262492 | 41 | 2.00E-21 | Helicobacter hepaticus ATCC 51449 | transcriptional regulator [Helicobacter hepaticus ATCC 51449] ref NP_860473.1 transcriptional regulator [Helicobacter hepaticus ATCC 51449] | | | | |
| 11241, 11242 | 52007358 | 40 | 2.00E-48 | Thiobacillus denitrificans ATCC 25259 | COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Thiobacillus denitrificans ATCC 25259] PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes] | Desc:M. capsulatus gene #41 for DNA array. Org:Methylococcus capsulatus | 88 | 4.00E-11 | 2.7.3.- |
| 11243, 11244 | 34557419 | 34 | 4.00E-27 | Wollinella succinogenes DSM 1740 | | | | | 2.7.3.- |

| | | | | | | | | |
|------------------------------------|----------------------|----------|----------------------|--|---|--|--|---------------|
| 11245, 11246 | 53715283 | 35 | 1.00E-08 | Bacteroides fragilis YCH46 | putative exodeoxyribonuclease VII large subunit [Bacteroides fragilis YCH46] dbj BAD50741.1 putative exodeoxyribonuclease VII large subunit [Bacteroides fragilis YCH46] | | | 3.1.11.6 |
| 11247, 11248 | 15643770 | 28 | 1.00E-10 | Thermotoga maritima MSB8 | hypothetical protein TM1012 [Thermotoga maritima MSB8] gb AAD36089.1 hypothetical protein TM1012 [Thermotoga maritima MSB8] pir D72305 hypothetical protein - Thermotoga maritima (strain MSB8) | | | |
| 11249, 11250 | 27364626 | 43 | 2.00E-14 | Vibrio vulnificus CMCP6 | Hemolysin [Vibrio vulnificus CMCP6] ref NP_935939.1 hemolysin [Vibrio vulnificus YJ016] gb AAO09681.1 Hemolysin [Vibrio vulnificus CMCP6] dbj BAC95910.1 hemolysin [Vibrio vulnificus YJ016] | | | |
| 11251, 11252 | 46201018 | 39 | 5.00E-55 | Magnetospirillum magnetotacticum MS-1 | COG2200: FOG: EAL domain [Magnetospirillum magnetotacticum MS-1] hypothetical protein aq_645 [Aquifex aeolicus VF5] gb AAC06850.1 putative protein [Aquifex aeolicus VF5] pir B70357 hypothetical protein aq_645 - Aquifex aeolicus | | | |
| 11255, 11256 11257, 11258 | 15606069 53795187 | 23 41 | 5.00E-12 2.00E-26 | Aquifex aeolicus VF5 Chloroflexus aurantiacus | COG1131: ABC-type multidrug transport system, ATPase component [Chloroflexus aurantiacus] | | | 1.8.- |
| 11261, 11262 | 15965924 | 45 | 3.00E-25 | Sinorhizobium meliloti 1021 | PROBABLE D-ALANINE-D-ALANINE LIGASE B PROTEIN [Sinorhizobium meliloti 1021] emb CAC46750.1 PROBABLE D-ALANINE-D-ALANINE LIGASE B PROTEIN [Sinorhizobium meliloti] sp Q92NM4 DDL_RHIME D- alanine-D-alanine ligase [D-alanylalanine synthetase] (D-Ala-D-Ala ligase) | | | 6.3.2.4 |
| 11263, 11264 | 48858155 | 25 | 1.00E-07 | Clostridium thermocellum ATCC 27405 | COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Clostridium thermocellum ATCC 27405] | | | 2.4.1.- |
| 11265, 11266 | 28854714 | 28 | 4.00E-19 | Pseudomonas syringae pv. tomato str. DC3000 | conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794082.1 hypothetical protein PSPT04326 [Pseudomonas syringae pv. tomato str. DC3000] | | | |
| 11269, 11270 | 34558188 | 63 | 4.00E-44 | Wolinnella succinogenes DSM 1740 | HOMOSERINE O-ACETYLTRANSFERASE PROTEIN [Wolinnella succinogenes DSM 1740] emb CAE10903.1 HOMOSERINE O- ACETYLTRANSFERASE PROTEIN [Wolinnella succinogenes] | | | 2.3.1.31 |
| 11271, 11272 | 32263208 | 35 | 4.00E-23 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861187.1 hypothetical protein HH1656 [Helicobacter hepaticus ATCC 51449] | | | 2.7.- |
| 11273, 11274 | AAW2085 7 | 44 | 1.00E-37 | | Desc.H: pylori outer membrane protein, 12ap11614orf8. Org:Helicobacter pylori | | | 2.7.1.13 0 |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|----|----------|----------|
| 11275, 11276 | 15896496 | 54 | 2.00E-55 | Clostridium acetobutylicum ATCC 824 | Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] gb AAK81185.1 Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] pir F97299 sensory transduction protein containing HD_GYP domain [Imported] - Clostridium acetobutylicum | Clostridium acetobutylicum ATCC 824 section 309 of 356 of the complete genome | 93 | 1.00E-07 | |
| 11279, 11280 | 53765610 | 29 | 1.00E-11 | Anabaena variabilis ATCC 29413 | COG2319: FOG: WD40 repeat [Anabaena variabilis ATCC 29413] | | | | |
| 11281, 11282 | 557887 | 40 | 1.00E-17 | | Integrase prf 2115270D Integrase | | | | |
| 11285, 11286 | 53735965 | 41 | 2.00E-12 | Crocospaera watsonii WH 8501 | hypothetical protein Cwat03001093 [Crocospaera watsonii WH 8501] conserved hypothetical protein-Uncharacterized ATPase [Wolinella succinogenes DSM 1740] emb CAE10743.1 conserved hypothetical protein- Uncharacterized ATPase [Wolinella succinogenes] | | | | |
| 11289, 11290 | 34558028 | 35 | 6.00E-48 | Wolinella succinogenes DSM 1740 | RIBONUCLEASE HII RNASE HII [Wolinella succinogenes DSM 1740] emb CAE10744.1 RIBONUCLEASE HII RNASE HII [Wolinella succinogenes] | | | | 3.1.26.4 |
| 11291, 11292 | 34558029 | 53 | 9.00E-49 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09963.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes] | | | | |
| 11293, 11294 | 34557248 | 35 | 2.00E-23 | Wolinella succinogenes DSM 1740 | sensory box sensor histidine kinase/response regulator [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230993.1 sensory box sensor histidine kinase/response regulator [Vibrio cholerae O1 biovar eltor str. N16961] pir H82211 sensory box sensor histidine kinase/response regulator VC1349 [Imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | 2.7.3.- |
| 11295, 11296 | 9655841 | 47 | 4.00E-40 | Vibrio cholerae O1 biovar eltor str. N16961 | Nitroreductase family protein [Clostridium acetobutylicum ATCC 824] gb AAK79386.1 Nitroreductase family protein [Clostridium acetobutylicum ATCC 824] pir G97074 nitroreductase family protein [Imported] - Clostridium acetobutylicum | | | | 1.6.- |
| 11299, 11300 | 15894697 | 36 | 3.00E-26 | Clostridium acetobutylicum ATCC 824 | EXCINUCLEASE ABC SUBUNIT A [Wolinella succinogenes DSM 1740] emb CAE10659.1 EXCINUCLEASE ABC SUBUNIT A [Wolinella succinogenes] | Helicobacter hepaticus ATCC 51449 section 1 of 6 of the complete genome | 89 | 1.00E-13 | |
| 11301, 11302 | 34557944 | 78 | 1.00E-106 | Wolinella succinogenes DSM 1740 | COG2010: Cytochrome c, mono- and diheme variants [Magnetospirillum magnetotacticum MS-1] | | | | 1.9.3.2 |
| 11303, 11304 | 46202056 | 53 | 6.00E-59 | Magnetospirillum magnetotacticum MS-1 | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|-----------|---|--|--|----|----------|----------|
| 11305, 11306 | 48953436 | 65 | 3.00E-85 | Cytophaga hutchinsonii | COG0677: UDP-N-acetyl-D-mannosaminuronate dehydrogenase [Cytophaga hutchinsonii] | Staphylococcus aureus M type 1 capsular polysaccharide biosynthesis gene cluster, complete sequence and unknown genes | 88 | 5.00E-10 | 1.1.1.- |
| 11307, 11308 | 34556660 | 49 | 4.00E-60 | Wolinella succinogenes DSM 1740 | METHIONYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE09375.1 METHIONYL-TRNA SYNTHETASE [Wolinella succinogenes] | | | | 6.1.1.10 |
| 11311, 11312 | 34557573 | 52 | 4.00E-28 | Wolinella succinogenes DSM 1740 | SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | 2.7.3.- |
| 11313, 11314 | 56460323 | 36 | 7.00E-16 | Idiomarina lohiensis L2TR | hypothetical protein IL1215 [Idiomarina lohiensis L2TR] gb AAV82055.1 Hypothetical protein IL1215 [Idiomarina lohiensis L2TR] | | | | |
| 11317, 11318 | 57241658 | 69 | 1.00E-123 | Campylobacter lari RM2100 | ribonucleoside reductase, alpha subunit [Campylobacter lari RM2100] gb EAL54328.1 ribonucleoside reductase, alpha subunit [Campylobacter lari RM2100] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 1/6 | 81 | 7.00E-07 | 1.17.4.1 |
| 11321, 11322 | 48862680 | 61 | 3.00E-51 | Microbulbifer degradans 2-40 | COG2077: Peroxiredoxin [Microbulbifer degradans 2-40] | | | | 1.11.1.- |
| 11325, 11326 | 57236944 | 38 | 7.00E-43 | Campylobacter jejuni RM1221 | RNB-like protein [Campylobacter jejuni RM1221] gb AAW34527.1 RNB-like protein [Campylobacter jejuni RM1221] | | | | 3.1.- |
| 11327, 11328 | 57158718 | 29 | 1.00E-12 | Thermococcus kodakaraensis | archaeal ATPase [Thermococcus kodakaraensis] ref YP_182872.1 archaeal ATPase [Thermococcus kodakaraensis] | | | | |
| 1133, 1134 | 29345503 | 66 | 1.00E-90 | Bacteroides thetaiotaomicron VPI-5482 | conserved protein found in conjugate transposon [Bacteroides thetaiotaomicron VPI-5482] gb AAO75200.1 conserved protein found in conjugate transposon [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 11331, 11332 | 34557235 | 46 | 4.00E-65 | Wolinella succinogenes DSM 1740 | PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes DSM 1740] emb CAE09950.1 PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes] | | | | |
| 11333, 11334 | 48854867 | 30 | 5.00E-18 | Cytophaga hutchinsonii | COG2815: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | 2.7.1.37 |
| 11335, 11336 | ABG9157 1 | 36 | 2.00E-33 | | Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus | | | | 2.7.7.13 |

| | | | | | | | | | |
|------------------------------------|----------------------|----------|----------------------|--|---|--|--|--|----------|
| 11337, 11338 | 15643658 | 36 | 1.00E-16 | Thermotoga maritima MSB8 | galactose-1-phosphate uridylyltransferase, putative [Thermotoga maritima MSB8] gb AAD35977.1 galactose-1-phosphate uridylyltransferase, putative [Thermotoga maritima MSB8] pir J72322 hypothetical protein TM0896 - Thermotoga maritima (strain MSB8) | | | | 2.7.7.10 |
| 11339, 11340 | 57168791 | 27 | 2.00E-08 | Campylobacter coli RM2228 | probable lipoprotein Cj1649 [Campylobacter coli RM2228] gb EAL56521.1 probable lipoprotein Cj1649 [Campylobacter coli RM2228] | | | | |
| 11341, 11342 | 23129382 | 36 | 2.00E-21 | Nostoc punctiforme PCC 73102 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 11343, 11344 | 21227244 | 35 | 4.00E-20 | Methanosarcina mazei Go1 | glycosyltransferase [Methanosarcina mazei Go1] gb AAM30838.1 glycosyltransferase [Methanosarcina mazei Goe1] | | | | 2.4.1.- |
| 11347, 11348 | 12580885 | 23 | 2.00E-07 | Guillardia theta | IAP100 protein [Guillardia theta] ref NP_113434.1 IAP100 protein [Guillardia theta] pir F90106 IAP100 protein [imported] - Guillardia theta nucleomorph | | | | |
| 1135, 1136 | 24214122 | 30 | 4.00E-26 | Leptospira interrogans serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] | | | | |
| 11351, 11352 | 42528087 | 26 | 2.00E-14 | Treponema denticola ATCC 35405 | endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405] gb AAS13104.1 endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405] | | | | |
| 11353, 11354 11357, 11358 | 29840673 23102242 | 47 33 | 1.00E-39 8.00E-15 | Chlamydomonas caviae GPIC Azotobacter vinelandii | helicase, Snf2 family [Chlamydomonas caviae GPIC] gb AAP05657.1 helicase, Snf2 family [Chlamydomonas caviae GPIC] | | | | 3.6.1.3 |
| 11359, 11360 | 34556741 | 50 | 5.00E-52 | Wolinella succinogenes DSM 1740 | COG1345: Flagellar capping protein [Azotobacter vinelandii] PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09456.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | 2.7.3.- |
| 11361, 11362 | 32262499 | 49 | 3.00E-13 | Helicobacter hepaticus ATCC 51449 | hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449] ref NP_860480.1 hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449] | | | | |
| 11363, 11364 | 34556768 | 72 | 1.00E-84 | Wolinella succinogenes DSM 1740 | DIAMINOPIMELATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes DSM 1740] emb CAE09483.1 DIAMINOPIMELATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes] | | | | 4.1.1.20 |
| 11365, 11366 | 19704720 | 23 | 7.00E-09 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | hypothetical protein FN1385 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95581.1 Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | |

| | | | | | | | | | |
|--------------|----------|----|-----------|------------------------------------|---|--|----|----------|-----------|
| 11369, 11370 | 57167845 | 55 | 2.00E-94 | Campylobacter coli RM2228 | glutamyl-tRNA synthetase [Campylobacter coli RM2228] gb EAL57631.1 | | | | 6.1.1.17 |
| 11371, 11372 | 48839710 | 28 | 1.00E-10 | Methanosarcina barkeri str. fusaro | glutamyl-tRNA synthetase [Campylobacter coli RM2228] COG0286: Type I restriction-modification system methyltransferase subunit [Methanosarcina barkeri str. fusaro] | | | | 2.1.1.72 |
| 11375, 11376 | 34556741 | 51 | 8.00E-63 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09456.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | 2.7.3.- |
| 11377, 11378 | 31241779 | 42 | 5.00E-24 | Anopheles gambiae | ENSANGP00000012858 [Anopheles gambiae] | Wolinella succinogenes, complete genome; segment 4/7 | | | 6.2.1.- |
| 11379, 11380 | 37678997 | 67 | 1.00E-107 | Vibrio vulnificus YJ016 | type I site-specific restriction-modification system, R (restriction) subunit [Vibrio vulnificus YJ016] dbj BAC93577.1 type I site-specific restriction-modification system, R (restriction) subunit [Vibrio vulnificus YJ016] | | 88 | 7.00E-10 | 3.1.21.3 |
| 11381, 11382 | 45524550 | 30 | 5.00E-09 | Crocospaera watsonii WH 8501 | hypothetical protein Cwat03005121 [Crocospaera watsonii WH 8501] | | | | |
| 11383, 11384 | 39995311 | 40 | 1.00E-48 | Geobacter sulfurreducens PCA | isoquinoline 1-oxidoreductase, beta subunit [Geobacter sulfurreducens PCA] gb AAR33535.1 isoquinoline 1-oxidoreductase, beta subunit [Geobacter sulfurreducens PCA] | | | | 1.3.99.16 |
| 11385, 11386 | 48868595 | 50 | 6.00E-50 | Haemophilus influenzae 86-028NP | COG0749: DNA polymerase I - 3'-5' exonuclease and polymerase domains [Haemophilus influenzae 86-028NP] | | | | 2.7.7.7 |
| 11387, 11388 | 34557172 | 32 | 2.00E-23 | Wolinella succinogenes DSM 1740 | SENSORY PROTEIN, CONTAINING EAL-DOMAIN [Wolinella succinogenes DSM 1740] emb CAE09887.1 SENSORY PROTEIN, CONTAINING EAL-DOMAIN [Wolinella succinogenes] | | | | |
| 11389, 11390 | 48856112 | 29 | 2.00E-19 | Cytophaga hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 11391, 11392 | 48855575 | 42 | 2.00E-45 | Cytophaga hutchinsonii | COG0553: Superfamily II DNA/RNA helicases, SNF2 family [Cytophaga hutchinsonii] | | | | 3.6.1.3 |
| 11393, 11394 | 48853532 | 42 | 5.00E-36 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | | |
| 11395, 11396 | 53798771 | 59 | 4.00E-26 | Chloroflexus aurantiacus | COG0305: Replicative DNA helicase [Chloroflexus aurantiacus] | | | | 3.6.1.- |
| 11397, 11398 | 34556836 | 56 | 4.00E-42 | Wolinella succinogenes DSM 1740 | ABC TRANSPORTER [Wolinella succinogenes DSM 1740] emb CAE09551.1 ABC TRANSPORTER [Wolinella succinogenes] | | | | |
| 11401, 11402 | 46120825 | 27 | 9.00E-12 | Methylobacillus flagellatus KT | COG1629: Outer membrane receptor proteins, mostly Fe transport [Methylobacillus flagellatus KT] | | | | |
| 11403, 11404 | 18311192 | 43 | 2.00E-33 | Clostridium perfringens str. 13 | hypothetical protein CPE2210 [Clostridium perfringens str. 13] dbj BAB81916.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | | 2.1.1.61 |

| | | | | | | |
|-----------------|----------|----|----------|---|--|----------|
| 11405, 11406 | 46140543 | 32 | 5.00E-20 | Dechloromonas aromatica RCB | COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Dechloromonas aromatica RCB] | 2.7.3.- |
| 11407, 11408 | 34556556 | 32 | 8.00E-25 | Wollinella succinogenes DSM 1740 | POSSIBLE PHOSPHATASE [Wollinella succinogenes DSM 1740] emb CAE09271.1 POSSIBLE PHOSPHATASE [Wollinella succinogenes] sodium:solute symporter family protein [Chlorobium tepidum TLS] gb AAM72210.1 sodium:solute symporter family protein [Chlorobium tepidum TLS] transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO76492.1 transcriptional regulator [Bacteroides thetaiotaomicron VPI- 5482] | 3.6.1.11 |
| 11409, 11410 | 21673803 | 57 | 2.00E-45 | Chlorobium tepidum TLS | | |
| 1141, 1142 | 29346795 | 27 | 8.00E-12 | Bacteroides thetaitaomicron VPI-5482 | | |
| 11411, 11412 | 53714574 | 65 | 9.00E-46 | Bacteroides fragilis YCH46 | lactoylglutathione lyase and related protein [Bacteroides fragilis YCH46] dbj BAD50032.1 lactoylglutathione lyase and related protein [Bacteroides fragilis YCH46] | 4.4.1.5 |
| 11413, 11414 | 34558230 | 38 | 8.00E-33 | Wollinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR-CheY like receiver domain [Wollinella succinogenes] hypothetical protein BT0660 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75767.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482] | |
| 11415, 11416 | 29346070 | 27 | 4.00E-14 | Bacteroides thetaitaomicron VPI-5482 | | |
| 11417, 11418 | 50085130 | 32 | 1.00E-15 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD1995 [Acinetobacter sp. ADP1] emb CAG68818.1 hypothetical protein [Acinetobacter sp. ADP1] | |
| 11419, 11420 | 34556534 | 45 | 7.00E-28 | Wollinella succinogenes DSM 1740 | APOLIPOPROTEIN N-ACYLTRANSFERASE [Wollinella succinogenes DSM 1740] emb CAE09249.1 APOLIPOPROTEIN N-ACYLTRANSFERASE [Wollinella succinogenes] sp Q7MAR3 LNT_WOLSU Apolipoprotein N- acyltransferase (ALP N-acyltransferase) | 2.3.1.- |
| 11421, 11422 | 48855199 | 42 | 5.00E-07 | Cytophaga hutchinsonii | hypothetical protein Chut02002271 [Cytophaga hutchinsonii] OSJNBa0079A21.19 [Oryza sativa (japonica cultivar-group)] emb CAD41475.2 OSJNBa0079A21.19 [Oryza sativa (japonica cultivar- group)] | |
| 11425, 11426 | 50927567 | 29 | 7.00E-08 | Oryza sativa (japonica cultivar- group) | cytochrome c family protein [Azoarcus sp. EbN1] emb CAI09074.1 Cytochrome c family protein [Azoarcus sp. EbN1] | |
| 11427, 11428 | 56478386 | 33 | 7.00E-10 | Azoarcus sp. EbN1 | | |
| 11429, 11430 | 4585802 | 41 | 7.00E-39 | Pseudomonas stutzeri | DnrS protein [Pseudomonas stutzeri] peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] dbj BAD47827.1 peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] | |
| 1143, 1144 | 53712369 | 31 | 4.00E-27 | Bacteroides fragilis YCH46 | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|----------|--|--|--|
| 11431, 11432 | 15643585 | 42 | 6.00E-55 | Thermotoga maritima MSB8 | phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] gb AAD35904.1 phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] pir A72330 phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Thermotoga maritima (strain MSB8) sp Q9WZS9 SYFB_THEMEA Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS) | 6.1.1.20 | | | |
| 11433, 11434 | 15643585 | 37 | 1.00E-38 | Thermotoga maritima MSB8 | phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] gb AAD35904.1 phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] pir A72330 phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Thermotoga maritima (strain MSB8) sp Q9WZS9 SYFB_THEMEA Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS) | 6.1.1.20 | | | |
| 11435, 11436 | 34557308 | 50 | 2.00E-35 | Wolinella succinogenes DSM 1740 | Nitrous oxidase accessory protein [Wolinella succinogenes DSM 1740] emb CAE10023.1 Nitrous oxidase accessory protein [Wolinella succinogenes] | | | | |
| 11437, 11438 | 15614433 | 29 | 6.00E-27 | Bacillus halodurans C-125 | hypothetical protein BH1870 [Bacillus halodurans C-125] dbj BAB05589.1 BH1870 [Bacillus halodurans C-125] pir F83883 hypothetical protein | 3.2.1.22 | | | |
| 11439, 11440 | 79388 | 42 | 2.00E-26 | | hypothetical protein - Bacillus halodurans (strain C-125) gb AAA22911.1 putative | | | | |
| 11441, 11442 | 15894773 | 32 | 5.00E-15 | Clostridium acetobutylicum ATCC 824 | Hypothetical protein, CF-32 family [Clostridium acetobutylicum ATCC 824] gb AAK79462.1 Hypothetical protein, CF-32 family [Clostridium acetobutylicum ATCC 824] pir C97084 hypothetical protein CAC1494 [Imported] - Clostridium acetobutylicum | | | | |
| 11445, 11446 | 57241158 | 29 | 1.00E-19 | Campylobacter lari RM2100 | ATP-dependent DNA helicase [Campylobacter lari RM2100] gb EAL54854.1 ATP-dependent DNA helicase [Campylobacter lari RM2100] | 3.6.1.- | | | |
| 11447, 11448 | 29348169 | 51 | 4.00E-49 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein B72760 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77866.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | 4.2.1.28 | | | |
| 11449, 11450 | 48855525 | 39 | 2.00E-30 | Cytophaga hutchinsonii | hypothetical protein Chut02001868 [Cytophaga hutchinsonii] | | | | |
| 1145, 1146 | 28211915 | 43 | 4.00E-53 | Clostridium tetani E88 | imidazolonepropionase [Clostridium tetani E88] gb AAO36796.1 imidazolonepropionase [Clostridium tetani E88] | 3.5.2.7 | | | |
| 11451, 11452 | 46140552 | 39 | 2.00E-18 | Dechloromonas aromatica RCB | COG0607: Rhodanese-related sulfurtransferase [Dechloromonas aromatica RCB] | | | | |
| 11455, 11456 | 48855525 | 43 | 4.00E-11 | Cytophaga hutchinsonii | hypothetical protein Chut02001868 [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|--|--|----------|
| 11459, 11460 | 16125567 | 23 | 7.00E-10 | Caulobacter crescentus CB15 | outer membrane protein TolC, putative [Caulobacter crescentus CB15] gb AAK23299.1 outer membrane protein TolC, putative [Caulobacter crescentus CB15] pir G87412 outer membrane protein TolC, probable CC1318 [imported] - Caulobacter crescentus | | | | |
| 11461, 11462 | 57505540 | 43 | 6.00E-58 | Campylobacter upsaliensis RM3195 | conserved hypothetical protein [Campylobacter upsaliensis RM3195] gb EAL52874.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195] | | | | |
| 11465, 11466 | 23014415 | 49 | 3.00E-25 | Magnetospirillum magnetotacticum MS-1 | COG0784: FOG: CheY-like receiver [Magnetospirillum magnetotacticum MS- 1] | | | | 2.7.3.- |
| 11467, 11468 | 38482512 | 44 | 1.00E-27 | Photobacterium luminescens | putative toxin transporter [Photobacterium luminescens] | | | | |
| 11469, 11470 | 29348726 | 40 | 3.00E-23 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3317 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78423.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 11471, 11472 | 34557096 | 74 | 1.00E-132 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0684 [Wolinella succinogenes DSM 1740] emb CAE09811.1 conserved hypothetical protein [Wolinella succinogenes] | | | | 1.17.4.2 |
| 11477, 11478 | 54639980 | 72 | 2.00E-71 | Campylobacter jejuni | putative adenylsulfate kinase [Campylobacter jejuni] | | | | 2.7.1.25 |
| 11479, 11480 | 56469773 | 24 | 4.00E-07 | Entamoeba histolytica HM- 1:IMSS | DNA repair protein Rad50, putative [Entamoeba histolytica HM-1:IMSS] | | | | |
| 11481, 11482 | 34558493 | 49 | 4.00E-62 | Wolinella succinogenes DSM 1740 | PUTATIVE ZINC PROTEASE [Wolinella succinogenes DSM 1740] emb CAE11208.1 PUTATIVE ZINC PROTEASE [Wolinella succinogenes] | | | | 3.4.-.- |
| 11483, 11484 | 48833487 | 58 | 4.00E-34 | Magnetococcus sp. MC-1 | COG2326: Uncharacterized conserved protein [Magnetococcus sp. MC-1] glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449] ref NP_860022.1 glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449] | | | | 2.-.-.- |
| 11485, 11486 | 32262039 | 41 | 5.00E-45 | Helicobacter hepaticus ATCC 51449 | COG0859: ADP-heptose:LPS heptosyltransferase [Geobacter metallireducens GS-15] | | | | 5.3.1.9 |
| 11489, 11490 | 48844440 | 22 | 2.00E-08 | Geobacter metallireducens GS- 15 | COG1843: Flagellar hook capping protein [Cytophaga hutchinsonii] | | | | |
| 1149, 1150 | 48853904 | 51 | 5.00E-43 | Cytophaga hutchinsonii | COG0535: Predicted Fe-S oxidoreductases [Magnetococcus sp. MC-1] | | | | |
| 11491, 11492 | 48834423 | 33 | 1.00E-20 | Magnetococcus sp. MC-1 | transketolase, N-terminal subunit [Thermotoga maritima MSB8] | | | | 2.2.1.1 |
| 11493, 11494 | 15644626 | 42 | 2.00E-55 | Thermotoga maritima MSB8 | | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---------------------------------------|---|--|-------------|--|----------|----------|
| 11495, 11496 | 32261558 | 33 | 9.00E-19 | 51449 | Helicobacter hepaticus ATCC | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859542.1 hypothetical protein HH0011 [Helicobacter hepaticus ATCC 51449] | | | | |
| 11499, 11500 | 48834077 | 50 | 6.00E-32 | MC-1 | Magnetococcus sp. | COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1] | | | | 2.7.3.- |
| 115, 116 | | | | | | Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence | ## 5.00E-30 | | | |
| 11503, 11504 | 57504860 | 30 | 5.00E-12 | RM2228 | Campylobacter coli | hypothetical protein CCO1785 [Campylobacter coli RM2228] gb EAL56124.1 hypothetical protein CCO1785 [Campylobacter coli RM2228] | | | | |
| 11505, 11506 | 57240928 | 57 | 6.00E-67 | RM2100 | Campylobacter lari | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55321.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 11507, 11508 | 41724578 | 30 | 2.00E-24 | Dechloromonas aromatica RCB | COG0842: ABC-type multidrug transport system, permease component | | | | | |
| 11509, 11510 | 48839711 | 46 | 9.00E-25 | Methanosarcina barkeri str. fusaro | COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro] | | | | 3.1.21.3 | |
| 1151, 1152 | 53711702 | 83 | 8.00E-58 | YCH46 | Bacteroides fragilis | topoisomerase IV subunit A [Bacteroides fragilis YCH46] dbj BAD47160.1 topoisomerase IV subunit A [Bacteroides fragilis YCH46] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | | | | |
| 11511, 11512 | 34557246 | 27 | 6.00E-12 | 1740 | Wolinella succinogenes DSM | hypothetical protein Mdeg02000469 [Microbulbifer degradans 2-40] aconitase [Aquifex aeolicus VF5] gb AAC07617.1 aconitase [Aquifex aeolicus VF5] pir F70453 aconitase - Aquifex aeolicus | | | | 4.2.1.3 |
| 11517, 11518 | 48864098 | 35 | 3.00E-12 | degradans 2-40 | Microbulbifer | COG0500: SAM-dependent methyltransferases [Nostoc punctiforme PCC 73102] | | | | |
| 11521, 11522 | 15606842 | 46 | 2.00E-35 | VF5 | Aquifex aeolicus | 2-isopropylmalate synthase [Chlorobium tepidum TLS] gb AAM73323.1 2-isopropylmalate synthase [Chlorobium tepidum TLS] COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii] | | | | 4.1.3.12 |
| 11525, 11526 | 23129257 | 43 | 6.00E-30 | PCC 73102 | Nostoc punctiforme | COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii] | | | | 3.1.1.24 |
| 11527, 11528 | 21674916 | 60 | 4.00E-28 | tepidum TLS | Chlorobium | ENSANGP00000016331 [Anopheles gambiae] | | | | 2.7.7.- |
| 11529, 11530 | 48854159 | 38 | 4.00E-37 | hutchinsonii | Cytophaga | | | | | |
| 11531, 11532 | 31195987 | 58 | 1.00E-38 | gambiae | Anopheles | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---------------------------------------|--|---|----|----------|----------|
| 11533, 11534 | 38045894 | 29 | 2.00E-09 | Homo sapiens | RAB6-interacting protein 2 isoform gamma [Homo sapiens] dbj BAC54108.1 ELKS gamma [Homo sapiens] | | | | |
| 11537, 11538 | 47525234 | 70 | 1.00E-113 | Geobacter sulfurreducens PCA | chromosomal replication initiator protein DnaA [Geobacter sulfurreducens PCA] gb AAR99581.1 chromosomal replication initiator protein DnaA | Oceanobacillus theyensis HTE831 genomic DNA, section 1/13 | 90 | 5.00E-17 | |
| 11539, 11540 | 47525234 | 60 | 6.00E-47 | Geobacter sulfurreducens PCA | [Geobacter sulfurreducens PCA] chromosomal replication initiator protein DnaA [Geobacter sulfurreducens PCA] gb AAR99581.1 chromosomal replication initiator protein DnaA | | | | |
| 11545, 11546 | 57505258 | 43 | 1.00E-30 | Campylobacter upsaliensis RM3195 | [Geobacter sulfurreducens PCA] conserved hypothetical protein [Campylobacter upsaliensis RM3195] gb EAL53179.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195] | | | | |
| 11549, 11550 | 46446323 | 37 | 6.00E-18 | Parachlamydia sp. UWE25 | putative exodeoxyribonuclease V [Parachlamydia sp. UWE25] emb CAF23413.1 putative exodeoxyribonuclease V [Parachlamydia sp. UWE25] | | | 3.1.11.5 | |
| 11553, 11554 | 34557295 | 23 | 1.00E-09 | Wolinella succinogenes DSM 1740 | hypothetical protein WSD905 [Wolinella succinogenes DSM 1740] emb CAE10010.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 11555, 11556 | 34557291 | 37 | 1.00E-46 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | 2.7.3.- | |
| 11557, 11558 | 53729414 | 30 | 9.00E-27 | Dechloromonas aromatica RCB | COG0515: Serine/threonine protein kinase [Dechloromonas aromatica RCB] | | | 3.1.3.16 | |
| 11559, 11560 | 23121691 | 50 | 5.00E-17 | Desulfotobacterium hafnense DCB-2 | COG0784: FOG: CheY-like receiver [Desulfotobacterium hafnense DCB-2] hypothetical protein CPE1705 [Clostridium perfringens str. 13] sp Q8XJQ1 YH05_CLOPE Hypothetical UPF0102 protein CPE1705 dbj BAB81411.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | 3.1.1.61 | |
| 11561, 11562 | 18310687 | 35 | 7.00E-13 | Clostridium perfringens str. 13 | ABC transporter, ATP-binding protein, MsbA family [Porphyromonas gingivalis W83] ref NP_905827.1 ABC transporter, ATP-binding protein, MsbA family [Porphyromonas gingivalis W83] | | | | |
| 11565, 11566 | 34397664 | 39 | 6.00E-42 | Porphyromonas gingivalis W83 | COG0642: Signal transduction histidine kinase [Thiobacillus denitrificans ATCC 25259] | | | 2.7.3.- | |
| 11567, 11568 | 52007424 | 36 | 1.00E-13 | Thiobacillus denitrificans ATCC 25259 | cGMP-dependent protein kinase 1, beta isozyme, putative [Plasmodium falciparum 3D7] gb AAN36959.1 cGMP-dependent protein kinase 1, beta isozyme, putative [Plasmodium falciparum 3D7] gb AAM22644.1 cGMP-dependent protein kinase [Plasmodium falciparum] | | | | |
| 11569, 11570 | 23509568 | 31 | 2.00E-08 | Plasmodium falciparum 3D7 | | | | | 2.7.1.37 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 11571, 11572 | 31195951 | 55 | 2.00E-53 | Anopheles gambiae | ENSANGP00000000471 [Anopheles gambiae] NAD dependent epimerase/dehydratase, UDP-glucose-4-epimerase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123157.1 hypothetical protein pp0827 [Legionella pneumophila str. Paris] gb AAU26850.1 NAD dependent epimerase/dehydratase, UDP- glucose-4-epimerase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAB65203.1 hypothetical protein [Legionella pneumophila] emb CAH11975.1 hypothetical protein [Legionella pneumophila str. Paris] | | | 1.1.1.95 |
| 11573, 11574 | 52840998 | 34 | 5.00E-17 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | | | | 5.1.3.- |

| | | | | | | | | |
|-------------------------------------|----------------------|----------|-----------------------|---|--|---|----------------------|----------|
| 11577, 11578, 11583, 11584 | 13491146 46934822 | 56 71 | 8.00E-41 1.00E-130 | Aneurinibacillus thermoaerophilus Wolinella succinogenes | D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [Aneurinibacillus thermoaerophilus] sp Q9AGY5 GMHB_ANETH D,D- heptose 1,7-bisphosphate phosphatase (D-glycero-D-manno-heptose 1,7- bisphosphate phosphatase) | Campylobacter jejuni putative ABC- type transport protein, putative UDP-glucose-4- epimerase, hypothetical protein, putative heptosyltransferase I, putative lipid A biosynthesis acyltransferase, putative two-domain glycosyltransferase, putative glycosyltransferase, putative beta-1,4-N- acetylglucosamin yltransferase, putative beta-1,3- galactosyltransferas e, putative alpha- 2,3- sialyltransferase, putative sialic acid synthase, putative UDP-N- acetylglucosamine 2-epimerase/N- acetylmannosamine synthase, putative> | 88 7.00E-09 3.1.3.15 | 1.7.99.6 |
| 11585, 11586 | 34556608 | 27 | 9.00E-27 | Wolinella succinogenes DSM 1740 | nitrous oxide reductase [Wolinella succinogenes] | | | |
| 11587, 11588 | 34556616 | 43 | 4.00E-35 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0160 [Wolinella succinogenes DSM 1740] emb CAE09323.1 conserved hypothetical protein [Wolinella succinogenes] CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|-------------|----------|
| 11589, 11590 | 57240404 | 61 | 4.00E-52 | Campylobacter lari RM2100 | tRNA (guanine-N1)-methyltransferase [Campylobacter lari RM2100] gb EAL55518.1 tRNA (guanine-N1)-methyltransferase [Campylobacter lari RM2100] | | | 2.1.1.31 |
| 1159, 1160 | 42520151 | 70 | 3.00E-68 | Wolbachia endosymbiont of Drosophila melanogaster | hypothetical protein WD0259 [Wolbachia endosymbiont of Drosophila melanogaster] gb AAS14000.1 conserved hypothetical protein [Wolbachia endosymbiont of Drosophila melanogaster] | | | |
| 11593, 11594 | 53714478 | 44 | 4.00E-39 | Bacteroides fragilis YCH46 | hypothetical protein BF3191 [Bacteroides fragilis YCH46] db BAD49936.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 11595, 11596 | 53713148 | 38 | 1.00E-53 | Bacteroides fragilis YCH46 | hypothetical protein BF1858 [Bacteroides fragilis YCH46] db BAD48606.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 11597, 11598 | 1197006 | 47 | 5.00E-33 | Bacteroides fragilis | unknown protein [Bacteroides fragilis] gb AAA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551) | | | |
| 11599, 11600 | 57241290 | 61 | 1.00E-40 | Campylobacter lari RM2100 | Uncharacterized BCR, YoeG family COG1559 [Campylobacter lari RM2100] gb EAL54986.1 Uncharacterized BCR, YoeG family COG1559 [Campylobacter lari RM2100] | | 97 3.00E-11 | 4.--- |
| 11601, 11602 | 3493599 | 24 | 3.00E-07 | Proteus mirabilis | ZapD [Proteus mirabilis] | | | |
| 11605, 11606 | 27117224 | 31 | 2.00E-23 | Bacillus megaterium | uroporphyrinogen III synthase [Bacillus megaterium] | | | 4.2.1.75 |
| 11607, 11608 | 48862680 | 63 | 4.00E-52 | Microbulbifer degradans 2-40 | COG2077: Peroxiredoxin [Microbulbifer degradans 2-40] proline-tRNA synthetase [Aquifex aeolicus VF5] gb AAC06648.1 proline- tRNA synthetase [Aquifex aeolicus VF5] pir F70332 proline-tRNA synthetase - Aquifex aeolicus | | | 1.11.1.- |
| 11609, 11610 | 15605873 | 44 | 1.00E-10 | Aquifex aeolicus VF5 | BpmI endonuclease-methyltransferase fusion protein type IIG [uncultured archaeon GZfos9D8] | | | 6.1.1.15 |
| 1161, 1162 | 52550522 | 32 | 2.00E-09 | uncultured archaeon GZfos9D8 | putative putative two-component sensor C0035 [Campylobacter fetus] | | | 2.7.3.- |
| 11613, 11614 | 28974235 | 33 | 2.00E-27 | Campylobacter fetus | hypothetical protein WS1227 [Wolbachia succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wolbachia succinogenes] sp P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridylyl synthase) (Uracil hydrolyase) | | | |
| 11615, 11616 | 34557593 | 42 | 1.00E-39 | Wolbachia succinogenes DSM 1740 | COG0849: Actin-like ATPase involved in cell division [Cytophaga hutchinsonii] | | | |
| 11617, 11618 | 48854568 | 50 | 2.00E-35 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|------------------|
| 11619, 11620 | 27365538 | 31 | 2.00E-15 | Vibrio vulnificus CMCP6 | hypothetical protein VV12211 [Vibrio vulnificus CMCP6] gb AAO10593.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] | | | 2.7.3.- |
| 11621, 11622 | 29349774 | 48 | 4.00E-33 | Bacteroides thetalaotomicron VPI-5482 | putative transcription regulator [Bacteroides thetalaotomicron VPI-5482] gb AAO7947.1.1 putative transcription regulator [Bacteroides thetalaotomicron VPI-5482] | | | 6.3.4.15 |
| 11625, 11626 | 48855427 | 30 | 1.00E-10 | Cytophaga hutchinsonii | COG1521: Putative transcriptional regulator, homolog of Bvg accessory factor [Cytophaga hutchinsonii] | | | |
| 1163, 1164 | 48856612 | 44 | 1.00E-32 | Cytophaga hutchinsonii | COG1331: Highly conserved protein containing a thioredoxin domain [Cytophaga hutchinsonii] | | | |
| 11631, 11632 | 46447193 | 60 | 1.00E-81 | Parachlamydia sp. UWE25 | putative ATP-dependent RNA helicase [Parachlamydia sp. UWE25] emb CAF24283.1 putative ATP-dependent RNA helicase [Parachlamydia sp. UWE25] | Lactobacillus johnsonii NCC 533, section 2 of 7 of the complete genome | 97 | 4.00E-08 2.7.7.- |
| 11633, 11634 | 34558815 | 75 | 1.00E-59 | Alvinella pompejana epibiont 7G3 | citrate lyase subunit 2 [Alvinella pompejana epibiont 7G3] PUTATIVE AMINOTRANSFERASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09898.1 PUTATIVE AMINOTRANSFERASE PROTEIN [Wolinella succinogenes] | Alvinella pompejana epibiont 7G3 fosmid clone 7G3, complete sequence | 90 | 2.00E-11 4.1.3.8 |
| 11635, 11636 | 34557183 | 47 | 3.00E-36 | Wolinella succinogenes DSM 1740 | putative translation initiation factor [Bradyrhizobium japonicum USDA 110] dbj BAC46226.1 br0961 [Bradyrhizobium japonicum USDA 110] | | | 2.6.1.- |
| 11639, 11640 | 27376072 | 60 | 4.00E-46 | Bradyrhizobium japonicum USDA 110 | COG0457: FOG: TPR repeat [Crocospaera watsonii WH 8501] | | | 5.2.1.8 |
| 11641, 11642 | 45528473 | 35 | 9.00E-32 | Crocospaera watsonii WH 8501 | site-specific DNA-methyltransferase (cytosine-specific) [Haemophilus parahaemolyticus] sp P50192 MTTHA_HAEPH Modification methylase HphIA (Cytosine-specific methyltransferase HphIA) (M.HphIA) (M.HphI(C)) pir S70707 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) HphI - Haemophilus parahaemolyticus (ATCC 49700) hypothetical protein BT3711 [Bacteroides thetalaotomicron VPI-5482] gb AAO78816.1 conserved hypothetical protein [Bacteroides thetalaotomicron VPI-5482] | | | 2.1.1.73 |
| 11649, 11650 | 732729 | 36 | 1.00E-15 | Haemophilus parahaemolyticus | acetylornithine aminotransferase [Helicobacter hepaticus ATCC 51449] ref NP_860500.1 acetylornithine aminotransferase [Helicobacter hepaticus ATCC 51449] | | | |
| 1165, 1166 | 29349119 | 35 | 2.00E-13 | Bacteroides thetalaotomicron VPI-5482 | | | | |
| 11653, 11654 | 32262519 | 52 | 2.00E-61 | Helicobacter hepaticus ATCC 51449 | | | | 2.6.1.11 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|----------|
| 11655, 11656 | 34558829 | 47 | 1.00E-56 | Alvinella pompejana epibiont 7G3 | succinylornithine transaminase [Alvinella pompejana epibiont 7G3] | | | | 2.6.1.- |
| 11657, 11658 | 48859331 | 23 | 3.00E-10 | Clostridium thermocellum ATCC 27405 | COG1670: Acetyltransferases, including N-acetylases of ribosomal proteins [Clostridium thermocellum ATCC 27405] | | | | |
| 11661, 11662 | 53736042 | 42 | 7.00E-20 | Crocospaera watsonii WH 8501 | hypothetical protein Cwat03001257 [Crocospaera watsonii WH 8501] | | | | |
| 11665, 11666 | 57240902 | 48 | 5.00E-39 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 11667, 11668 | 32473317 | 43 | 7.00E-39 | Rhodopirellula baltica SH 1 | gb EAL55295.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 11671, 11672 | 34556560 | 50 | 4.00E-55 | Wolinella succinogenes DSM 1740 | N-acetylglucosamine-6-sulfatase [Rhodopirellula baltica SH 1] emb CAD78091.1 N-acetylglucosamine-6-sulfatase [Pirellula sp.] | | | | 3.1.6.- |
| 11673, 11674 | 34556560 | 37 | 3.00E-38 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | |
| 11675, 11676 | 34557033 | 59 | 3.00E-40 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | |
| 11677, 11678 | 34557161 | 58 | 7.00E-40 | Wolinella succinogenes DSM 1740 | GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09748.1 GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes] sp Q7M9X0 HIS5_WOLSU [imidazole glycerol phosphate synthase subunit hisH (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (IGP subunit hisH)] | | | | 2.4.2.- |
| 11685, 11686 | 56418878 | 62 | 2.00E-73 | Geobacillus kaustophilus HTA426 | PUTATIVE ARSENATE REDUCTASE [Wolinella succinogenes DSM 1740] emb CAE09876.1 PUTATIVE ARSENATE REDUCTASE [Wolinella succinogenes] | | | | 1.97.1.5 |
| 11687, 11688 | 48853288 | 36 | 2.00E-28 | Ferroplasma acidarmanus | type I restriction modification system M subunit (site-specific DNA- methyltransferase subunit) [Geobacillus kaustophilus HTA426] | | | | |
| 1169, 1170 | 148397 | 59 | 3.00E-35 | Pantoea agglomerans | dbj BAD74628.1 type I restriction modification system M subunit (site- specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426] | | | | 2.1.1.72 |
| 11691, 11692 | 34558827 | 50 | 2.00E-63 | Alvinella pompejana epibiont 7G3 | COG0732: Restriction endonuclease S subunits [Ferroplasma acidarmanus] phytoene dehydrogenase [Pantoea agglomerans] pfl S52586 phytoene dehydrogenase (EC 1.3.-.-) - Erwinia herbicola | | | | 3.1.21.3 |
| | | | | | | | | | 1.3.3.4 |
| | | | | | | | | | 3.5.4.26 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 11693, 11694 | 46143552 | 43 | 5.00E-21 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | |
| 11697, 11698 | 57167857 | 37 | 9.00E-16 | Campylobacter coli RM2228 | ferric uptake regulation protein, putative [Campylobacter coli RM2228] gb EAL57643.1 ferric uptake regulation protein, putative [Campylobacter coli RM2228] | | | |
| 11699, 11700 | 42523774 | 33 | 6.00E-24 | Bdellovibrio bacteriovorus HD100 | HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] emb CAE0147.1 HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] | | | |
| 117, 118 | | | | | Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence ## 5.00E-30 | | | |
| 11701, 11702 | 34557750 | 40 | 3.00E-25 | Wolinella succinogenes DSM 1740 | FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10465.1 FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT [Wolinella succinogenes] | | | 1.3.99.1 |
| 11703, 11704 | 30249464 | 40 | 1.00E-21 | Nitrosomonas europaea ATCC 19718 | Cytochrome c, class IC: Cytochrome c, class I [Nitrosomonas europaea ATCC 19718] emb CAD85404.1 Cytochrome c, class IC: Cytochrome c, class I [Nitrosomonas europaea ATCC 19718] | | | |
| 11705, 11706 | 34558322 | 50 | 9.00E-19 | Wolinella succinogenes DSM 1740 | UDP-N-ACETYL MURAMOYLALANINE-D-GLUTAMATE LIGASE [Wolinella succinogenes DSM 1740] emb CAE11037.1 UDP-N- ACETYL MURAMOYLALANINE-D-GLUTAMATE LIGASE [Wolinella succinogenes] | | | 6.3.2.9 |
| 11707, 11708 | 51245977 | 54 | 8.00E-40 | Desulfotalea psychrophila LSV54 | related to DNA repair photolyase [Desulfotalea psychrophila LSV54] emb CAG36854.1 related to DNA repair photolyase [Desulfotalea psychrophila LSV54] | | | 4.1.99.- |
| 11709, 11710 | 15679599 | 28 | 8.00E-08 | Methanothermobac ter thermautotrophicus str. Delta H | acetyl-CoA synthetase [Methanothermobacter thermotrophicus str. Delta H] gb AAB86077.1 acetyl-CoA synthetase [Methanothermobacter thermautotrophicus str. Delta H] pir C69081 acetyl-CoA synthetase - Methanothermobacterium thermotrophicum (strain Delta H) | | | 6.2.1.1 |
| 11711, 11712 | 39995927 | 48 | 5.00E-49 | Geobacter sulfurreducens PCA | hypothetical protein GSU0821 [Geobacter sulfurreducens PCA] gb AAR34151.1 conserved hypothetical protein [Geobacter sulfurreducens PCA] | | | |
| 11713, 11714 | 48855392 | 33 | 1.00E-27 | Cytophaga hutchinsonii | COG0823: Periplasmic component of the Tol biopolymer transport system [Cytophaga hutchinsonii] | | | |
| 11719, 11720 | 48834051 | 48 | 9.00E-39 | Magnetococcus sp. MC-1 | COG2602: Beta-lactamase class D [Magnetococcus sp. MC-1] | | | 3.5.2.6 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 11721, 11722 | 17229972 | 41 | 7.00E-26 | Nostoc sp. PCC 7120 | beta-lactamase [Nostoc sp. PCC 7120] dbj BAB74179.1 beta-lactamase [Nostoc sp. PCC 7120] pir A12115 beta-lactamase [imported] - Nostoc sp. (strain PCC 7120) | | | 3.5.2.6 |
| 11725, 11726 | 17232265 | 36 | 5.00E-20 | Nostoc sp. PCC 7120 | alpha-glucosidase [Nostoc sp. PCC 7120] pir AE2402 alpha-glucosidase [imported] - Nostoc sp. (strain PCC 7120) dbj BAB78472.1 alpha-glucosidase [Nostoc sp. PCC 7120] | | | 3.2.1.20 |
| 11727, 11728 | 52841063 | 24 | 6.00E-11 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | agglutination protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123217.1 hypothetical protein lpp0889 [Legionella pneumophila str. Paris] gb AAU26915.1 agglutination protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH12040.1 hypothetical protein [Legionella pneumophila str. Paris] | | | |
| 11729, 11730 | 33147750 | 50 | 6.00E-18 | Haemophilus ducreyi 35000HP | possible type II DNA modification enzyme (methyltransferase) [Haemophilus ducreyi 35000HP] ref NP_872883.1 possible type II DNA modification enzyme (methyltransferase) [Haemophilus ducreyi 35000HP] | | | 2.1.1.72 |
| 11731, 11732 | 34763071 | 31 | 1.00E-22 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | Restriction enzyme BcgI beta subunit [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24368.1 Restriction enzyme BcgI beta subunit [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | |
| 11735, 11736 | 57240635 | 46 | 4.00E-58 | Campylobacter lari RM2100 | peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL55749.1 peptidase, M23/M37 family [Campylobacter lari RM2100] | | | 3.5.1.- |
| 11737, 11738 | 57240636 | 46 | 6.00E-54 | Campylobacter lari RM2100 | magnesium transporter, putative [Campylobacter lari RM2100] gb EAL55750.1 magnesium transporter, putative [Campylobacter lari RM2100] | | | 3.6.1.- |
| 11739, 11740 | 56707454 | 35 | 5.00E-33 | Francisella tularensis subsp. tularensis Schu 4 | hypothetical protein FTT0301 [Francisella tularensis subsp. tularensis Schu 4] gb AAV29706.1 NT02F70891 [synthetic construct] emb CAG44934.1 hypothetical protein [Francisella tularensis subsp. tularensis] | | | |
| 11741, 11742 | 40062476 | 39 | 8.00E-43 | uncultured bacterium 105 | hypothetical protein EBAC750-01A01.2 [uncultured bacterium 105] | | | 2.7.9.2 |
| 11745, 11746 | 53713382 | 48 | 1.00E-40 | Bacteroides fragilis YCH46 | outer membrane efflux protein [Bacteroides fragilis YCH46] dbj BAD48840.1 outer membrane efflux protein [Bacteroides fragilis YCH46] | | | |
| 11747, 11748 | 57237698 | 36 | 7.00E-23 | Campylobacter jejuni RM1221 | molybdopterin biosynthesis MoeA protein, putative [Campylobacter jejuni RM1221] gb AAW35281.1 molybdopterin biosynthesis MoeA protein, putative [Campylobacter jejuni RM1221] | | | |
| 11749, 11750 | 30020150 | 26 | 2.00E-07 | Bacillus cereus ATCC 14579 | Alpha/beta hydrolase [Bacillus cereus ATCC 14579] gb AAP08982.1 Alpha/beta hydrolase [Bacillus cereus ATCC 14579] | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|--|--|--|--|--|----------|
| 1175, 1176 | AAE0569 8 | 32 | 2.00E-20 | | | Desc: <i>Bacillus deramificans</i> pullulanase variant G794P. Org: <i>Bacillus deramificans</i> Synthetic | | | 3.2.1.41 |
| 11751, 11752 | 7481995 | 26 | 1.00E-06 | | | protein P120 - Mycoplasma hominis gb AAA67449.1 P120 ATPase involved in DNA replication [Vibrio vulnificus CMCP6] gb AAO10830.1 ATPase involved in DNA replication [Vibrio vulnificus CMCP6] | | | |
| 11753, 11754 | 27365775 | 35 | 2.00E-36 | Vibrio vulnificus CMCP6 | | hypothetical protein WS0958 [Wolinnella succinogenes DSM 1740] emb CAE10061.1 hypothetical protein [Wolinnella succinogenes] hypothetical protein BT1328 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76435.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 11757, 11758 | 34557346 | 55 | 3.00E-14 | Wolinnella succinogenes DSM 1740 | | Desc: <i>H. pylori</i> HPC099 protein. Org: <i>Helicobacter pylori</i> | | | |
| 11759, 11760 | 29346738 | 42 | 1.00E-52 | Bacteroides thetaitotaomicron VPI-5482 | | hypothetical protein SO1978 [Shewanella oneidensis MR-1] gb AAN55029.1 conserved hypothetical protein [Shewanella oneidensis MR-1] Rhodanese-like domain protein [Geobacter sulfurreducens PCA] gb AAR34258.1 Rhodanese-like domain protein [Geobacter sulfurreducens PCA] | | | |
| 11765, 11766 | AAB4639 9 | 33 | 4.00E-23 | | | putative transposase [Microscilla sp. PRE1] gb AAK62881.1 MS159, putative transposase [Microscilla sp. PRE1] COG0715: ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components [Magnetococcus sp. MC-1] | | | |
| 11767, 11768 | 24373542 | 41 | 1.00E-38 | Shewanella oneidensis MR-1 | | Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihiensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihiensis L2TR] hydrolase, haloacid dehalogenase-like family [Chlorobium tepidum TLS] gb AAM72545.1 hydrolase, haloacid dehalogenase-like family [Chlorobium tepidum TLS] | | | 5.4.2.6 |
| 1177, 1178 | 39996034 | 35 | 5.00E-27 | PCA | | PUTATIVE CHEMOTAXIS PROTEIN [Wolinnella succinogenes DSM 1740] emb CAE09412.1 PUTATIVE CHEMOTAXIS PROTEIN [Wolinnella succinogenes] | | | 2.7.3.- |
| 11771, 11772 | 14518364 | 44 | 1.00E-58 | Microscilla sp. PRE1 | | COG0778: Nitroreductase [Microbulifer degradans 2-40] | | | |
| 11775, 11776 | 48833468 | 27 | 8.00E-24 | Magnetococcus sp. MC-1 | | COG0778: Nitroreductase [Nostoc punctiforme PCC 73102] | | | |
| 11779, 11780 | 56460818 | 32 | 2.00E-31 | Idiomarina loihiensis L2TR | | | | | |
| 11781, 11782 | 21674138 | 52 | 1.00E-65 | Chlorobium tepidum TLS | | | | | |
| 11783, 11784 | 34556697 | 36 | 8.00E-25 | Wolinnella succinogenes DSM 1740 | | | | | |
| 11787, 11788 | 48862510 | 42 | 5.00E-17 | Microbulifer degradans 2-40 | | | | | |
| 11789, 11790 | 23130537 | 37 | 6.00E-35 | Nostoc punctiforme PCC 73102 | | | | | |

| | | | | | | | | | |
|-------------------------------------|----------------------------------|----------|----------------------|--|--|----|----------|----------|----------|
| 11791, 11792, 11793, 11794 | 53763585 53711768 53711768 | 35 22 | 1.00E-18 3.00E-17 | Anabaena variabilis ATCC 29413 Bacteroides fragilis YCH46 | COG4938: Uncharacterized conserved protein [Anabaena variabilis ATCC 29413] hypothetical protein BF0477 [Bacteroides fragilis YCH46] dbj BAD47226.1 hypothetical protein [Bacteroides fragilis YCH46] 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228] gb EAL57510.1 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228] | | | | |
| 11795, 11796 | 57167724 | 43 | 1.00E-26 | Campylobacter coli RM2228 | Vibrio vulnificus CMCP6 chromosome I section 9 of 11 of the complete sequence | 85 | 2.00E-09 | | |
| 11797, 11798 | 1197006 | 56 | 8.00E-49 | Bacteroides fragilis | unknown protein [Bacteroides fragilis] gb AAA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for Insertion sequence element IS4351 (Transposon TN4551) | | | | |
| 11799, 11800 | 23126261 | 49 | 6.00E-53 | Nostoc punctiforme PCC 73102 | COG2755: Lysophospholipase L1 and related esterases [Nostoc punctiforme PCC 73102] | | | | |
| 11801, 11802, 11805, 11806 | 34556591 38016672 | 57 41 | 8.00E-77 4.00E-20 | Wolinella succinogenes DSM 1740 Klebsiella pneumoniae | PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE09306.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes] YebB [Klebsiella pneumoniae] ref NP_943343.1 YebB [Klebsiella pneumoniae] | | | 4.2.1.70 | |
| 11809, 11810 | 57241075 | 51 | 2.00E-81 | Campylobacter lari RM2100 | glycyl-tRNA synthetase, beta subunit [Campylobacter lari RM2100] gb EAL54771.1 glycyl-tRNA synthetase, beta subunit [Campylobacter lari RM2100] | | | | 6.1.1.14 |
| 1181, 1182 | 48854372 | 76 | 5.00E-67 | Cytophaga hutchinsonii | COG0114: Fumarase [Cytophaga hutchinsonii] | | | | |
| 11811, 11812 | 46143552 | 44 | 2.00E-35 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | | 2.7.3.- |
| 11813, 11814 | 23127773 | 43 | 3.00E-35 | Nostoc punctiforme PCC 73102 | COG0337: 3-dehydroquinase synthetase [Nostoc punctiforme PCC 73102] | | | | 4.2.3.4 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|---------|
| 11815, 11816 | 45658172 | 41 | 8.00E-35 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 11817, 11818 | 51244491 | 30 | 8.00E-20 | Desulfotalea psychrophila LSV54 | hypothetical membrane protein (BatB) [Desulfotalea psychrophila LSV54] emb CAG35368.1 hypothetical membrane protein (BatB) [Desulfotalea psychrophila LSV54] | | | | |
| 11823, 11824 | 34556560 | 41 | 5.00E-56 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | |
| 11825, 11826 | 48855584 | 37 | 6.00E-42 | Cytophaga hutchinsonii | COG0010: Arginase/agmatinase/formiminonoglutamate hydrolase, arginase family [Cytophaga hutchinsonii] | | | | 3.5.3.1 |
| 11827, 11828 | 15607089 | 63 | 1.00E-43 | Aquifex aolicus VF5 | hypothetical protein aq_2146 [Aquifex aolicus VF5] gb AAC07873.1 hypothetical protein [Aquifex aolicus VF5] pir B70484 conserved hypothetical protein aq_2146 - Aquifex aolicus | | | | 2.7.4.9 |
| 11829, 11830 | 34396965 | 37 | 2.00E-11 | Porphyromonas gingivalis W83 | hypothetical protein PG0883 [Porphyromonas gingivalis W83] ref NP_905130.1 hypothetical protein PG0883 [Porphyromonas gingivalis W83] | | | | |
| 1183, 1184 | 15603823 | 34 | 7.00E-10 | Pasteurella multocida subsp. multocida str. Pm70 | hypothetical protein PM1958 [Pasteurella multocida subsp. multocida str. Pm70] gb AAK04042.1 unknown [Pasteurella multocida subsp. multocida str. Pm70] sp Q9CJN9 J58_PASMU Hypothetical UPF0306 protein PM1958 | | | | |
| 11831, 11832 | 34556779 | 26 | 1.00E-17 | Wolinella succinogenes DSM 1740 | GGDEF DOMAIN PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09494.1 GGDEF DOMAIN PROTEIN [Wolinella succinogenes] | | | | |
| 11837, 11838 | 57237396 | 76 | 4.00E-38 | Campylobacter jejuni RM1221 | excinuclease ABC, A subunit [Campylobacter jejuni RM1221] gb AAW34979.1 excinuclease ABC, A subunit [Campylobacter jejuni RM1221] | | | | |
| 11839, 11840 | 48832174 | 25 | 6.00E-17 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | | |
| 11841, 11842 | 48833886 | 54 | 4.00E-32 | Magnetococcus sp. MC-1 | COG2202: FOG: PAS/PAC domain [Magnetococcus sp. MC-1] | | | | |
| 11843, 11844 | 48786283 | 54 | 8.00E-66 | Burkholderia fungorum LB400 | COG0436: Aspartate/tyrosine/aromatic aminotransferase [Burkholderia fungorum LB400] | | | | 2.6.1.1 |
| 11845, 11846 | 32262039 | 41 | 2.00E-46 | Helicobacter hepaticus ATCC 51449 | glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449] ref NP_860022.1 glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449] | | | | 5.3.1.9 |
| 11851, 11852 | 53714985 | 33 | 1.00E-27 | Bacteroides fragilis YCH46 | putative membrane peptidase [Bacteroides fragilis YCH46] db BAD50443.1 putative membrane peptidase [Bacteroides fragilis YCH46] | | | | |

| | | | | | | | | |
|-----------------|--------------|----|-----------|---|--|--|----|----------|
| 11857, 11858 | 34556460 | 56 | 2.00E-53 | Wolnella succinogenes DSM 1740 | DNA POLYMERASE III, BETA CHAIN [Wolnella succinogenes DSM 1740] embjCAE09175.1] DNA POLYMERASE III, BETA CHAIN [Wolnella succinogenes] | | | 2.7.7.7 |
| 11859, 11860 | 34558792 | 31 | 4.00E-18 | Alvinella pompejana epibiont 6C6 | conserved hypothetical protein [Alvinella pompejana epibiont 6C6] | | | |
| 11861, 11862 | 54302166 | 29 | 2.00E-10 | Photobacterium profundum SS9 | hypothetical protein PBRB0486 [Photobacterium profundum SS9] embjCAG23359.1] hypothetical protein [Photobacterium profundum] | | | |
| 11863, 11864 | 34104262 | 33 | 1.00E-09 | Chromobacterium violaceum ATCC 12472 | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] refjNP_902623.1] hypothetical protein CV2953 [Chromobacterium violaceum ATCC 12472] | | | 2.7.3.- |
| 11865, 11866 | 34557749 | 53 | 2.00E-34 | Wolnella succinogenes DSM 1740 | hypothetical protein WS1398 [Wolnella succinogenes DSM 1740] embjCAE10464.1] conserved hypothetical protein [Wolnella succinogenes] | | | |
| 1187, 1188 | 48855923 | 46 | 9.00E-35 | Cytophaga hutchinsonii | COG2812: DNA polymerase III, gamma/tau subunits [Cytophaga hutchinsonii] | | | 2.7.7.7 |
| 11873, 11874 | AAU3577 1 | 80 | 1.00E-123 | | Desc:Helicobacter pylori cellular proliferation protein #84. Org:Helicobacter pylori | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 80 | 1.00E-11 |
| 11875, 11876 | 57168227 | 45 | 4.00E-40 | Campylobacter coli RM2228 | probable flagellar protein Cj1312 [Campylobacter coli RM2228] gbjEAL57270.1] probable flagellar protein Cj1312 [Campylobacter coli RM2228] | | | |
| 11877, 11878 | 6968747 | 46 | 1.00E-24 | Campylobacter jejuni subsp. jejuni NCTC 11168 | possible flagellar protein [Campylobacter jejuni subsp. jejuni NCTC 11168] refjNP_282459.1] possible flagellar protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pirjF81274 probable flagellar protein Cj1313 [Imported] - Campylobacter jejuni (strain NCTC 11168) | | | |
| 11879, 11880 | 26247620 | 24 | 5.00E-09 | Escherichia coli CFT073 | Hypothetical protein yciR [Escherichia coli CFT073] gbjAAN80222.1] Hypothetical protein yciR [Escherichia coli CFT073] | | | |
| 11881, 11882 | 34556462 | 71 | 6.00E-49 | Wolnella succinogenes DSM 1740 | hypothetical protein WS0003 [Wolnella succinogenes DSM 1740] embjCAE09177.1] conserved hypothetical protein [Wolnella succinogenes] | | | |
| 11883, 11884 | 34556772 | 61 | 1.00E-69 | Wolnella succinogenes DSM 1740 | ENDOPEPTIDASE CLP ATP-BINDING CHAIN A [Wolnella succinogenes DSM 1740] embjCAE09487.1] ENDOPEPTIDASE CLP ATP-BINDING CHAIN A [Wolnella succinogenes] | Desc:Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1142. Org:Staphylococcus epidermidis | 87 | 3.00E-08 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|----|----------|----------|
| 11885, 11886 | 57240902 | 49 | 8.00E-35 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55295.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 11889, 11890 | 19703759 | 29 | 9.00E-23 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Type III restriction-modification system restriction subunit [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94620.1 Type III restriction-modification system restriction subunit [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | 3.1.21.5 | |
| 11891, 11892 | 34557016 | 52 | 3.00E-23 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0599 [Wolinella succinogenes DSM 1740] emb CAE09731.1 conserved hypothetical protein [Wolinella succinogenes] COG0840: Methyl-accepting chemotaxis protein [Microbulifer degradans 2- 40] | | | | |
| 11893, 11894 | 48863731 | 30 | 9.00E-19 | Microbulifer degradans 2-40 | | | | | |
| 11895, 11896 | 51891413 | 30 | 3.00E-07 | Symbiobacterium thermophilum IAM 14863 | transposase [Symbiobacterium thermophilum IAM 14863] db BAD39260.1 transposase [Symbiobacterium thermophilum IAM 14863] | | | | |
| 11897, 11898 | 34557509 | 48 | 7.00E-30 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 11899, 11900 | 53795617 | 36 | 1.00E-42 | Chloroflexus aurantiacus | COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Chloroflexus aurantiacus] | | | 2.7.3.- | |
| 119, 120 | 48854510 | 57 | 5.00E-44 | Cytophaga hutchinsonii | COG0622: Predicted phosphoesterase [Cytophaga hutchinsonii] | | | | |
| 11901, 11902 | 34557246 | 55 | 6.00E-74 | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | | | 2.7.3.- | |
| 11903, 11904 | 57236987 | 51 | 3.00E-85 | Campylobacter jejuni RM1221 | primosomal protein N' [Campylobacter jejuni RM1221] gb AAW34570.1 primosomal protein N' [Campylobacter jejuni RM1221] | | | | |
| 11905, 11906 | 34556865 | 56 | 3.00E-58 | Wolinella succinogenes DSM 1740 | PUTATIVE D-ALANINE-D-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09580.1 PUTATIVE D-ALANINE-D-ALANINE LIGASE [Wolinella succinogenes] sp Q7MA71 DDL_WOLSU D-alanine-D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase) | | | 6.3.2.4 | |
| 11909, 11910 | 22651592 | 68 | 9.00E-98 | Sulfurospirillum barnesii | periplasmic nitrate reductase [Sulfurospirillum barnesii] | Sulfurospirillum barnesii SES-3 periplasmic nitrate reductase (napA) gene, partial cds | 86 | 4.00E-08 | 1.7.99.4 |
| 11913, 11914 | 52426060 | 41 | 2.00E-29 | Mannheimia succiniciproducens MBEL 55E | hypothetical protein MS2005 [Mannheimia succiniciproducens MBEL55E] gb AAU38612.1 unknown [Mannheimia succiniciproducens MBEL55E] | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|----|----------|
| 11915, 11916 | 34558488 | 61 | 2.00E-42 | Wolinella succinogenes DSM 1740 | PUTATIVE ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11203.1 PUTATIVE ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes] | | | 1.8.-:- |
| 11917, 11918 | 18310884 | 28 | 8.00E-10 | Clostridium perfringens str. 13 | hypothetical protein CPE1902 [Clostridium perfringens str. 13] dbj BAB81608.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | |
| 11919, 11920 | 34556640 | 75 | 3.00E-57 | Wolinella succinogenes DSM 1740 | 30S RIBOSOMAL PROTEIN S2 [Wolinella succinogenes DSM 1740] emb CAE09355.1 30S RIBOSOMAL PROTEIN S2 [Wolinella succinogenes] uracil phosphoribosyltransferase [Aquifex aeolicus VF5] gb AAC07880.1 uracil phosphoribosyltransferase [Aquifex aeolicus VF5] pir F70485 uracil phosphoribosyltransferase (EC 2.4.2.9) upp-type - Aquifex aeolicus sp Q67914 UUP_AQUAE Uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTase) | Helicobacter hepaticus ATCC 51449 section 4 of 6 of the complete genome | 82 | 1.00E-12 |
| 11921, 11922 | 15607101 | 41 | 1.00E-42 | Aquifex aeolicus VF5 | PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] gb AAD05690.1 PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] pir E71972 pyruvate, water dikinase (EC 2.7.9.2) - Helicobacter pylori (strain J99) sp Q9ZMV4 PPSA_HELPJ Phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase) | | | 2.4.2.9 |
| 11923, 11924 | 15611181 | 58 | 6.00E-86 | Helicobacter pylori J99 | dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46097.1 dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis] gb AAS60284.1 sugar dehydratase [Francisella tularensis subsp. tularensis] | | | 2.7.9.2 |
| 11925, 11926 | 56708505 | 63 | 4.00E-50 | Francisella tularensis subsp. tularensis Schu 4 | probable flavoprotein [Desulfotalea psychrophila LSV54] emb CAG36848.1 probable flavoprotein [Desulfotalea psychrophila LSV54] hypothetical protein GSU1360 [Geobacter sulfurreducens PCA] gb AAR34736.1 hypothetical protein GSU1360 [Geobacter sulfurreducens PCA] | | | 4.2.1.- |
| 11927, 11928 | 51245971 | 68 | 1.00E-105 | Desulfotalea psychrophila LSV54 | COG3735: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 11929, 11930 | 39996462 | 38 | 1.00E-25 | Geobacter sulfurreducens PCA | hypothetical protein Rub02001299 [Rhodospirillum rubrum] | | | |
| 1193, 1194 | 48856757 | 38 | 5.00E-07 | Cytophaga hutchinsonii | hypothetical protein Reut02000360 [Ralstonia metallidurans CH34] | | | |
| 11931, 11932 | 48764556 | 29 | 9.00E-13 | Rhodospirillum rubrum | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |
| 11935, 11936 | 48771616 | 29 | 2.00E-21 | Ralstonia metallidurans CH34 | | | | |
| 11937, 11938 | 48853332 | 31 | 2.00E-32 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | |
|-----------------|--------------|----|----------|---|---|--|--|---------|
| 11939, 11940 | 48853332 | 26 | 2.00E-13 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |
| 11941, 11942 | 34557573 | 33 | 1.00E-30 | Wolinella succinogenes DSM 1740 | SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 11943, 11944 | 34557118 | 46 | 6.00E-23 | Wolinella succinogenes DSM 1740 | MOLYBDOPTERIN OXIDOREDUCTASE, IRON-SULFUR BINDING SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE09833.1 MOLYBDOPTERIN OXIDOREDUCTASE, IRON-SULFUR BINDING SUBUNIT [Wolinella succinogenes] | | | 1.2.7.- |
| 11945, 11946 | 28851369 | 59 | 4.00E-19 | Pseudomonas syringae pv. tomato str. DC3000 | methyl-accepting chemotaxis protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_790751.1 methyl-accepting chemotaxis protein [Pseudomonas syringae pv. tomato str. DC3000] | | | |
| 11947, 11948 | ABP3072 8 | 56 | 5.00E-34 | | Desc:Streptococcus polypeptide SEQ ID NO 10632. Org:Streptococcus agalactiae | | | |
| 11949, 11950 | ABP3072 8 | 47 | 4.00E-28 | | Desc:Streptococcus polypeptide SEQ ID NO 10632. Org:Streptococcus agalactiae | | | |
| 11951, 11952 | 48855487 | 73 | 2.00E-37 | Cytophaga hutchinsonii | COG1048: Aconitase A [Cytophaga hutchinsonii] | | | 4.2.1.3 |
| 11953, 11954 | 42521967 | 43 | 7.00E-37 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd0347 [Bdellovibrio bacteriovorus HD100] emb CAE78001.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100] | | | |
| 11955, 11956 | 34558795 | 50 | 9.00E-80 | Alvinella pompejana epibiont 6C6 | TonB-dependent receptor [Alvinella pompejana epibiont 6C6] | | | |
| 11957, 11958 | 40063642 | 43 | 9.00E-12 | uncultured bacterium 582 | oxidoreductase, 2OG-Fe(II) oxygenase family [uncultured bacterium 582] PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR | | | |
| 11959, 11960 | 34557235 | 47 | 4.00E-26 | Wolinella succinogenes DSM 1740 | [Wolinella succinogenes DSM 1740] emb CAE09950.1 PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes] | | | |
| 11963, 11964 | 34558815 | 57 | 5.00E-51 | Alvinella pompejana epibiont 7G3 | citrate lyase subunit 2 [Alvinella pompejana epibiont 7G3] | | | 4.1.3.8 |
| 11965, 11966 | 42525634 | 34 | 4.00E-14 | Treponema denticola ATCC 35405 | hypothetical protein TDE0115 [Treponema denticola ATCC 35405] gb AA510613.1 conserved hypothetical protein [Treponema denticola ATCC 35405] | | | |
| 11969, 11970 | 48854887 | 43 | 1.00E-41 | Cytophaga hutchinsonii | COG0538: Isocitrate dehydrogenases [Cytophaga hutchinsonii] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|----------|
| 11971, 11972 | 34556565 | 30 | 4.00E-19 | Wolnella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes DSM 1740] emb CAE09280.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes] emb CAD23185.1 putative transcriptional regulator protein [Wolnella succinogenes] | | | |
| 11973, 11974 | 23102480 | 42 | 6.00E-45 | Azotobacter vinelandii | COG3649: Uncharacterized protein predicted to be involved in DNA repair [Azotobacter vinelandii] | | | |
| 11978, 11980 | 23103021 | 31 | 1.00E-23 | Azotobacter vinelandii | COG3321: Polyketide synthase modules and related proteins [Azotobacter vinelandii] | | | 2.3.1.39 |
| 11981, 11982 | 19704257 | 29 | 4.00E-11 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Homoserine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95118.1 Homoserine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | 2.7.1.39 |
| 11983, 11984 | 37787364 | 45 | 1.00E-33 | Thiocapsa roseopersicina | HoxY [Thiocapsa roseopersicina] | | | 1.12.-- |
| 11985, 11986 | 57237690 | 29 | 3.00E-16 | Campylobacter jejuni RM1221 | hypothetical protein CJE0936 [Campylobacter jejuni RM1221] gb AAW35273.1 hypothetical protein CJE0936 [Campylobacter jejuni RM1221] | | | |
| 11987, 11988 | 57241378 | 56 | 5.00E-53 | Campylobacter lari RM2100 | molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100] gb EAL54490.1 molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100] | | | |
| 11989, 11990 | 37528276 | 41 | 6.00E-54 | Photobacterium luminescens subsp. laumondii TTO1 | hypothetical protein plu4453 [Photobacterium luminescens subsp. laumondii TTO1] emb CAE16825.1 unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1] | | | |
| 11991, 11992 | 57241378 | 56 | 5.00E-49 | Campylobacter lari RM2100 | molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100] gb EAL54490.1 molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100] | | | |
| 11993, 11994 | 34556682 | 61 | 3.00E-66 | Wolnella succinogenes DSM 1740 | TYROSYL-TRNA SYNTHETASE [Wolnella succinogenes DSM 1740] emb CAE09397.1 TYROSYL-TRNA SYNTHETASE [Wolnella succinogenes] | | | 6.1.1.1 |
| 12001, 12002 | 23128981 | 32 | 1.00E-13 | Nostoc punctiforme PCC 73102 | COG2319: FOG: WD40 repeat [Nostoc punctiforme PCC 73102] | | | 2.7.1.37 |
| 12003, 12004 | 48870994 | 32 | 2.00E-09 | Pedococcus pentosaceus ATCC 25745 | COG0679: Predicted permeases [Pedococcus pentosaceus ATCC 25745] Protein containing HTH-type DNA-binding domain and DOC/FIC domain involved in death-on-curing system [Idiomarina loihiensis L2TR] gb AAV82879.1 Protein containing HTH-type DNA-binding domain and DOC/FIC domain involved in death-on-curing system [Idiomarina loihiensis L2TR] | | | |
| 12005, 12006 | 56461147 | 37 | 5.00E-44 | Idiomarina loihiensis L2TR | | | | |

| | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|----------|
| 12007, | 50122189 | 24 | 2.00E-13 | Erwinia carotovora subsp. atroseptica SCRI1043 | agglutination protein [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76165.1 agglutination protein [Erwinia carotovora subsp. atroseptica SCRI1043] | | | |
| 12008, | 18858717 | 36 | 9.00E-10 | Danio rerio | alpha(1,3)fucosyltransferase [Danio rerio] | | | 2.4.1.- |
| 12009, | 32477759 | 39 | 5.00E-26 | Rhodopirellula baltica SH 1 | hypothetical protein RB12866 [Rhodopirellula baltica SH 1] | | | |
| 1201, | 32262039 | 36 | 1.00E-14 | Helicobacter hepaticus ATCC 51449 | emb CAD77830.1 conserved hypothetical protein [Pirellula sp.] glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449] ref NP_860022.1 glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449] | | | 5.3.1.9 |
| 12013, | 53756727 | 23 | 6.00E-12 | Methylococcus capsulatus str. Bath | conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_115226.1 hypothetical protein MCA2832 [Methylococcus capsulatus str. Bath] | | | |
| 12014, | 56387326 | 38 | 6.00E-34 | Clostridium saccharoperbutylacetonicum | uptake hydrogenase [Clostridium saccharoperbutylacetonicum] | | | 1.6.5.3 |
| 12021, | 53685438 | 37 | 5.00E-41 | Desulfitobacterium hafniense DCB-2 | COG2081: Predicted flavoproteins [Desulfitobacterium hafniense DCB-2] | | | |
| 12022, | 56707780 | 59 | 3.00E-84 | Francisella tularensis subsp. tularensis Schu 4 | DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45292.1 DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis] | | | |
| 12023, | 18310859 | 31 | 1.00E-11 | Clostridium perfringens str. 13 | probable glycerophosphodiester phosphodiesterase [Clostridium perfringens str. 13] dbj BAB81583.1 probable glycerophosphodiester phosphodiesterase [Clostridium perfringens str. 13] | | | 3.1.4.46 |
| 12027, | 48891084 | 30 | 1.00E-14 | Trichodesmium erythraeum IMS101 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] | | | 2.4.1.- |
| 12032, | 34397216 | 50 | 8.00E-23 | Porphyromonas gingivalis W83 | conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_905380.1 hypothetical protein PG1179 [Porphyromonas gingivalis W83] | | | |
| 12035, | 53713673 | 42 | 7.00E-30 | Bacteroides fragilis YCH46 | hypothetical protein BF2382 [Bacteroides fragilis YCH46] dbj BAD49131.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 12036, | 34558322 | 46 | 4.00E-52 | Wolinella succinogenes DSM 1740 | UDP-N-ACETYLMURAMOYLALANINE-D-GLUTAMATE LIGASE [Wolinella succinogenes DSM 1740] emb CAE11037.1 UDP-N-ACETYLMURAMOYLALANINE-D-GLUTAMATE LIGASE [Wolinella succinogenes] | | | 6.3.2.9 |
| 12037, | 46118943 | 49 | 8.00E-19 | Crocospaera watsonii WH 8501 | COG0545: FKBP-type peptidyl-prolyl cis-trans isomerases 1 [Crocospaera watsonii WH 8501] | | | 5.2.1.8 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|-------------------|
| 12049, 12050 | 48864040 | 22 | 1.00E-11 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02000406 [Microbulbifer degradans 2-40] | | | |
| 1205, 1206 | 15602459 | 59 | 7.00E-16 | Pasteurella multocida subsp. multocida str. Pm70 | hypothetical protein PM0594 [Pasteurella multocida subsp. multocida str. Pm70] gb AAK02678.1 unknown [Pasteurella multocida subsp. multocida str. Pm70] | | | |
| 12057, 12058 | 48846045 | 35 | 2.00E-21 | Geobacter metallireducens GS-15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 12059, 12060 | 15639357 | 39 | 5.00E-11 | Treponema pallidum subsp. pallidum str. Nichols | chemotaxis response regulator (cheY) [Treponema pallidum subsp. pallidum str. Nichols] gb AAC65351.1 chemotaxis response regulator (cheY) [Treponema pallidum subsp. pallidum str. Nichols] gb AAD45223.1 chemotaxis protein CheY [Treponema pallidum subsp. pertenue] gb AAC45558.1 chemotaxis protein CheY pir[D71335 probable chemotaxis response regulator (cheY) - syphilis spirochete sp P96126 CHEY_TREPA Chemotaxis protein cheY | | | 2.7.3.- |
| 12061, 12062 | 34557846 | 43 | 1.00E-34 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1513 [Wolinella succinogenes DSM 1740] emb CAE10561.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 12063, 12064 | 34557848 | 61 | 2.00E-72 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-2-methylthioadenine synthetase [Wolinella succinogenes DSM 1740] emb CAE10563.1 conserved hypothetical protein-2-methylthioadenine synthetase [Wolinella succinogenes] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 89 | 5.00E-07 1.8.- |
| 12065, 12066 | 37694419 | 41 | 6.00E-51 | Flavobacterium columnare | membrane-associated zinc metalloprotease [Flavobacterium columnare] | Flavobacterium columnare strain G4 membrane- associated zinc metalloprotease gene, complete cds | 81 | 4.00E-14 3.4.24.- |
| 12067, 12068 | 29349509 | 45 | 8.00E-57 | Bacteroides thetaiotaomicron VPI-5482 | alanine racemase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79206.1 alanine racemase [Bacteroides thetaiotaomicron VPI-5482] | | | 5.1.1.1 |
| 12069, 12070 | 53736047 | 43 | 2.00E-60 | Crocospaera watsonii WH 8501 | COG4889: Predicted helicase [Crocospaera watsonii WH 8501] | | | |
| 1207, 1208 | 48854861 | 43 | 3.00E-35 | Cytophaga hutchinsonii | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | 2.4.1.- |
| 12071, 12072 | 57241408 | 36 | 2.00E-25 | Campylobacter lari RM2100 | rod shape-determining protein (mreC), putative [Campylobacter lari RM2100] gb EAL54520.1 rod shape-determining protein (mreC), putative [Campylobacter lari RM2100] | | | |

| | | | | | | | | |
|--------|----------|----|-----------|---------------------------------------|---|--|-------------|----------|
| 12073, | 48853984 | 59 | 1.00E-104 | Cytophaga hutchinsonii | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | 3.6.1.- |
| 12074 | 48853984 | 41 | 1.00E-56 | Cytophaga hutchinsonii | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | |
| 12075, | 48853984 | 41 | 1.00E-56 | Wolinella succinogenes DSM 1740 | PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wolinella succinogenes DSM 1740] emb CAE11049.1 PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wolinella succinogenes] | | | 2.4.2.- |
| 12076 | 34558334 | 49 | 3.00E-44 | Microbulbifer degradans 2-40 | COG3176: Putative hemolysin [Microbulbifer degradans 2-40] | Wolinella succinogenes, complete genome; segment 6/7 | 89 5.00E-10 | |
| 12081, | 48861085 | 48 | 1.00E-56 | Magnetospirillum magnetotacticum MS-1 | COG2200: FOG: EAL domain [Magnetospirillum magnetotacticum MS-1] | | | |
| 12082 | 46201018 | 35 | 3.00E-37 | Campylobacter lari RM2100 | ParB family protein [Campylobacter lari RM2100] | | | |
| 12083, | 57240722 | 33 | 2.00E-11 | Synechocystis sp. PCC 6803 | hypothetical protein sir2110 [Synechocystis sp. PCC 6803] dbj BAA18047.1 sir2110 [Synechocystis sp. PCC 6803] pir S75486 hypothetical protein sir2110 - Synechocystis sp. (strain PCC 6803) | | | |
| 12084 | 16330639 | 41 | 4.00E-18 | Bacteroides fragilis YCH46 | tRNA nucleotidyltransferase [Bacteroides fragilis YCH46] dbj BAD50383.1 tRNA nucleotidyltransferase [Bacteroides fragilis YCH46] | | | 2.7.7.19 |
| 12085, | 53714925 | 62 | 6.00E-74 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2505 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77612.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 12086 | 29347915 | 36 | 3.00E-31 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2211 [Wolinella succinogenes DSM 1740] emb CAE11200.1 hypothetical protein [Wolinella succinogenes] | | | |
| 12089, | 34558485 | 38 | 2.00E-40 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR-CheY like receiver domain [Wolinella succinogenes DSM 1740] emb CAE10945.1 PUTATIVE TWO-COMPONENT REGULATOR-CheY like receiver domain [Wolinella succinogenes] | | | |
| 1209, | 34558485 | 38 | 2.00E-40 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1588 [Wolinella succinogenes DSM 1740] emb CAE10627.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 1210, | 53714925 | 62 | 6.00E-74 | Bacteroides thetaiotaomicron VPI-5482 | type I restriction-modification system methyltransferase subunit [Vibrio vulnificus YJ016] dbj BAC93580.1 type I restriction-modification system methyltransferase subunit [Vibrio vulnificus YJ016] | | | 2.1.1.72 |
| 12097, | 29347915 | 36 | 3.00E-31 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein TIGR00486 [Campylobacter upsaliensis RM3195] gb EAL53410.1 conserved hypothetical protein TIGR00486 [Campylobacter upsaliensis RM3195] | | | |
| 12098 | 34558230 | 50 | 8.00E-25 | Wolinella succinogenes DSM 1740 | | | | |
| 12099, | 34558485 | 38 | 2.00E-40 | Wolinella succinogenes DSM 1740 | | | | |
| 12100 | 34558485 | 38 | 2.00E-40 | Wolinella succinogenes DSM 1740 | | | | |
| 12101, | 34558230 | 50 | 8.00E-25 | Wolinella succinogenes DSM 1740 | | | | |
| 12102 | 34558230 | 50 | 8.00E-25 | Wolinella succinogenes DSM 1740 | | | | |
| 12103, | 34558230 | 50 | 8.00E-25 | Wolinella succinogenes DSM 1740 | | | | |
| 12104 | 34558230 | 50 | 8.00E-25 | Wolinella succinogenes DSM 1740 | | | | |
| 12105, | 37679000 | 68 | 3.00E-69 | Vibrio vulnificus YJ016 | | | | |
| 12106 | 37679000 | 68 | 3.00E-69 | Vibrio vulnificus YJ016 | | | | |
| 12107, | 57242697 | 47 | 1.00E-58 | Campylobacter upsaliensis RM3195 | | | | |
| 12108 | 57242697 | 47 | 1.00E-58 | Campylobacter upsaliensis RM3195 | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|---------------|
| 1211, 1212 | 21226234 | 63 | 2.00E-38 | Methanosarcina mazel Go1 | hypothetical protein MM0132 [Methanosarcina mazel Go1] gb AAM29828.1 conserved protein [Methanosarcina mazel Go1] | | | |
| | | | | | hypothetical protein c5144 [Escherichia coli CFT073] ref NP_755482.1 | | | |
| | | | | | hypothetical protein c3607 [Escherichia coli CFT073] ref NP_753439.1 | | | |
| | | | | | hypothetical protein c1530 [Escherichia coli CFT073] gb AAN83566.1 | | | |
| 12113, 12114 | 26250952 | 36 | 3.00E-23 | Escherichia coli CFT073 | Hypothetical protein [Escherichia coli CFT073] gb AAN82055.1 Hypothetical protein [Escherichia coli CFT073] gb AAN79999.1 Hypothetical protein [Escherichia coli CFT073] | | | |
| 12115, 12116 | 48892683 | 28 | 2.00E-11 | Trichodesmium erythraeum IMS101 | COG0515: Serine/threonine protein kinase [Trichodesmium erythraeum IMS101] | | | 2.7.1.37 |
| 12121, 12122 | 29347740 | 27 | 1.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2330 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77437.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 12123, 12124 | 45658174 | 39 | 1.00E-18 | Leptospira interrogans serovar Copenhagen str. Flocruz L1-130 | hypothetical protein LIC12326 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70897.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 12125, 12126 | 51245405 | 41 | 2.00E-32 | Desulfotalea psychrophila LSV54 | hypothetical protein DP1553 [Desulfotalea psychrophila LSV54] emb CAG36282.1 unknown protein [Desulfotalea psychrophila LSV54] | | | |
| 12127, 12128 | 34556927 | 60 | 9.00E-81 | Wolinella succinogenes DSM 1740 | PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09642.1 PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes] | | | |
| 1213, 1214 | 31195995 | 54 | 1.00E-39 | Anopheles gambiae | ENSANGP00000000470 [Anopheles gambiae] | | | 2.3.1.- |
| 12131, 12132 | 20559765 | 41 | 6.00E-52 | Pseudomonas aeruginosa | ORF_15; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa] gb AAO17396.1 glycosyl transferases group 1-like protein [Pseudomonas aeruginosa] | | | 2.4.1.- |
| 12135, 12136 | 48855632 | 32 | 8.00E-25 | Cytophaga hutchinsonii | COG0712: F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein) [Cytophaga hutchinsonii] | | | 3.6.3.14 |
| 12137, 12138 | 48857000 | 35 | 3.00E-16 | Cytophaga hutchinsonii | COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | |
| 12139, 12140 | 57506236 | 65 | 1.00E-35 | Campylobacter upsaliensis RM3195 | malate:quinone oxidoreductase, putative [Campylobacter upsaliensis RM3195] gb EAL52259.1 malate:quinone oxidoreductase, putative [Campylobacter upsaliensis RM3195] | | | 1.1.99.1 6 |
| 12141, 12142 | 34557578 | 41 | 2.00E-38 | Wolinella succinogenes DSM 1740 | CIAB PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10293.1 CIAB PROTEIN [Wolinella succinogenes] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|---|----|-----------|
| 12143, 12144 | 24372513 | 31 | 1.00E-19 | Shewanella oneidensis MR-1 | acetyltransferase, GNAT family [Shewanella oneidensis MR-1] gb AAAN54000.1 acetyltransferase, GNAT family [Shewanella oneidensis MR-1] | | | |
| 12145, 12146 | 17549647 | 60 | 5.00E-40 | Ralstonia solanacearum GMI1000 | hypothetical protein RS03114 [Ralstonia solanacearum GMI1000] emb CAD18579.1 CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] | | | |
| 12147, 12148 | 48854194 | 42 | 7.00E-23 | Cytophaga hutchinsonii | COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii] | | | |
| 12149, 12150 | 52007438 | 67 | 1.00E-72 | Thiobacillus denitrificans ATCC 25259 | COG0677: UDP-N-acetyl-D-mannosaminuronate dehydrogenase [Thiobacillus denitrificans ATCC 25259] | Shigella sonnei O antigen gene cluster, complete sequence; insertion sequences IS1 InsB (InsB), InsA (InsA), IS630 transposase, IS628 ORFA (orfA), IS91 transposase (InsB) and InsA (InsA), and IS911 InsB (InsB) genes, complete cds | 91 | 2.00E-09 |
| 12151, 12152 | 53612047 | 51 | 1.00E-49 | Azotobacter vinelandii | COG0419: ATPase involved in DNA repair [Azotobacter vinelandii] Lysyl-tRNA synthetase class II [Thermoanaerobacter tengcongensis MB4] | | | |
| 12153, 12154 | 20808736 | 48 | 2.00E-71 | Thermoanaerobact er tengcongensis MB4 | gb AAM2551.1 Lysyl-tRNA synthetase class II [Thermoanaerobacter tengcongensis MB4] sp Q8R7N1 SYK_THETN Lysyl-tRNA synthetase (Lysine-tRNA ligase) (LysRS) oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter jejuni RM1221] gb AAW35807.1 oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter jejuni RM1221] emb CAB75216.1 putative oxidoreductase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281763.1 putative oxidoreductase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81405 probable oxidoreductase Cj0580c [imported] - Campylobacter jejuni (strain NCTC 11168) | Prochlorococcus marinus MED4 complete genome; segment 5/5 | 86 | 1.00E-08 |
| 12155, 12156 | 57238224 | 44 | 3.00E-49 | Campylobacter jejuni RM1221 | | | | 1.1.1.1.6 |
| 12159, 12160 | 48846045 | 40 | 1.00E-27 | Geobacter metallireducens GS-15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|--|----------|
| 12161, 12162 | 48825033 | 38 | 7.00E-20 | Enterococcus faecium | COG0463: Glycosyltransferases involved in cell wall biogenesis [Enterococcus faecium] | | | 2.4.-.- |
| 12165, 12166 | 21673395 | 49 | 1.00E-60 | Chlorobium tepidum TLS | NH(3)-dependent NAD+ synthetase [Chlorobium tepidum TLS] gb AAAM71802.1 NH(3)-dependent NAD+ synthetase [Chlorobium tepidum TLS] sp Q8KEX2 NADE_CHLTE NH(3)-dependent NAD(+) synthetase | | | 6.3.5.1 |
| 12167, 12168 | 48861330 | 39 | 5.00E-21 | Microbulbifer degradans 2-40 | COG0457: FOG: TPR repeat [Microbulbifer degradans 2-40] | | | |
| 12169, 12170 | 34557419 | 36 | 2.00E-36 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | 2.7.3.- |
| 1217, 1218 | 5360168 | 33 | 6.00E-27 | Flavobacterium johnsoniae | GldB [Flavobacterium johnsoniae] | | | |
| 12171, 12172 | 34556479 | 41 | 4.00E-15 | Wolinella succinogenes DSM 1740 | POSSIBLE NUCLEOTIDYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09194.1 POSSIBLE NUCLEOTIDYLTRANSFERASE [Wolinella succinogenes] | | | |
| 12173, 12174 | 34556480 | 66 | 1.00E-63 | Wolinella succinogenes DSM 1740 | GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes DSM 1740] emb CAE09195.1 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes] | | | 2.6.1.16 |
| 12175, 12176 | 57236944 | 46 | 2.00E-43 | Campylobacter jejuni RM1221 | RNB-like protein [Campylobacter jejuni RM1221] gb AAW34527.1 RNB-like protein [Campylobacter jejuni RM1221] | | | 3.1.-.- |
| 12177, 12178 | 34557504 | 71 | 1.00E-109 | Wolinella succinogenes DSM 1740 | HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella succinogenes DSM 1740] emb CAE10219.1 HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella succinogenes] | | | 3.1.21.3 |
| 12185, 12186 | 48855392 | 28 | 8.00E-16 | Cytophaga hutchinsonii | COG0823: Periplasmic component of the Tol biopolymer transport system [Cytophaga hutchinsonii] | | | |
| 12189, 12190 | 21228324 | 28 | 4.00E-17 | Methanosarcina mazel Go1 | Galactosyltransferase [Methanosarcina mazel Go1] gb AAM31918.1 Galactosyltransferase [Methanosarcina mazel Goe1] | | | 2.4.1.- |
| 1219, 1220 | 30023200 | 42 | 4.00E-55 | Bacillus cereus ATCC 14579 | Excinuclease ABC subunit A [Bacillus cereus ATCC 14579] gb AAP12032.1 Excinuclease ABC subunit A [Bacillus cereus ATCC 14579] | | | |
| 12191, 12192 | 24214122 | 34 | 1.00E-30 | Leptospira interrogans serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] | | | |
| 12193, 12194 | 32262126 | 63 | 5.00E-75 | Helicobacter hepaticus ATCC 51449 | UTP-glucose-1-phosphate uridylyltransferase [Helicobacter hepaticus ATCC 51449] ref NP_860109.1 UTP-glucose-1-phosphate uridylyltransferase [Helicobacter hepaticus ATCC 51449] | | | 2.7.7.9 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|--|
| 12197, 12198 | 57242699 | 51 | 5.00E-39 | Campylobacter upsallensis RM3195 | conserved hypothetical protein [Campylobacter upsallensis gb EAL53412.1 conserved hypothetical protein [Campylobacter upsallensis RM3195] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 80 | 8.00E-11 | |
| 12199, 12200 | 48846029 | 36 | 1.00E-45 | Geobacter metallireducens GS-15 | COG0747: ABC-type dipeptide transport system, periplasmic component [Geobacter metallireducens GS-15] | | | | |
| 12201, 12202 | 57505780 | 44 | 2.00E-33 | Campylobacter upsallensis RM3195 | Phosphoglycolate phosphatase [Campylobacter upsallensis gb EAL52841.1 Phosphoglycolate phosphatase [Campylobacter upsallensis RM3195] | | | 3.1.3.18 | |
| 12203, 12204 | 34556865 | 58 | 3.00E-72 | Wolinella succinogenes DSM 1740 | PUTATIVE D-ALANINE--D-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09580.1 PUTATIVE D-ALANINE--D-ALANINE LIGASE [Wolinella succinogenes] sp Q7MA71 DDL_WOLSU D-alanine--D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase) | | | 6.3.2.4 | |
| 12205, 12206 | 21241197 | 25 | 7.00E-08 | Xanthomonas axonopodis pv. citri str. 306 | hypothetical protein XAC0424 [Xanthomonas axonopodis pv. citri str. 306] gb AAM35315.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 12207, 12208 | 34556865 | 53 | 2.00E-46 | Wolinella succinogenes DSM 1740 | PUTATIVE D-ALANINE--D-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09580.1 PUTATIVE D-ALANINE--D-ALANINE LIGASE [Wolinella succinogenes] sp Q7MA71 DDL_WOLSU D-alanine--D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase) | | | 6.3.2.4 | |
| 12209, 12210 | 21674916 | 59 | 4.00E-35 | Chlorobium tepidum TLS | 2-Isopropylmalate synthase [Chlorobium tepidum TLS] gb AAM73323.1 2- isopropylmalate synthase [Chlorobium tepidum TLS] | | | 4.1.3.12 | |
| 1221, 1222 | 29349121 | 46 | 1.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | gb AAO79818.1 D-alanine--D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine--D-alanine ligase (D- alanylalanine synthetase) (D-Ala-D-Ala ligase) | | | 6.3.2.4 | |
| 12211, 12212 | 48855427 | 42 | 6.00E-48 | Cytophaga hutchinsonii | COG1521: Putative transcriptional regulator, homolog of Bvg accessory factor [Cytophaga hutchinsonii] | | | | |
| 12213, 12214 | 52840981 | 40 | 8.00E-15 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | GGDEF domain protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123139.1 hypothetical protein lpp0809 [Legionella pneumophila str. Paris] gb AAU26833.1 GGDEF domain protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH11957.1 hypothetical protein [Legionella pneumophila str. Paris] | | | 2.7.3.- | |
| 12215, 12216 | 48890755 | 37 | 8.00E-29 | Trichodesmium erythraeum IMS101 | COG4121: Uncharacterized conserved protein [Trichodesmium erythraeum IMS101] | | | | |

| | | | | | | | | |
|-------------------------------------|----------|----|----------|---|---|--|----|----------|
| 12217, 12218, 12219, 12220 | 34557949 | 47 | 1.00E-64 | Wolinella succinogenes DSM 1740 | ADENYLATE CYCLASE [Wolinella succinogenes DSM 1740] emb CAE10864.1 ADENYLATE CYCLASE [Wolinella succinogenes] | | | 4.6.1.1 |
| 12221, 12222 | 48832299 | 48 | 4.00E-35 | Magnetococcus sp. MC-1 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | 3.1.4.17 |
| 12227, 12228 | 34557782 | 43 | 1.00E-16 | Wolinella succinogenes DSM 1740 | SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes DSM 1740] emb CAE10864.1 SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes] | | | 2.7.3.- |
| 12229, 12230 | 34558149 | 22 | 1.00E-10 | Wolinella succinogenes DSM 1740 | COG1505: Serine proteases of the peptidase family S9A [Crocospaera watsonii WH 8501] | Nostoc sp. PCC 7120 DNA, complete genome | 86 | 6.00E-07 |
| 12231, 12232 | 53735717 | 54 | 8.00E-77 | Crocospaera watsonii WH 8501 | COG0162: Tyrosyl-tRNA synthetase [Cytophaga hutchinsonii] | | | 6.1.1.1 |
| 12235, 12236 | 48853873 | 65 | 1.00E-92 | Cytophaga hutchinsonii | COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242] putative integral membrane protein [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282423.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir F81335 probable integral membrane protein Cj1276c [imported] - Campylobacter jejuni (strain NCTC 11168) | | | |
| 12239, 12240 | 46142567 | 35 | 1.00E-31 | Methanococcoides burtonii DSM 6242 | MutS-like ATPases involved in mismatch repair, family 1 [Thermoanaerobacter tengcongensis MB4] gb AAM24886.1 MutS-like ATPases involved in mismatch repair, family 1 [Thermoanaerobacter tengcongensis MB4] sp Q8R9D0 MUS2_THETN MutS2 protein | | | |
| 12241, 12242 | 6968709 | 35 | 2.00E-43 | Campylobacter jejuni subsp. jejuni NCTC 11168 | hypothetical protein plu3521 [Photothabdus luminescens subsp. laumondii TTO1] emb CAE15894.1 unnamed protein product [Photothabdus luminescens subsp. laumondii TTO1] PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09185.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes] | | | 2.7.-.- |
| 12243, 12244 | 20808111 | 28 | 1.00E-10 | Thermoanaerobacter tengcongensis MB4 | hypothetical protein PG0290 [Porphyromonas gingivalis W83] ref NP_904610.1 hypothetical protein PG0280 [Porphyromonas gingivalis W83] | | | |
| 12245, 12246 | 34396443 | 33 | 2.00E-21 | Photothabdus luminescens subsp. laumondii TTO1 | | | | |
| | 37527394 | 29 | 6.00E-20 | Wolinella succinogenes DSM 1740 | | | | |
| | 34558670 | 50 | 4.00E-47 | Porphyromonas gingivalis W83 | | | | |

| | | | | | | | | | | |
|---|----------------------------------|----------------|----------------------------------|--|---|---|----|----------|-------|----------|
| 12247, 12248, 12249, 12250, 1225, 1226 | 57233639 46119473 48855955 | 38 48 45 | 3.00E-36 9.00E-40 6.00E-16 | Dehalococcoides ethenogenes 195 Crocosphaera watsonii WH 8501 Cytophaga hutchinsonii | DNA internalization-related competence protein ComEC/Rec2 [Dehalococcoides ethenogenes 195] gb AAW39144.1 DNA internalization- related competence protein ComEC/Rec2 [Dehalococcoides ethenogenes 195] COG2200: FOG: EAL domain [Crocosphaera watsonii WH 8501] COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] hypothetical protein BT0882 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75989.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482] | | | | | 1.11.1.5 |
| 12251, 12252, 12255, 12256 | 29346292 48832069 | 50 36 | 1.00E-43 8.00E-31 | Bacteroides thetaitaomicron VPI-5482 Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] putative outer membrane protein [Bacteroides fragilis YCH46] dbj BAD49029.1 putative outer membrane protein [Bacteroides fragilis YCH46] COG1666: Uncharacterized protein conserved in bacteria [Desulfovibrio desulfuricans G20] | | | | | 2.7.3.- |
| 12257, 12258, 12259, 12260 | 53713571 23474131 | 29 50 | 4.00E-22 1.00E-42 | Bacteroides fragilis YCH46 Desulfovibrio desulfuricans G20 | | | | | | |
| 12261, 12262, 12263, 12264 | 48855897 13542183 | 64 48 | 9.00E-99 3.00E-46 | Cytophaga hutchinsonii Thermoplasma volcanium GSS1 Wolinella succinogenes DSM 1740 | COG1123: ATPase components of various ABC-type transport systems, contain duplicated ATPase [Cytophaga hutchinsonii] Pyruvate-formate lyase-activating enzyme [Thermoplasma volcanium GSS1] hypothetical protein WS0005 [Wolinella succinogenes DSM 1740] emb CAE09179.1 hypothetical protein [Wolinella succinogenes] predicted Zn-dependent protease and their inactivated homologs [Thermoanaerobacter tengcongensis MB4] gb AAM25841.1 predicted Zn- dependent protease and their inactivated homologs [Thermoanaerobacter tengcongensis MB4] | Desc:Staphylococ- us epidermidis ORF nucleic acid sequence SEQ ID NO:1156. Org:Staphylococcus epidermidis | 91 | 4.00E-11 | 1.8.- | |
| 12265, 12266 | 34556464 | 30 | 5.00E-07 | | | | | | | 1.97.1.4 |
| 12269, 12270 | 20809066 | 48 | 6.00E-67 | Thermoanaerobact er tengcongensis MB4 | | | | | | 4.1.2.25 |
| | | | | | | | | | | 3.4.24.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|----------|----------|
| 12271, 12272 | 17934430 | 38 | 4.00E-29 | Agrobacterium tumefaciens str. C58 | chemotaxis methyltransferase [Agrobacterium tumefaciens str. C58] gb AAL41536.1 chemotaxis methyltransferase [Agrobacterium tumefaciens str. C58] gb AAK86332.1 AGR_C_914p [Agrobacterium tumefaciens str. C58] gb AAC25078.1 CheR homolog [Agrobacterium tumefaciens str. C58] ref NP_353547.1 hypothetical protein AGR_C_914 [Agrobacterium tumefaciens str. C58] pir AB2640 chemotaxis methyltransferase [Imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir C97422 cheR homolog (AF044495) [Imported] - Agrobacterium tumefaciens (strain C58, Cereon) | | | | 2.1.1.80 |
| 12273, 12274 | 39935922 | 23 | 7.00E-10 | Rhodopseudomonas palustris CGA009 | hypothetical protein RPA2857 [Rhodopseudomonas palustris CGA009] emb CAE28298.1 unknown protein [Rhodopseudomonas palustris CGA009] | | | | |
| 12275, 12276 | 38482512 | 35 | 2.00E-38 | Photobacterium luminescens | putative toxin transporter [Photobacterium luminescens] HlyD family secretion protein [Pseudomonas putida KT2440] gb AAN70493.1 HlyD family secretion protein [Pseudomonas putida KT2440] | | | | |
| 12277, 12278 | 26991604 | 35 | 5.00E-10 | Pseudomonas putida KT2440 | hypothetical protein PBPRB0708 [Photobacterium profundum SS9] emb CAG22580.1 hypothetical protein [Photobacterium profundum] | | | | |
| 12279, 12280 | 54302387 | 41 | 3.00E-59 | Photobacterium profundum SS9 | weak similarity to chloramphenicol phosphotransferase [Mesorhizobium loti MAFF303099] db BAB50605.1 mlr3789 [Mesorhizobium loti MAFF303099] | | | | |
| 12281, 12282 | 13473252 | 34 | 2.00E-22 | Mesorhizobium loti MAFF303099 | COG0500: SAM-dependent methyltransferases [Nostoc punctiforme PCC 73102] | | | | |
| 12285, 12286 | 23129257 | 39 | 6.00E-23 | Nostoc punctiforme PCC 73102 | 2-isopropylmalate synthase [Clostridium acetobutylicum ATCC 824] gb AAK78254.1 2-isopropylmalate synthase [Clostridium acetobutylicum ATCC 824] pir C96933 2-isopropylmalate synthase [Imported] - Clostridium acetobutylicum sp Q97MC5 LEU1_CLOAB 2-isopropylmalate synthase (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase) DIGUANYLATE CYCLASE (FRAGMENT) [Wolnelia succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolnelia succinogenes] | | | 4.1.3.12 | |
| 12289, 12290 | 34557407 | 31 | 3.00E-30 | Wolnelia succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolnelia succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolnelia succinogenes] | | | | 2.7.3.- |
| 12291, 12292 | 34556560 | 36 | 2.00E-38 | Wolnelia succinogenes DSM 1740 | ENSANGP00000000374 [Anopheles gambiae] putative endonuclease [Bacteroides fragilis YCH46] db BAD48444.1 putative endonuclease [Bacteroides fragilis YCH46] | | | | 3.4.21.- |
| 12293, 12294 | 31195611 | 57 | 4.00E-87 | Anopheles gambiae | | | | | 3.1.30.- |
| 12295, 12296 | 53712986 | 46 | 1.00E-12 | Bacteroides fragilis YCH46 | | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|--|----------|
| 12297, 12298 | 48854967 | 55 | 4.00E-25 | Cytophaga hutchinsonii | COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii] hypothetical protein PA0172 [Pseudomonas aeruginosa PAO1] pir[E83623 hypothetical protein PA0172 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_248862.1 hypothetical protein PA0172 [Pseudomonas aeruginosa PAO1] | | | | | |
| 12299, 12300 | 9946005 | 33 | 2.00E-28 | Pseudomonas aeruginosa PAO1 | pilus assembly protein [Bradyrhizobium japonicum USDA 110] dbj BAC46701.1 pilus assembly protein [Bradyrhizobium japonicum USDA 110] | | | | | 2.7.3.- |
| 12301, 12302 | 27376547 | 32 | 3.00E-28 | Bradyrhizobium japonicum USDA 110 | hypothetical protein MMP1269 [Methanococcus maripaludis S2] emb CAF30825.1 unnamed protein product [Methanococcus maripaludis S2] | | | | | |
| 12303, 12304 | 45358832 | 50 | 5.00E-23 | Methanococcus maripaludis S2 | lactoylglutathione lyase and related protein [Bacteroides fragilis YCH46] dbj BAD50032.1 lactoylglutathione lyase and related protein [Bacteroides fragilis YCH46] | | | | | 4.4.1.5 |
| 12309, 12310 | 53714574 | 65 | 9.00E-46 | Bacteroides fragilis YCH46 | L-aspartate oxidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78290.1 L-aspartate oxidase [Bacteroides thetaiotaomicron VPI- 5482] | | | | | 1.4.3.16 |
| 1231, 1232 | 29348593 | 50 | 1.00E-33 | Bacteroides thetaitaomicron VPI-5482 | histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_712713.1 two-component hybrid sensor and regulator [Leptospira interrogans serovar Lai str. 56601] gb AAN49731.1 two-component hybrid sensor and regulator [Leptospira interrogans serovar lai str. 56601] gb AAS70039.1 histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | | 2.7.3.- |
| 12313, 12314 | 45657316 | 34 | 6.00E-26 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein WS2202 [Wollinella succinogenes DSM 1740] emb CAE11192.1 hypothetical protein [Wollinella succinogenes] | | | | | |
| 12315, 12316 | 34558477 | 36 | 8.00E-15 | Wollinella succinogenes DSM 1740 | hypothetical protein WS1135 [Wollinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wollinella succinogenes] hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1 hypothetical protein [Bacteroides fragilis YCH46] | Wollinella succinogenes, complete genome; segment 4/7 | 92 | 3.00E-11 | | |
| 12317, 12318 | 34557509 | 53 | 8.00E-55 | Wollinella succinogenes DSM 1740 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] | | | | | 2.7.3.- |
| 12321, 12322 | 53712193 | 32 | 7.00E-14 | Bacteroides fragilis YCH46 | COG4261: Predicted acyltransferase [Cytophaga hutchinsonii] | | | | | |
| 12323, 12324 | 24214122 | 35 | 8.00E-32 | Leptospira interrogans serovar Lai str. 56601 | | | | | | |
| 12325, 12326 | 48856697 | 30 | 4.00E-22 | Cytophaga hutchinsonii | | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---------------------------------------|---|--|----|----------|-----------|
| 12329, 12330 | 34557169 | 37 | 9.00E-47 | Wolinella succinogenes DSM 1740 | ACRIFLAVIN RESISTANCE A PRECURSOR [Wolinella succinogenes DSM 1740] emb CAE09884.1 ACRIFLAVIN RESISTANCE A PRECURSOR [Wolinella succinogenes] | | | | |
| 1233, 1234 | 15606535 | 25 | 1.00E-09 | Aquifex aeolicus VF5 | hypothetical protein aq_1332 [Aquifex aeolicus VF5] gb AAC07320.1 hypothetical protein [Aquifex aeolicus VF5] pir D70415 conserved hypothetical protein aq_1332 - Aquifex aeolicus | | | | |
| 12331, 12332 | 34556919 | 27 | 8.00E-09 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0496 [Wolinella succinogenes DSM 1740] emb CAE09634.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 12333, 12334 | 34557848 | 59 | 2.00E-74 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-2-methylthioadenine synthetase [Wolinella succinogenes DSM 1740] emb CAE10563.1 conserved hypothetical protein- 2-methylthioadenine synthetase [Wolinella succinogenes] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 89 | 5.00E-07 | 1.8-- |
| 12335, 12336 | AAW9853 5 | 56 | 1.00E-36 | Wolinella succinogenes DSM 1740 | Desc:H. pylori GHPO 1479 protein. Org:Helicobacter pylori dnaA, probable chromosomal replication initiator protein [Wolinella succinogenes DSM 1740] emb CAE09174.1 dnaA, probable chromosomal replication initiator protein [Wolinella succinogenes] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 95 | 2.00E-08 | 1.8-- |
| 12337, 12338 | 34556459 | 64 | 4.00E-82 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0806 [Wolinella succinogenes DSM 1740] emb CAE09919.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 12339, 12340 | 34557204 | 38 | 8.00E-40 | Wolinella succinogenes DSM 1740 | (MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228] gb EAL56394.1 MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228]) | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 89 | 4.00E-07 | 1.8-- |
| 12341, 12342 | 57168872 | 56 | 2.00E-54 | Campylobacter coli RM2228 | hypothetical protein WS1513 [Wolinella succinogenes DSM 1740] emb CAE10561.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 12345, 12346 | 34557846 | 43 | 9.00E-35 | Wolinella succinogenes DSM 1740 | COG0006: Xaa-Pro aminopeptidase [Crocospaera watsonii WH 8501] | | | | 3.4, 11.9 |
| 12347, 12348 | 45525497 | 37 | 2.00E-38 | Crocospaera watsonii WH 8501 | COG0195: Transcription elongation factor [Cytophaga hutchinsonii] | | | | |
| 1235, 1236 | 48853541 | 41 | 7.00E-29 | Cytophaga hutchinsonii | phosphatase, YrbI family [Campylobacter jejuni RM1221] gb AAW34543.1 phosphatase, YrbI family [Campylobacter jejuni RM1221] | | | | 3.1, 3.29 |
| 12351, 12352 | 57236960 | 57 | 6.00E-29 | Campylobacter jejuni RM1221 | | | | | |

| | | | | | | | | |
|-------------------------------------|----------------------------------|----------------|----------------------------------|--|--|---|-------------|--------------------|
| 12353, 12354, 12357, 12358 | 24374626 14600147 29654029 | 47 39 48 | 3.00E-35 4.00E-47 1.00E-26 | Shewanella oneidensis MR-1 Coxiella burnetii Coxiella burnetii RSA 493 | hypothetical protein SO3107 [Shewanella oneidensis MR-1] gb AAN56113.1 conserved hypothetical protein [Shewanella oneidensis MR-1] S-adenosyl-dependent methyl transferase [Coxiella burnetii] NDP-hexose 3-C-methyltransferase TyICIII [Coxiella burnetii] RSA 493 gb AAO90235.1 NDP-hexose 3-C-methyltransferase TyICIII [Coxiella burnetii] RSA 493 | | | 2.1.1.- 2.1.1.- |
| 12363, 12364 | 57240289 | 56 | 4.00E-35 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55403.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 12369, 12370 | 6968343 | 42 | 2.00E-34 | Campylobacter jejuni subsp. jejuni NCTC 11168 | alanine racemase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81364 alanine racemase (EC 5.1.1.1) Cj0905c [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282058.1 alanine racemase [Campylobacter jejuni subsp. jejuni NCTC 11168] sp Q9PP26 ALR_CAMJE Alanine racemase | | | 5.1.1.1 |
| 12371, 12372 | 48134374 | 46 | 9.00E-07 | Anabaena variabilis ATCC 29413 | hypothetical protein Avar03006438 [Anabaena variabilis ATCC 29413] | | | |
| 12373, 12374 | 34558185 | 81 | 1.00E-103 | Wolinella succinogenes DSM 1740 | RNA POLYMERASE SIGMA FACTOR [Wolinella succinogenes DSM 1740] emb CAE10900.1 RNA POLYMERASE SIGMA FACTOR [Wolinella succinogenes] | Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis DNA, complete genome | 83 7.00E-28 | |
| 12375, 12376 | 48855741 | 62 | 1.00E-46 | Cytophaga hutchinsonii | COG0151: Phosphoribosylamine-glycine ligase [Cytophaga hutchinsonii] | | | 6.3.4.13 |
| 12377, 12378 | 30020326 | 50 | 8.00E-40 | Bacillus cereus ATCC 14579 | Dihydrofolate reductase [Bacillus cereus ATCC 14579] gb AAP09158.1 Dihydrofolate reductase [Bacillus cereus ATCC 14579] | | | 1.5.1.3 |
| 12379, 12380 | 56459673 | 65 | 7.00E-51 | Idiomarina loihensis L2TR | Nucleoside-diphosphate-sugar epimerase [Idiomarina loihensis L2TR] gb AAV81405.1 Nucleoside-diphosphate-sugar epimerase [Idiomarina loihensis L2TR] | Vibrio parahaemolyticus DNA, chromosome 1, complete sequence | 90 5.00E-12 | 5.1.3.- |
| 12383, 12384 | 48855208 | 53 | 6.00E-52 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | |
| 12385, 12386 | 29348675 | 58 | 6.00E-74 | Bacteroides thetaiotaomicron VPI-5482 | exonuclease ABC subunit C [Bacteroides thetaiotaomicron VPI-5482] gb AAO78372.1 exonuclease ABC subunit C [Bacteroides thetaiotaomicron VPI-5482] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|--|----------|
| 12387, | 34556919 | 27 | 8.00E-09 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0496 [Wolinella succinogenes DSM 1740] emb CAE09634.1 hypothetical protein [Wolinella succinogenes] outer membrane assembly protein [Bacteroides fragilis YCH46] dbj BAD47737.1 outer membrane assembly protein [Bacteroides fragilis YCH46] | | | | |
| 12389, | | | | Bacteroides fragilis YCH46 | | | | | |
| 12390 | 53712279 | 31 | 1.00E-37 | Cytophaga hutchinsonii | COG0719: ABC-type transport system involved in Fe-S cluster assembly, permease component [Cytophaga hutchinsonii] | | | | |
| 1239, | 48854815 | 64 | 2.00E-48 | Geobacter metallireducens GS-15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | | 2.7.3.- |
| 12391, | 48845271 | 47 | 6.00E-54 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1362 [Wolinella succinogenes DSM 1740] emb CAE10430.1 hypothetical protein [Wolinella succinogenes] hypothetical protein BT4373 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79478.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482] | | | | |
| 12393, | | | | Bacteroides thetaitaomicron VPI-5482 | | | | | |
| 12394 | 34557715 | 26 | 4.00E-16 | Cytophaga hutchinsonii | COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii] hypothetical protein BF5085 [Bacteroides fragilis YCH46] dbj BAD49830.1 hypothetical protein [Bacteroides fragilis YCH46] COG1887: Putative glycosylglycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC [Desulfovibrio desulfuricans G20] | | | | |
| 12395, | 29349781 | 31 | 1.00E-16 | Desulfovibrio desulfuricans G20 | putative teichoic acid biosynthesis protein F [Bacteroides thetaiotaomicron VPI-5482] gb AAO76757.1 putative teichoic acid biosynthesis protein F [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 12396 | | | | Bacteroides thetaitaomicron VPI-5482 | | | | | |
| 12397, | 48853591 | 57 | 1.00E-85 | Yersinia enterocolitica | putative NTP-binding protein [Yersinia enterocolitica] KIAA1706-like protein [Danio rerio] ref NP_991322.1 hypothetical protein zgc:77395 [Danio rerio] | | | | |
| 12398 | 53714372 | 28 | 6.00E-07 | Danio rerio | phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides fragilis YCH46] dbj BAD49800.1 phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides fragilis YCH46] | | | | 5.3.1.16 |
| 12403, | 23474406 | 25 | 3.00E-12 | Bacteroides thetaitaomicron VPI-5482 | | | | | |
| 12404 | | | | Yersinia enterocolitica | | | | | |
| 12405, | 29347060 | 39 | 1.00E-18 | Danio rerio | | | | | |
| 12406 | | | | | | | | | |
| 1241, | 55163168 | 34 | 9.00E-25 | | | | | | |
| 1242 | 37682097 | 27 | 3.00E-08 | | | | | | |
| 12411, | | | | | | | | | |
| 12412 | | | | | | | | | |
| 12413, | | | | | | | | | |
| 12414 | 53714342 | 51 | 8.00E-48 | Bacteroides fragilis YCH46 | | | | | |
| 12415, | | | | | | | | | |
| 12416 | 3769356 | 40 | 2.00E-29 | Helicobacter pylori Listeria monocytogenes str. 1/2a F6854 | icaA1 [Helicobacter pylori] DNA helicase II, putative [Listeria monocytogenes str. 1/2a F6854] gb EAL06694.1 DNA helicase II, putative [Listeria monocytogenes str. 1/2a F6854] | | | | 3.1.21.4 |
| 12417, | | | | | | | | | |
| 12418 | 47095888 | 39 | 4.00E-21 | | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|-----------|--|--|--|----|----------|----------|
| 12419, 12420 | 45523887 | 26 | 1.00E-09 | Crocospaera watsonii WH 8501 | COG5433: Transposase [Crocospaera watsonii WH 8501] hypothetical protein BT2330 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77437.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 12425, 12426 | 29347740 | 28 | 9.00E-25 | Bacteroides thetaitaomlcron VPI-5482 | related to ATP-dependent dsDNA exonuclease (SBCC) [Desulfotalea psychrophila Lsv54] embjCAG35255.1 related to ATP-dependent dsDNA exonuclease (SBCC) [Desulfotalea psychrophila Lsv54] | | | 3.1.11.- | |
| 12427, 12428 | 51244378 | 32 | 7.00E-32 | Desulfotalea psychrophila Lsv54 | response regulator lytR [Bacillus anthracis str. 'Ames Ancestor'] ref YP_039431.1 response regulator [Bacillus thuringiensis serovar konkukian str. 97-27] ref YP_031532.1 response regulator LytR [Bacillus anthracis str. Sterne] ref NP_847837.1 response regulator LytR [Bacillus anthracis str. Ames] ref NP_653909.1 response_reg, Response regulator receiver domain [Bacillus anthracis str. A2012] gb AAP29323.1 response regulator LytR [Bacillus anthracis str. Ames] gb AAT62659.1 response regulator [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT35470.1 response regulator LytR [Bacillus anthracis str. 'Ames Ancestor'] gb AAT57582.1 response regulator LytR [Bacillus anthracis str. Sterne] sp Q81JL3 LYT_BACAN Sensory transduction protein lytT | | | 3.1.1.61 | |
| 12429, 12430 | 47778428 | 35 | 2.00E-22 | Bacillus anthracis str. 'Ames 'Ancestor' | putative UDP-glucose 4-epimerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75730.1 putative UDP-glucose 4-epimerase [Bacteroides thetaiotaomicron VPI-5482] | | | 5.1.3.2 | |
| 12437, 12438 | 29346033 | 45 | 1.00E-18 | Bacteroides thetaitaomlcron VPI-5482 | COG3459: Cellobiose phosphorylase [Microbulbifer degradans 2-40] | Clostridium thermocellum YIM4 cellobiose phosphorylase (cbp) gene, complete cds | 83 | 1.00E-11 | 2.4.1.20 |
| 12443, 12444 | 48862917 | 75 | 1.00E-121 | Microbulbifer degradans 2-40 | glycosyl transferase [Pyrococcus furiosus DSM 3638] gb AAL81482.1 glycosyl transferase [Pyrococcus furiosus DSM 3638] Desc:Drosophila melanogaster polypeptide SEQ ID NO 20241. Org:Drosophila melanogaster | | | | |
| 12447, 12448 | 18977730 | 29 | 6.00E-12 | Pyrococcus furiosus DSM 3638 | | | | | |
| 12451, 12452 | ABB6448 3 | 24 | 1.00E-07 | | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|---------------|
| 12455, 12456 | 18977973 | 33 | 3.00E-07 | Pyrococcus furiosus DSM 3638 | transcriptional regulatory protein, asnC family [Pyrococcus furiosus DSM 3638] gblAAL81725.1] transcriptional regulatory protein, asnC family [Pyrococcus furiosus DSM 3638] gblAAD20389.1] transcriptional regulator LrpA [Pyrococcus furiosus] plj]T46972 transcription regulator lrpA [validated] - Pyrococcus furiosus pdb]111G]B Chain B, Crystal Structure Of The Lrp-Like Transcriptional Regulator From The Archaeon Pyrococcus Furiosus (pdb]111G]A Chain A, Crystal Structure Of The Lrp-Like Transcriptional Regulator From The Archaeon Pyrococcus Furiosus sp]P42180]REG7_PYRFU HTH-type transcriptional regulator lrpA | | | | |
| 12457, 12458 | 29348750 | 38 | 7.00E-30 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3341 [Bacteroides thetaiotaomicron VPI-5482] gblAAO78447.1] conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 12459, 12460 | 29347220 | 45 | 7.00E-15 | Bacteroides thetaiotaomicron VPI-5482 | GAF domain-containing protein, involved in signal transduction [Bacteroides thetaiotaomicron VPI-5482] gblAAO76917.1] GAF domain-containing protein, involved in signal transduction [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 12461, 12462 | 53715640 | 44 | 4.00E-52 | Bacteroides fragilis YCH46 | Xaa-Pro aminopeptidase [Bacteroides fragilis YCH46] dbj]BAD51098.1] Xaa-Pro aminopeptidase [Bacteroides fragilis YCH46] | | | | 3.4.13.9 |
| 12463, 12464 | 53685204 | 25 | 3.00E-12 | Desulfotobacterium hafnense DCB-2 | COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Desulfotobacterium hafnense DCB-2] | | | | 1.2.1.2 |
| 12465, 12466 | 45505347 | 41 | 8.00E-35 | Anabaena variabilis ATCC 29413 | COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Anabaena variabilis ATCC 29413] | | | | 1.1.1.10 0 |
| 12467, 12468 | 42522911 | 31 | 2.00E-21 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd1393 [Bdellovibrio bacteriovorus HD100] emb]CAE79284.1] hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100] | | | | |
| 12469, 12470 | 34556972 | 51 | 3.00E-16 | Wolinella succinogenes DSM 1740 | SERINE ACETYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb]CAE09687.1] SERINE ACETYLTRANSFERASE [Wolinella succinogenes] | | | | |
| 1247, 1248 | 20807036 | 39 | 5.00E-23 | Thermoanaerobacter tengcongensis MB4 | predicted ATPase or kinase [Thermoanaerobacter tengcongensis MB4] gblAAM23811.1] predicted ATPase or kinase [Thermoanaerobacter tengcongensis MB4] | | | | |
| 12471, 12472 | 21673150 | 45 | 5.00E-53 | Chlorobium tepidum TLS | isoleucyl-tRNA synthetase [Chlorobium tepidum TLS] gblAAM71557.1] isoleucyl-tRNA synthetase [Chlorobium tepidum TLS] | | | | 6.1.1.5 |
| 12473, 12474 | 48853745 | 32 | 6.00E-50 | Cytophaga hutchinsonii | hypothetical protein Chut02003380 [Cytophaga hutchinsonii] | | | | |
| 12477, 12478 | 48833211 | 45 | 2.00E-31 | Magnetococcus sp. MC-1 | COG2114: Adenylate cyclase, family 3 (some proteins contain HAMP domain) [Magnetococcus sp. MC-1] | | | | 4.6.1.1 |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|----|------------------|
| 12479, 12480 | 53711472 | 40 | 1.00E-13 | Bacteroides fragilis YCH46 | signal peptidase I [Bacteroides fragilis YCH46] dbj BAD46930.1 signal peptidase I [Bacteroides fragilis YCH46] | | | |
| 12485, 12486 | 34558058 | 64 | 1.00E-100 | Wolinella succinogenes DSM 1740 | OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE [Wolinella succinogenes DSM 1740] emb CAE10773.1 OXYGEN- INDEPENDENT COPROPORPHYRINOGEN III OXIDASE [Wolinella succinogenes] | Wolinella succinogenes, complete genome; segment 5/7 | 83 | 1.00E-08 1.-.-.- |
| 12489, 12490 | 16648662 | 27 | 1.00E-11 | Edwardsiella ictaluri | UDP-glucose 4-epimerase [Edwardsiella ictaluri] | | | 5.1.3.- |
| 12491, 12492 | 15643366 | 56 | 8.00E-77 | Thermotoga maritima MSB8 | hypothetical protein TM0600 [Thermotoga maritima MSB8] gb AAD35685.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir A72358 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | |
| 12493, 12494 | 48839007 | 27 | 8.00E-27 | Methanosarcina barkeri str. fusaro | COG1721: Uncharacterized conserved protein (some members contain a von Willebrand factor type A (VWA) domain) [Methanosarcina barkeri str. fusaro] | | | |
| 12495, 12496 | 34557573 | 38 | 9.00E-39 | Wolinella succinogenes DSM 1740 | SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 12497, 12498 | 46202456 | 42 | 7.00E-51 | Magnetospirillum magnetotacticum MS-1 | COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1] | | | 2.7.3.- |
| 12499, 12500 | 46202456 | 29 | 7.00E-12 | Magnetospirillum magnetotacticum MS-1 | COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1] | | | |
| 12501, 12502 | 39937848 | 39 | 3.00E-25 | Rhodopseudomonas palustris CGA009 | response regulator receiver:histidine kinase [Rhodopseudomonas palustris CGA009] emb CAE30230.1 response regulator receiver:histidine kinase [Rhodopseudomonas palustris CGA009] | | | 2.7.3.- |
| 12505, 12506 | 20091276 | 47 | 2.00E-22 | Methanosarcina acetivorans C2A | response regulator receiver [Methanosarcina acetivorans C2A] gb AAM05831.1 response regulator receiver [Methanosarcina acetivorans str. C2A] | | | 2.7.3.- |
| 12507, 12508 | 53735771 | 34 | 3.00E-18 | Crocospaera watsonii WH 8501 | hypothetical protein Cwat03001968 [Crocospaera watsonii WH 8501] | | | |
| 12509, 12510 | 48853585 | 34 | 4.00E-31 | Cytophaga hutchinsonii | COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii] | | | |
| 12511, 12512 | 48856170 | 29 | 3.00E-24 | Cytophaga hutchinsonii | COG1452: Organic solvent tolerance protein OstA [Cytophaga hutchinsonii] | | | |
| 12515, 12516 | 48853184 | 25 | 6.00E-09 | Ferroplasma acidarmanus | COG3547: Transposase and inactivated derivatives [Ferroplasma acidarmanus] | | | |
| 12517, 12518 | 53763644 | 28 | 4.00E-11 | Anabaena variabilis ATCC 29413 | COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Anabaena variabilis ATCC 29413] | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|--|----|----------|--|
| 12519, 12520 | 14521387 | 24 | 8.00E-09 | Pyrococcus abyssi GE5 | hypothetical protein PAB0790 [Pyrococcus abyssi GE5] emb CAB50093.1 Hypothetical protein [Pyrococcus abyssi] pir H75098 hypothetical protein PAB0790 - Pyrococcus abyssi (strain Orsay) | | | 3.6.1.- |
| 12521, 12522 | 16077745 | 66 | 1.00E-116 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU06770 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12497.1 yeeB [Bacillus subtilis subsp. subtilis str. 168] gb AA066475.1 yeeB [Bacillus subtilis] pir F69792 hypothetical protein yeeB - Bacillus subtilis | 97 | 2.00E-07 | Bacillus subtilis complete genome (section 4 of 21): from 611631 to 813719 |
| 12525, 12526 | 48832594 | 29 | 2.00E-17 | Magnetococcus sp. MC-1 | COG0438: Glycosyltransferase [Magnetococcus sp. MC-1] | | | |
| 12527, 12528 | 51891165 | 48 | 5.00E-30 | Symbiobacterium thermophilum IAM 14863 | hypothetical protein STH27 [Symbiobacterium thermophilum IAM 14863] dbj BAD39012.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863] | | | |
| 12529, 12530 | 48844902 | 50 | 2.00E-37 | Geobacter metallireducens GS 15 | COG0582: Integrase [Geobacter metallireducens GS-15] | | | |
| 1253, 1254 | 48895710 | 39 | 8.00E-18 | Trichodesmium erythraeum IMS101 | hypothetical protein Tery02000770 [Trichodesmium erythraeum IMS101] | | | |
| 12531, 12532 | 53730726 | 28 | 5.00E-12 | Dechloromonas aromatica RCB | COG0642: Signal transduction histidine Kinase [Dechloromonas aromatica RCB] | | | |
| 12535, 12536 | 34397371 | 71 | 1.00E-105 | Porphyrromonas gingivalis W83 | lysyl-tRNA synthetase [Porphyrromonas gingivalis W83] ref NP_905535.1 lysyl-tRNA synthetase [Porphyrromonas gingivalis W83] sp Q7MUV7 SYK_PORGI Lysyl-tRNA synthetase (Lysine-tRNA ligase) (LysRS) | 97 | 7.00E-10 | Mesoplasma florum L1 complete genome |
| 12537, 12538 | 45157173 | 41 | 3.00E-53 | Escherichia coli | endonuclease [Escherichia coli] sp P25239 T257_ECOLI Type IIS restriction enzyme Eco57I (Endonuclease Eco57I) [Includes: Adenine-specific methyltransferase activity Eco57IA (M.Eco57IA)] | | | |
| 12539, 12540 | 57238087 | 53 | 3.00E-23 | Campylobacter jejuni RM1221 | peptidase, M23/M37 family [Campylobacter jejuni RM1221] gb AAW35670.1 peptidase, M23/M37 family [Campylobacter jejuni RM1221] | | | 3.5.1.- |
| 12541, 12542 | 48892348 | 27 | 8.00E-23 | Trichodesmium erythraeum IMS101 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] fibronectin/fibrinogen-binding protein, putative [Campylobacter upsaliensis RM3195] gb EAL53665.1 fibronectin/fibrinogen-binding protein, putative [Campylobacter upsaliensis RM3195] | | | |
| 12543, 12544 | 57242203 | 44 | 3.00E-18 | Campylobacter upsaliensis RM3195 | | | | |
| 12545, 12546 | 23126057 | 22 | 3.00E-07 | Nostoc punctiforme PCC 73102 | COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----------|----------|
| 12547, 12548 | 48853732 | 48 | 1.00E-28 | Cytophaga hutchinsonii | COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Cytophaga hutchinsonii] | | | 3.1.1.61 |
| 12549, 12550 | 48853733 | 31 | 3.00E-07 | Cytophaga hutchinsonii | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | |
| 12551, 12552 | 48853332 | 34 | 1.00E-35 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |
| 12555, 12556 | 52840989 | 29 | 3.00E-20 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | N-acetylneuraminic acid synthetase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU26841.1 N-acetylneuraminic acid synthetase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] hypothetical protein sir2110 [Synecocystis sp. PCC 6803] dbj BAA18047.1 | | 4.1.3.19 | |
| 12557, 12558 | 16330639 | 44 | 1.00E-13 | Synechocystis sp. PCC 6803 | sir2110 [Synecocystis sp. PCC 6803] pir S75486 hypothetical protein sir2110 - Synechocystis sp. (strain PCC 6803) | | | |
| 12561, 12562 | 34557050 | 50 | 6.00E-31 | Wolinella succinogenes DSM 1740 | FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolinella succinogenes DSM 1740] emb CAE09765.1 FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolinella succinogenes] | | | |
| 12563, 12564 | 57238052 | 58 | 4.00E-65 | Campylobacter jejuni RM1221 | ABC transporter, ATP-binding protein [Campylobacter jejuni RM1221] gb AAW35635.1 ABC transporter, ATP-binding protein [Campylobacter jejuni RM1221] | | 1.8.-.- | |
| 12567, 12568 | 14591451 | 36 | 1.00E-15 | Pyrococcus horikoshii OT3 | hypothetical protein PH1688 [Pyrococcus horikoshii OT3] dbj BAA30800.1 352aa long hypothetical protein [Pyrococcus horikoshii OT3] pir JA71176 hypothetical protein PH1688 - Pyrococcus horikoshii | | | |
| 1257, 1258 | 53715375 | 34 | 3.00E-24 | Bacteroides fragilis YCH46 | hypothetical protein BF4091 [Bacteroides fragilis YCH46] dbj BAD50833.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 12571, 12572 | 45357761 | 37 | 1.00E-33 | Methanococcus maripaludis S2 | ABC-type iron(III) transport system, ATP binding protein [Methanococcus maripaludis S2] emb CAF29754.1 ABC-type iron(III) transport system, ATP binding protein [Methanococcus maripaludis S2] | | 3.4.21.- | |
| 12573, 12574 | 57284261 | 26 | 9.00E-07 | Staphylococcus aureus subsp. aureus COL | iron compound ABC transporter, iron compound-binding protein, putative [Staphylococcus aureus subsp. aureus COL] ref YP_185549.1 iron compound ABC transporter, iron compound-binding protein, putative [Staphylococcus aureus subsp. aureus COL] | | | |
| 12575, 12576 | 14591054 | 35 | 7.00E-13 | Pyrococcus horikoshii OT3 | ferrichrome transport ATP-binding protein [Pyrococcus horikoshii OT3] dbj BAA30335.1 250aa long hypothetical ferrichrome transport ATP-binding protein [Pyrococcus horikoshii OT3] pir E71067 probable ferrichrome transport ATP-binding protein - Pyrococcus horikoshii | | | |

| | | | | | | | | | | |
|-----------------|-------------|----|-----------|--------------|--|---|---|----|----------|----------|
| 12577, 12578 | 2314022 | 59 | 2.00E-71 | 26695 | Helicobacter pylori | cysteinyI-tRNA synthetase (cysS) [Helicobacter pylori 26695] pir F64630 cysteine-tRNA ligase (EC 6.1.1.16) - Helicobacter pylori (strain 26695) ref NP_207679.1 cysteinyI-tRNA synthetase (cysS) [Helicobacter pylori 26695] sp P41259 SYC_HELPY CysteinyI-tRNA synthetase (Cysteine-tRNA ligase) (CysRS) | Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 8 of 197 of the complete genome | 91 | 6.00E-10 | 6.1.1.16 |
| 12579, 12580 | 9654643 | 31 | 4.00E-27 | N16961 | Vibrio cholerae O1 biovar eltor str. | lipopolysaccharide biosynthesis protein, putative [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229892.1 lipopolysaccharide biosynthesis protein, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir E82349 probable lipopolysaccharide biosynthesis protein VC0235 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 12581, 12582 | AA4378 0 | 22 | 6.00E-08 | | | Desc:Amino acid sequence of the eps4 of Lactobacillus helveticus LH59. Org:Lactobacillus helveticus | | | | |
| 12585, 12586 | 52082595 | 56 | 2.00E-81 | 14580 | Bacillus licheniformis ATCC | hypothetical protein BL02386 [Bacillus licheniformis ATCC 14580] gb AAU25748.1 hypothetical protein BL02386 [Bacillus licheniformis ATCC 14580] | | | | |
| 12587, 12588 | 20808081 | 38 | 3.00E-24 | MB4 | Thermoanaerobact er tengcongensis | hypothetical protein TTE1654 [Thermoanaerobacter tengcongensis MB4] gb AAM24856.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4] sp Q8R9F8 MRZ_THETN Protein mraZ | | | | |
| 12589, 12590 | 32472855 | 32 | 6.00E-17 | ba1tica SH 1 | Rhodopirellula ba1tica SH 1 | transposase [Rhodopirellula ba1tica SH 1] emb CAD73534.1 transposase [Pirellula sp.] | | | | |
| 1259, 1260 | 53715375 | 36 | 8.00E-19 | YCH46 | Bacteroides fragilis | hypothetical protein BF4091 [Bacteroides fragilis YCH46] dbj BAD50833.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 12591, 12592 | 34557638 | 66 | 3.00E-31 | 1740 | Wolinella succinogenes DSM | QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes] | | | | |
| 12593, 12594 | 53713904 | 74 | 1.00E-110 | YCH46 | Bacteroides fragilis | excinuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46] | Coxiella burnetii strain RSA 493, section 1 of 7 of the complete genome | 93 | 6.00E-07 | |
| 12597, 12598 | 33861871 | 33 | 8.00E-13 | CCMP1986 | Prochlorococcus marinus subsp. pastoris str. | Ketol-acid reductoisomerase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19774.1 Ketol-acid reductoisomerase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] sp Q7V0F0 ILVC_PROMP Ketol-acid reductoisomerase (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydroxyacyl reductoisomerase) | | | | 1.1.1.86 |

| | | | | | | | | | |
|-----------------|--------------|----|----------|--|---|--|--|--|---------|
| 12599, 12600 | 46578913 | 29 | 1.00E-17 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | iron-sulfur cluster-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94980.1 iron-sulfur cluster-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAM06751.1 glutamate-ammonia ligase [Methanosarcina acetivorans C2A] str. C2A] | | | | 6.3.1.2 |
| 12601, 12602 | 20092196 | 60 | 3.00E-48 | Methanosarcina acetivorans C2A | hypothetical protein DP2996 [Desulfohalobium psychrophila LSV54] emb CAG37725.1 unknown protein [Desulfohalobium psychrophila LSV54] | | | | |
| 12603, 12604 | 51246848 | 22 | 3.00E-07 | Desulfohalobium psychrophila LSV54 | thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861359.1 thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449] | | | | 2.5.1.3 |
| 12605, 12606 | 32263380 | 51 | 3.00E-17 | Helicobacter hepaticus ATCC 51449 | hypothetical protein Chut02003091 [Cytophaga hutchinsonii] | | | | |
| 12613, 12614 | 48854003 | 30 | 1.00E-18 | Cytophaga hutchinsonii | COG0726: Predicted xylanase/chitin deacetylase [Magnetospirillum magnetotacticum MS-1] | | | | |
| 12615, 12616 | 46201112 | 30 | 3.00E-22 | Magnetospirillum magnetotacticum MS-1 | flavocytochrome C sulfide dehydrogenase [Aquifex aeolicus VF5] gb AAC06555.1 flavocytochrome C sulfide dehydrogenase [Aquifex aeolicus VF5] pir B70321 flavocytochrome C sulfide dehydrogenase - Aquifex aeolicus | | | | 1.8.2.- |
| 12617, 12618 | 15605781 | 42 | 1.00E-57 | Aquifex aeolicus VF5 | hypothetical iron-regulated protein [Photobacterium profundum SS9] emb CAG21164.1 hypothetical iron-regulated protein [Photobacterium profundum] | | | | |
| 12619, 12620 | 54309946 | 31 | 2.00E-21 | Photobacterium profundum SS9 | iron transport protein [Synechocystis sp. PCC 6803] dbj BAA16842.1 iron transport protein [Synechocystis sp. PCC 6803] pir S74691 iron transport protein - Synechocystis sp. (strain PCC 6803) | | | | |
| 12625, 12626 | 16329434 | 51 | 1.00E-72 | Synechocystis sp. PCC 6803 | Carbamoyltransferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19705.1 Carbamoyltransferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] | | | | 2.-.-.- |
| 12629, 12630 | 33861802 | 41 | 2.00E-32 | Prochlorococcus marinus subsp. pastoris str. CCMP1986 | DNA POLYMERASE III SUBUNITS GAMMA AND TAU [Wolfinella succinogenes DSM 1740] emb CAE11094.1 DNA POLYMERASE III SUBUNITS GAMMA AND TAU [Wolfinella succinogenes] | | | | 2.7.7.7 |
| 12633, 12634 | 34558379 | 38 | 1.00E-45 | Wolfinella succinogenes DSM 1740 | Desc: Mouse protein kinase #5. Org: Mus sp | | | | 2.7.1.- |
| 12635, 12636 | AAY4394 1 | 41 | 1.00E-09 | Wolfinella succinogenes DSM 1740 | CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN [Wolfinella succinogenes DSM 1740] emb CAE11050.1 CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN [Wolfinella succinogenes] | | | | 6.3.5.5 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|------------------|
| 12639, 12640 | 34558810 | 33 | 1.00E-27 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09525.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | 2.7.3.- |
| 12641, 12642 | 45655762 | 29 | 8.00E-25 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | response regulator [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714779.1 probable protein contain EAL family signaling protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51794.1 probable protein contain EAL family signaling protein [Leptospira interrogans serovar lai str. 56601] gb AAS72208.1 response regulator [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 12643, 12644 | 13474570 | 29 | 2.00E-26 | Mesorhizobium loti MAFF303099 | hypothetical protein mlf5479 [Mesorhizobium loti MAFF303099] db BAB51925.1 mlf5479 [Mesorhizobium loti MAFF303099] | | | |
| 12649, 12650 | 57238220 | 50 | 3.00E-22 | Campylobacter jejuni RM1221 | DNA polymerase III, delta prime subunit, homolog [Campylobacter jejuni RM1221] gb AAW35803.1 DNA polymerase III, delta prime subunit, homolog [Campylobacter jejuni RM1221] | | | 2.7.7.7 |
| 1265, 1266 | 53714275 | 44 | 7.00E-27 | Bacteroides fragilis YCH46 | UDP-N-acetylenolpyruvoylglucosamine reductase [Bacteroides fragilis YCH46] db BAD49733.1 UDP-N-acetylenolpyruvoylglucosamine reductase [Bacteroides fragilis YCH46] | | | 1.1.1.15 8 |
| 12651, 12652 | 48857483 | 42 | 5.00E-18 | Clostridium thermocellum ATCC 27405 | COG2217: Cation transport ATPase [Clostridium thermocellum ATCC 27405] | | | 3.6.3.4 |
| 12653, 12654 | 53612326 | 49 | 8.00E-53 | Azotobacter vinelandii | COG1391: Glutamine synthetase adenylyltransferase [Azotobacter vinelandii] | | | 2.7.7.42 |
| 12655, 12656 | 54311293 | 36 | 3.00E-35 | Xenopus laevis | Unknown (protein for MGC:86416) [Xenopus laevis] | | | 1.1.3.8 |
| 12657, 12658 | 34558426 | 59 | 6.00E-74 | Wolinella succinogenes DSM 1740 | CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes DSM 1740] emb CAE1114.1 CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes] | Efflatouniella aegyptiaca CAD (r) gene, partial cds | 87 | 4.00E-08 6.3.5.5 |
| 12659, 12660 | 34557622 | 75 | 4.00E-89 | Wolinella succinogenes DSM 1740 | PREPROTEIN TRANSLOCASE SECA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10337.1 PREPROTEIN TRANSLOCASE SECA SUBUNIT [Wolinella succinogenes] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 79 | 1.00E-32 |
| 12663, 12664 | 53766156 | 34 | 2.00E-17 | Rubrobacter xylanophilus DSM 9941 | COG1583: Uncharacterized protein predicted to be involved in DNA repair (RAMP superfamily) [Rubrobacter xylanophilus DSM 9941] | | | |
| 12665, 12666 | 57237408 | 40 | 4.00E-19 | Campylobacter jejuni RM1221 | phosphatase, Ppx/GppA family [Campylobacter jejuni RM1221] gb AAW34991.1 phosphatase, Ppx/GppA family [Campylobacter jejuni RM1221] | | | 3.6.1.40 |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|----------|----------|
| 12667, 12668 | 29346111 | 55 | 8.00E-58 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0701 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75808.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | Bacteroides fragilis YCH46 DNA, complete genome | 86 | 5.00E-07 | | |
| 12669, 12670 | 34556867 | 54 | 1.00E-47 | Wolinella succinogenes DSM 1740 | PUTATIVE HOLLIDAY JUNCTION DNA HELICASE [Wolinella succinogenes DSM 1740] emb CAE09582.1 PUTATIVE HOLLIDAY JUNCTION DNA HELICASE [Wolinella succinogenes] sp Q7MA70 RUVA_WOLSU Holliday junction DNA helicase ruva conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55132.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | | |
| 12671, 12672 | 57240739 | 51 | 4.00E-24 | Campylobacter lari RM2100 | | | | | | |
| 12673, 12674 | 34558426 | 73 | 4.00E-95 | Wolinella succinogenes DSM 1740 | CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes DSM 1740] emb CAE11141.1 CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes] aspartate carbamoyltransferase [Campylobacter lari RM2100] gb EAL55577.1 aspartate carbamoyltransferase [Campylobacter lari RM2100] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 1/6 | 81 | 5.00E-41 | 6.3.5.5 | |
| 12675, 12676 | 57240463 | 54 | 3.00E-40 | Campylobacter lari RM2100 | | | | | | 2.1.3.2 |
| 12677, 12678 | 42628871 | 31 | 2.00E-10 | Haemophilus influenzae R2846 | COG0147: Anthranilate/para-aminobenzoate synthases component I [Haemophilus influenzae R2846] | | | | | 4.1.3.- |
| 12679, 12680 | 34557248 | 36 | 2.00E-25 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09963.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes] | | | | | |
| 12681, 12682 | 34557101 | 40 | 2.00E-19 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0690 [Wolinella succinogenes DSM 1740] emb CAE09816.1 conserved hypothetical protein [Wolinella succinogenes] GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes DSM 1740] emb CAE09195.1 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes] | | | | 4.-.-.- | |
| 12683, 12684 | 34556480 | 65 | 5.00E-76 | Wolinella succinogenes DSM 1740 | | | | | | 2.6.1.16 |
| 12685, 12686 | 15606338 | 64 | 2.00E-87 | Aquifex aeolicus VF5 | phosphate transport ATP binding protein [Aquifex aeolicus VF5] gb AAC07112.1 phosphate transport ATP binding protein [Aquifex aeolicus VF5] pir G70390 phosphate transport ATP binding protein - Aquifex aeolicus sp O67154 PSTB_AQUAE Phosphate import ATP-binding protein pstB (Phosphate-transporting ATPase) [ABC phosphate transporter] hypothetical protein aq_367 [Aquifex aeolicus VF5] gb AAC06656.1 hypothetical protein [Aquifex aeolicus VF5] pir G70332 conserved hypothetical protein aq_367 - Aquifex aeolicus | | | | 3.4.21.- | |
| 12687, 12688 | 15605874 | 29 | 6.00E-09 | Aquifex aeolicus VF5 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 12689, 12690 | 34556462 | 70 | 3.00E-48 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0003 [Wolinella succinogenes DSM 1740] emb CAE09177.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 12691, 12692 | 15606018 | 42 | 1.00E-34 | Aquifex aeolicus VF5 | hypothetical protein aq_563 [Aquifex aeolicus VF5] gb AAC06808.1 hypothetical protein [Aquifex aeolicus VF5] pir G70350 conserved hypothetical protein aq_563 - Aquifex aeolicus | | | 2.7.3.- |
| 12693, 12694 | 52842284 | 57 | 9.00E-88 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28136.1 reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | 2.7.7.49 |
| 12695, 12696 | 34556575 | 60 | 5.00E-97 | Wolinella succinogenes DSM 1740 | PUTATIVE FORMATE DEHYDROGENASE, ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE09290.1 PUTATIVE FORMATE DEHYDROGENASE, ALPHA SUBUNIT [Wolinella succinogenes] | | | 1.2.1.2 |
| 12697, 12698 | 53714874 | 38 | 3.00E-26 | Bacteroides fragilis YCH46 | putative outer membrane protein [Bacteroides fragilis YCH46] dbj BAD50332.1 putative outer membrane protein [Bacteroides fragilis YCH46] | | | |
| 12701, 12702 | 24375806 | 25 | 1.00E-16 | Shewanella oneidensis MR-1 | GGDEF domain protein [Shewanella oneidensis MR-1] gb AAN57293.1 GGDEF domain protein [Shewanella oneidensis MR-1] | | | 2.7.3.- |
| 12703, 12704 | 6967929 | 65 | 1.00E-89 | Campylobacter jejuni subsp. jejuni NCTC 11168 | hypothetical protein Cj0458c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281645.1 hypothetical protein Cj0458c [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81390 hypothetical protein Cj0458c [Imported] - Campylobacter jejuni (strain NCTC 11168) | | | 1.8.- |
| 12705, 12706 | 57240857 | 64 | 1.00E-60 | Campylobacter lari RM2100 | tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter lari RM2100] gb EAL55250.1 tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter lari RM2100] | | | 1.8.- |
| 12707, 12708 | 34558204 | 30 | 6.00E-12 | Wolinella succinogenes DSM 1740 | GUANOSINE PENTAPHOSPHATE PHOSPHOHYDROLASE GPPA [Wolinella succinogenes DSM 1740] emb CAE10919.1 GUANOSINE PENTAPHOSPHATE PHOSPHOHYDROLASE GPPA [Wolinella succinogenes] | | | 3.6.1.11 |
| 12711, 12712 | 29348760 | 61 | 2.00E-94 | Bacteroides thetaiotaomicron VPI-5482 | cysteinyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78457.1 cysteinyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | 6.1.1.16 |
| 12713, 12714 | 34397363 | 38 | 4.00E-25 | Porphyromonas gingivalis W83 | conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_905527.1 hypothetical protein PG1362 [Porphyromonas gingivalis W83] | | | 2.1.1.- |
| 12715, 12716 | 29348664 | 50 | 3.00E-37 | Bacteroides thetaiotaomicron VPI-5482 | putative N6-adenine-specific DNA methylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78361.1 putative N6-adenine-specific DNA methylase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.1.1.- |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|--|--|--|--|----------|
| 12719, 12720 | 29346657 | 29 | 2.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1247 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76354.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 12721, 12722 | 54302195 | 27 | 2.00E-10 | Photobacterium profundum SS9 | hypothetical protein PBPRB0515 [Photobacterium profundum SS9] emb CAG22388.1 hypothetical protein [Photobacterium profundum] | | | | |
| 12723, 12724 | 15896082 | 40 | 2.00E-15 | Clostridium acetobutylicum ATCC 824 | S-adenosylmethionine-dependent methyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK80771.1 S-adenosylmethionine- dependent methyltransferase [Clostridium acetobutylicum ATCC 824] pir H97247 S-adenosylmethionine-dependent methyltransferase [imported] - Clostridium acetobutylicum | | | | |
| 12727, 12728 | 48858098 | 54 | 2.00E-29 | Clostridium thermocellum ATCC 27405 | COG2172: Anti-sigma regulatory factor (Ser/Thr protein kinase) [Clostridium thermocellum ATCC 27405] | | | | |
| 12729, 12730 | 48854896 | 69 | 1.00E-104 | Cytophaga hutchinsonii | COG0825: Acetyl-CoA carboxylase alpha subunit [Cytophaga hutchinsonii] | | | | 6.4.1.2 |
| 12731, 12732 | 51244185 | 23 | 6.00E-08 | Desulfotalea psychrophila LSv54 | hypothetical protein DP0333 [Desulfotalea psychrophila LSv54] emb CAG35062.1 unknown protein [Desulfotalea psychrophila LSv54] | | | | |
| 12733, 12734 | 42629381 | 48 | 1.00E-32 | Haemophilus influenzae R2846 | hypothetical protein Hfla103001140 [Haemophilus influenzae R2846] | | | | |
| 12737, 12738 | 6969058 | 53 | 3.00E-65 | Campylobacter jejuni subsp. jejuni NCTC 11168 | UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diamine ligase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282769.1 UDP-N- acetylmuramoylalanyl-D-glutamate-2,6-diamine ligase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir G81260 UDP-N-acetylmuramoylalanyl-D- glutamate-2,6-diamino-pimelate ligase (EC 6.3.2.13) Cj1641 [imported] - Campylobacter jejuni (strain NCTC 11168) sp O69290 MURE_CAMJE UDP- N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase (UDP-N- acetylmuramyl-tripeptide synthetase) (Meso-diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase) | | | | 6.3.2.13 |
| 12739, 12740 | 34557608 | 26 | 2.00E-24 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1243 [Wolinella succinogenes DSM 1740] emb CAE10323.1 conserved hypothetical protein [Wolinella succinogenes] | | | | 2.7.3.- |
| 12743, 12744 | 34556884 | 47 | 4.00E-60 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0457 [Wolinella succinogenes DSM 1740] emb CAE09599.1 conserved hypothetical protein [Wolinella succinogenes] protein of unknown function / conserved hypothetical protein TIGR00296 [Dehalococcoides ethenogenes 195] gb AAW39480.1 protein of unknown function / conserved hypothetical protein TIGR00296 [Dehalococcoides ethenogenes 195] | | | | 1.-.-.- |
| 12745, 12746 | 57233975 | 29 | 2.00E-21 | Dehalococcoides ethenogenes 195 | | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|------------|--|---|--|--|--|----------|
| 12747, 12748 | 28210824 | 44 | 5.00E-47 | E88 | Clostridium tetani | transcriptional regulatory protein [Clostridium tetani E88] gb AAO35705.1 transcriptional regulatory protein [Clostridium tetani E88] | | | | 2.7.3.- |
| 12749, 12750 | 23097516 | 37 | 7.00E-28 | | Oceanobacillus lheyensis HTE831 | stage V sporulation protein C [Oceanobacillus lheyensis HTE831] dbj BAC12017.1 stage V sporulation protein C (peptidyl-rRNA hydrolase (PTH)) [Oceanobacillus lheyensis HTE831] sp Q8CXP8 PTH_OCEIH Peptidyl-rRNA hydrolase (PTH) | | | | 3.1.1.29 |
| 1275, 1276 | 57169064 | 54 | 1.00E-22 | RM2228 | Campylobacter coli | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 12751, 12752 | 6968169 | 49 | 1.00E-37 | NCTC 11168 | Campylobacter jejuni subsp. jejuni | putative 16S rRNA processing protein [Campylobacter jejuni subsp. jejuni] NCTC 11168] pir C81342 probable 16S rRNA processing protein Cj0712 [Imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281884.1 putative 16S rRNA processing protein [Campylobacter jejuni subsp. jejuni] NCTC 11168] sp Q9PPJ5 RIMM_CAMJE Probable 16S rRNA processing protein rimM | | | | |
| 12753, 12754 | 33861802 | 44 | 1.00E-43 | CCMP1986 | Prochlorococcus marinus subsp. pastoris str. | Carbamoyltransferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19705.1 Carbamoyltransferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] | | | | 2.-.- |
| 12757, 12758 | 33864985 | 39 | 2.00E-31 | WH 8102 | Synechococcus sp. | putative N-acetylglucosamine-6-phosphate 2-epimerase/N-acetyl... [Synechococcus sp. WH 8102] emb CAE06964.1 putative N- acetylglucosamine-6-phosphate 2-epimerase/N-acetylglucosamine-6- phosphatase [Synechococcus sp. WH 8102] | | | | 5.1.3.- |
| 12763, 12764 | 38233578 | 47 | 9.00E-30 | 13129 | Corynebacterium diphtheriae NCTC | hypothetical protein DIP0983 [Corynebacterium diphtheriae NCTC 13129] emb CAE49501.1 Conserved hypothetical protein [Corynebacterium diphtheriae] | | | | 1.1.1.85 |
| 12765, 12766 | 34557329 | 37 | 3.00E-45 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS0940 [Wolinella succinogenes DSM 1740] emb CAE10044.1 conserved hypothetical protein [Wolinella succinogenes] | | | | 2.7.3.- |
| 12767, 12768 | 1769991 | 52 | 4.00E-19 | | Geobacillus stearothermophilus | site-specific DNA-methyltransferase [Geobacillus stearothermophilus] | | | | 2.1.1.72 |
| 12769, 12770 | 50083438 | 54 | 2.00E-50 | ADP1 | Acinetobacter sp. | hypothetical protein ACIAD0152 [Acinetobacter sp. ADP1] emb CAG67126.1 conserved hypothetical protein [Acinetobacter sp. ADP1] COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii] | | | | |
| 1277, 1278 | 48853912 | 48 | 2.00E-33 | | Cytophaga hutchinsonii | | | | | |

| | | | | | | | | | | |
|--------|----------|----|----------|-----|--|---|--|--|--|----------|
| 12773, | 27383072 | 40 | 1.00E-13 | 110 | Bradyrhizobium japonicum USDA | probable HspC2 heat shock protein [Bradyrhizobium japonicum USDA 110] dbj BAC53226.1 bfr7961 [Bradyrhizobium japonicum USDA 110] | | | | |
| 12774 | | | | | | transposase [Methanosarcina acetivorans C2A] gb AAM07337.1 | | | | |
| 12775, | 20092782 | 51 | 1.00E-55 | | Methanosarcina acetivorans C2A | transposase [Methanosarcina acetivorans str. C2A] | | | | |
| 12776 | | | | | | | | | | |
| 12777, | 48854025 | 37 | 1.00E-16 | | Cytophaga hutchinsonii | hypothetical protein Chut02003116 [Cytophaga hutchinsonii] | | | | |
| 12778 | | | | | | | | | | |
| 12779, | 15793038 | 64 | 1.00E-58 | | Neisseria meningitidis Z2491 | hypothetical protein NMA0004 [Neisseria meningitidis Z2491] emb CAB83324.1 hypothetical protein NMA0004 [Neisseria meningitidis Z2491] gb AAF40709.1 cell filamentation protein Fic-related protein Fic-related protein NMB0255 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain Z2491 serogroup A) ref NP_273311.1 cell filamentation protein Fic-related protein [Neisseria meningitidis MC58] | | | | |
| 12780 | | | | | | | | | | |
| 12781, | 48854252 | 26 | 6.00E-08 | | Cytophaga hutchinsonii | COG1125: ABC-type proline/glycine betaine transport systems, ATPase components [Cytophaga hutchinsonii] | | | | |
| 12782 | | | | | | | | | | |
| 12783, | 48854252 | 26 | 7.00E-08 | | Cytophaga hutchinsonii | COG1125: ABC-type proline/glycine betaine transport systems, ATPase components [Cytophaga hutchinsonii] | | | | |
| 12784 | | | | | | | | | | |
| 12789, | 56808559 | 30 | 6.00E-07 | | Streptococcus pyogenes M49 591 | COG3754: Lipopolysaccharide biosynthesis protein [Streptococcus pyogenes M49 591] | | | | |
| 12790 | | | | | | | | | | |
| 1279, | | | | | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | precortin methylase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS72156.1 precortin methylase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | 2.1.1.13 |
| 1280 | 45655710 | 34 | 3.00E-26 | | Neisseria meningitidis MC58 | conserved hypothetical protein [Neisseria meningitidis MC58] pir A81107 conserved hypothetical protein NMB1232 [imported] - Neisseria meningitidis (strain MC58 serogroup B) ref NP_274256.1 hypothetical protein NMB1232 [Neisseria meningitidis MC58] | | | | 2.1.1.- |
| 12791, | 7226471 | 41 | 2.00E-16 | | Rhodopirellula ballica SH 1 | hypothetical protein RB711 [Rhodopirellula ballica SH 1] emb CAD71713.1 conserved hypothetical protein [Pirellula sp.] | | | | |
| 12792 | | | | | | | | | | |
| 12795, | 32471046 | 44 | 9.00E-30 | | Vibrio parahaemolyticus | hypothetical ATP-binding protein [Vibrio parahaemolyticus] | | | | |
| 12796 | | | | | | | | | | |
| 12797, | 22036085 | 37 | 1.00E-11 | | Bacteroides fragilis YCH46 | hypothetical protein BF0635 [Bacteroides fragilis YCH46] dbj BAD47384.1 | | | | |
| 12798 | | | | | | | | | | |
| 12799, | 53711926 | 38 | 1.00E-09 | | Methanosarcina acetivorans C2A | hypothetical protein MA0186 [Methanosarcina acetivorans C2A] gb AAM03641.1 hypothetical protein (multi-domain) [Methanosarcina acetivorans str. C2A] | | | | 2.4.1.- |
| 12800 | | | | | | | | | | |
| 12801, | 20089086 | 40 | 5.00E-35 | | Methanosarcina acetivorans C2A | | | | | |
| 12802 | | | | | | | | | | |

| | | | | | | | | |
|---|--------------------------------------|----------------|----------------------------------|---|---|---|----------|-------------------------------|
| 12805, 12806, 12807, 12808 1281, 1282 | 21674062 32417538 AAG8240 1 | 49 30 28 | 1.00E-54 2.00E-18 1.00E-07 | Chlorobium tepidum TLS Neurospora crassa | preprotein translocase SecA subunit [Chlorobium tepidum TLS] gb AAM72469.1 preprotein translocase SecA subunit [Chlorobium tepidum TLS] hypothetical protein [Neurospora crassa] gb EAA34777.1 hypothetical protein [Neurospora crassa] Desc:S. epidermidis open reading frame protein sequence SEQ ID NO:1896. Org:Staphylococcus epidermidis | Arabis thaliana chromosome 1 BAC F8K7 sequence, complete sequence 95 | 2.00E-09 | |
| 12813, 12814 12815, 12816 12817, 12818 | 57240977 34557665 46202294 | 62 41 41 | 5.00E-98 3.00E-41 5.00E-42 | Campylobacter lari RM2100 Wolinella succinogenes DSM 1740 Magnetospirillum magnetotacticum MS-1 | DNA-directed RNA polymerase, beta subunit [Campylobacter lari RM2100] gb EAL55370.1 DNA-directed RNA polymerase, beta subunit [Campylobacter lari RM2100] DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] COG0840: Methyl-accepting chemotaxis protein [Magnetospirillum magnetotacticum MS-1] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 6.00E-32 | 2.7.3.- 2.7.3.- 2.7.3.- |
| 12819, 12820 12821, 12822 12823, 12824 | 24214445 24374136 28262612 | 24 56 52 | 9.00E-20 5.00E-84 2.00E-74 | Leptospira interrogans serovar Lai str. 56601 Shewanella oneidensis MR-1 Rickettsia sibirica 246 | two-component hybrid sensor and regulator [Leptospira interrogans serovar Lai str. 56601] gb AAN49944.1 two-component hybrid sensor and regulator [Leptospira interrogans serovar lai str. 56601] hypothetical protein SO2593 [Shewanella oneidensis MR-1] gb AAN55623.1 conserved hypothetical protein [Shewanella oneidensis MR-1] unknown [Rickettsia sibirica 246] ref ZP_00142707.1 hypothetical protein [Rickettsia sibirica 246] | | | 2.7.3.- 1.4.1.2 1.4.1.2 |
| 12825, 12826 12827, 12828 | 15606018 34556481 | 30 44 | 9.00E-16 1.00E-37 | Aquifex aeolicus VF5 Wolinella succinogenes DSM 1740 | hypothetical protein aq_563 [Aquifex aeolicus VF5] gb AAC06808.1 hypothetical protein [Aquifex aeolicus VF5] pir G70350 conserved hypothetical protein aq_563 - Aquifex aeolicus hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes] | | | 2.7.3.- |

| | | | | | | |
|---|--|----------------------|--|--|--|--|
| 12829, 12830, 12831, 12832, 12833, 12834 | 20807293 48853434 48856692 48831001 | 33 68 40 38 | 1.00E-39 3.00E-73 4.00E-15 2.00E-53 | Thermoanaerobacter tengcongensis MB4 Cytophaga hutchinsonii Cytophaga hutchinsonii Magnetococcus sp. MC-1 | Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Thermoanaerobacter tengcongensis MB4] gb AAM24068.1 Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Thermoanaerobacter tengcongensis MB4] sp Q8RBK5 PURL_THETN Phosphoribosylformylglycinamide synthase II (FGAM synthase II) COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] COG0304: 3-oxoacyl-(acyl-carrier-protein) synthase [Cytophaga hutchinsonii] COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] sulfite synthesis pathway protein CysQ [Bacteroides fragilis YCH46] db BAD48413.1 sulfite synthesis pathway protein CysQ [Bacteroides fragilis YCH46] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] COG1088: dTDP-D-glucose 4,6-dehydratase [Cytophaga hutchinsonii] COG0517: FOG: CBS domain [Chloroflexus aurantiacus] putative putative two-component sensor C10035 [Campylobacter fetus] | 6.3.5.3 2.7.7.24 2.7.3.- 3.1.3.25 2.7.3.- 2.7.3.- 2.7.3.- 2.7.3.- |
| 12835, 12836 | 53712955 | 50 | 2.00E-41 | Bacteroides fragilis YCH46 | | |
| 12837, 12838 | 34557246 | 55 | 3.00E-78 | Wolinella succinogenes DSM 1740 | | |
| 12839, 12840 | 34557246 | 33 | 3.00E-32 | Wolinella succinogenes DSM 1740 | | |
| 12843, 12844 | 45658172 | 30 | 2.00E-31 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | | |
| 12847, 12848 | 48846045 | 43 | 2.00E-22 | Geobacter metallireducens GS-15 | | 2.7.3.- |
| 12849, 12850 | 48846045 | 34 | 1.00E-09 | Geobacter metallireducens GS-15 | | |
| 1285, 1286 | 48853435 | 70 | 5.00E-55 | Cytophaga hutchinsonii | Prochlorococcus marinus MIT9313 complete genome; segment 1/7 | 94 1.00E-06 4.2.1.46 1.1.1.20 5 |
| 12851, 12852 | 53796794 | 41 | 9.00E-20 | Chloroflexus aurantiacus | | |
| 12857, 12858 | 28974235 | 41 | 4.00E-43 | Campylobacter fetus | | 2.7.3.- |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|----------|
| 12859, 12860 | 23129844 | 29 | 1.00E-11 | Nostoc punctiforme PCC 73102 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] | | | 2.7.3.- |
| 12861, 12862 | 48846045 | 48 | 1.00E-20 | Geobacter metallireducens GS-15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 12863, 12864 | 23012315 | 49 | 4.00E-22 | Magnetospirillum magnetotacticum MS-1 | COG0834: ABC-type amino acid transport/signal transduction systems, periplasmic component/domain [Magnetospirillum magnetotacticum MS-1] | | | 4.2.- |
| 12865, 12866 | 21674940 | 48 | 2.00E-31 | Chlorobium tepidum TLS | hypothetical protein CT2131 [Chlorobium tepidum TLS] gb AAM73347.1 | | | |
| 12867, 12868 | 40062786 | 31 | 1.00E-09 | uncultured bacterium 439 | conserved domain protein [uncultured bacterium 439] | | | |
| 1287, 1288 | AAY80126 | 29 | 2.00E-17 | Methanosarcina barkeri str. fusaro | Desc:Sphaerotilus natans SnaBI endonuclease protein SEQ ID NO:4. Org:Sphaerotilus natans | | | |
| 12871, 12872 | 48841399 | 28 | 2.00E-07 | Methanosarcina barkeri str. fusaro | COG2244: Membrane protein involved in the export of O-antigen and teichoic acid [Methanosarcina barkeri str. fusaro] | | | |
| 12873, 12874 | 14591370 | 35 | 2.00E-08 | Pyrococcus horikoshii OT3 | transcriptional regulator [Pyrococcus horikoshii OT3] | | | |
| 12875, 12876 | ABP73922 | 46 | 5.00E-53 | Pyrococcus horikoshii | spi059256[REG7_PYRHO HTH-type transcriptional regulator lrpA dbj BAA30704.1 141aa long hypothetical transcriptional regulator [Pyrococcus horikoshii OT3] pir H71037 probable transcription regulator - Pyrococcus horikoshii Desc:Candida albicans essential protein SEQ ID NO 7759. Org:Candida albicans | | | 4.2.1.36 |
| 12877, 12878 | 32477370 | 35 | 5.00E-19 | Rhodopirella baltica SH 1 | phosphoribosylaminoimidazole-succinocarboxamide synthase [Rhodopirella baltica SH 1] emb CAD77441.1 | | | 6.3.2.6 |
| 12879, 12880 | 30249527 | 50 | 7.00E-28 | Nitrosomonas europaea ATCC 19718 | phosphoribosylaminoimidazole-succinocarboxamide synthase [Pirella sp.] putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718] | | | |
| 12881, 12882 | 41724578 | 30 | 4.00E-24 | Dechloromonas aromatica RCB | COG0842: ABC-type multidrug transport system, permease component [Dechloromonas aromatica RCB] | | | |
| 12883, 12884 | 48855825 | 29 | 9.00E-18 | Cytophaga hutchinsonii | COG0304: 3-oxoacyl-(acyl-carrier-protein) synthase [Cytophaga hutchinsonii] | | | 2.3.1.41 |
| 12885, 12886 | 15603871 | 37 | 2.00E-40 | Pasteurella multocida subsp. multocida str. Pm70 | hypothetical protein PM2006 [Pasteurella multocida subsp. multocida str. Pm70] gb AAK04090.1 unknown [Pasteurella multocida subsp. multocida str. Pm70] | | | |

| | | | | | | | | |
|-------------------------------------|----------|----|----------|---|--|--|--|----------|
| 12887, 12888 | 29348444 | 36 | 1.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO78141.1 carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 12889, 12890, 12891, 12892 | 45658026 | 36 | 2.00E-13 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | CMP-N-acetylneuraminic acid synthetase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711786.1 Probable acylneuraminase cytidyltransferase [Leptospira interrogans serovar Lai str. 56601] gb AAN4804.1 Probable acylneuraminase cytidyltransferase [Leptospira interrogans serovar lai str. 56601] gb AAS70749.1 CMP-N- acetylneuraminic acid synthetase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.7.7.43 |
| 12893, 12894 | 48853351 | 63 | 1.00E-50 | Cytophaga hutchinsonii | COG4804: Uncharacterized conserved protein [Cytophaga hutchinsonii] conserved hypothetical protein TIGR00486 [Campylobacter coli RM2228] gb EAL57503.1 conserved hypothetical protein TIGR00486 [Campylobacter coli RM2228] | | | |
| 12895, 12896 | 5740646 | 50 | 5.00E-29 | Campylobacter lari RM2100 | UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate ligase [Campylobacter lari RM2100] gb EAL55039.1 UDP-N-acetylmuramoylalanine- D-glutamate-2, 6-diaminopimelate ligase [Campylobacter lari RM2100] | | | 6.3.2.13 |
| 12897, 12898 | 34556481 | 37 | 1.00E-15 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 12899, 12900 | 34556481 | 49 | 6.00E-55 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes] | | | 2.7.3.- |
| 129, 130 | 48854463 | 55 | 1.00E-35 | Cytophaga hutchinsonii | COG0193: Peptidyl-tRNA hydrolase [Cytophaga hutchinsonii] | | | 3.1.1.29 |
| 12901, 12902 | 57505271 | 43 | 4.00E-41 | Campylobacter upsaliensis RM3195 | nicotinate (nicotinamide) nucleotide adenyltransferase [Campylobacter upsaliensis RM3195] gb EAL53192.1 nicotinate (nicotinamide) nucleotide adenyltransferase [Campylobacter upsaliensis RM3195] | | | 2.7.7.18 |
| 12903, 12904 | 32263376 | 59 | 2.00E-53 | Helicobacter hepaticus ATCC 51449 | phosphoenolpyruvate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861355.1 phosphoenolpyruvate synthase [Helicobacter hepaticus ATCC 51449] | | | 2.7.9.2 |
| 12905, 12906 | 45658435 | 52 | 6.00E-65 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | adenylate/guanylate cyclase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS71158.1 adenylate/guanylate cyclase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 4.6.1.2 |

| | | | | | | | | |
|---|--|------------------------|--|--|--|--|-------------|----------|
| 12907, 12908 | AAU3593 1 | 56 | 2.00E-18 | | Desc:Helicobacter pylori cellular proliferation protein #244. Org:Helicobacter pylori | | | 1.17.4.1 |
| 12909, 12910 12911, 12912 12913, 12914 | 56479307 48853884 14531035 | 35 37 37 | 5.00E-13 5.00E-29 2.00E-07 | Azoarcus sp. EbN1 Cytophaga hutchinsonii Flavobacterium johnsoniae | transposition helper protein [Azoarcus sp. EbN1] ref YP_160652.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_160194.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_158869.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_158141.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_157415.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_157215.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI09995.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI09751.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI09293.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI07968.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI07240.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI06514.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI06314.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI10704.1 IstB, ATP-binding protein [Azoarcus sp. EbN1] emb CAI10643.1 transposase OrfB protein [Azoarcus sp. EbN1] emb CAI10603.1 orfB protein, similar to Isr3 COG3225: ABC-type uncharacterized transport system involved in gliding motility, auxiliary component [Cytophaga hutchinsonii] | | | |
| 12915, 12916 12917, 12918 | 34558438 48833884 | 46 28 | 9.00E-56 2.00E-11 | Wolinella succinogenes DSM 1740 Magnetococcus sp. MC-1 | gliding motility protein GldG [Flavobacterium johnsoniae] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 4/6 | 92 4.00E-08 | |
| 12919, 12920 | 34558399 | 42 | 6.00E-18 | Wolinella succinogenes DSM 1740 | CYTOCHROME C BIOGENESIS PROTEIN (YCF5) [Wolinella succinogenes DSM 1740] emb CAE11153.1 CYTOCHROME C BIOGENESIS PROTEIN (YCF5) [Wolinella succinogenes] COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] 3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE KDTA [Wolinella succinogenes DSM 1740] emb CAE11114.1 3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE KDTA [Wolinella succinogenes] | | 2.4.99.- | |
| 12921, 12922 | 15896496 | 44 | 3.00E-39 | Clostridium acetobutylicum ATCC 824 | Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] gb AAK81185.1 Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] pir F97299 sensory transduction protein containing HD_GYP domain [Imported] - Clostridium acetobutylicum | | | |
| 12923, 12924 | 21674362 | 40 | 5.00E-41 | Chlorobium tepidum TLS | molybdenum transport protein ModE [Chlorobium tepidum TLS] gb AAM72769.1 molybdenum transport protein ModE [Chlorobium tepidum TLS] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|----------|
| 12925, 12926 | 17231298 | 26 | 5.00E-16 | Nostoc sp. PCC 7120 | hypothetical protein alr3806 [Nostoc sp. PCC 7120] pir JAG2281 hypothetical protein alr3806 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75505.1 alr3806 [Nostoc sp. PCC 7120] | | | |
| 12929, 12930 | 29346209 | 24 | 4.00E-10 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0799 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75906.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 1293, 1294 | 53712627 | 38 | 2.00E-26 | Bacteroides fragilis YCH46 | putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD48085.1 putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] | | | |
| 12931, 12932 | 57241729 | 48 | 7.00E-25 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54399.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 12935, 12936 | 46141858 | 35 | 2.00E-30 | Methanococcus burtonii DSM 6242 | COG0598: Mg2+ and Co2+ transporters [Methanococcus burtonii DSM 6242] | | | |
| 12939, 12940 | 34104254 | 32 | 3.00E-12 | Chromobacterium violaceum ATCC 12472 | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_902615.1 hypothetical protein CV2945 [Chromobacterium violaceum ATCC 12472] | | | |
| 12941, 12942 | 48858108 | 61 | 3.00E-36 | Clostridium thermocellum ATCC 27405 | COG0281: Malic enzyme [Clostridium thermocellum ATCC 27405] | | | 1.1.1.38 |
| 12943, 12944 | 29346750 | 34 | 2.00E-13 | Bacteroides thetaiotaomicron VPI-5482 | putative lipopolysaccharide biosynthesis glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76447.1 putative lipopolysaccharide biosynthesis glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 12947, 12948 | 48854416 | 49 | 2.00E-72 | Cytophaga hutchinsonii Wolinella succinogenes DSM 1740 | COG3275: Putative regulator of cell autolysis [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 12949, 12950 | 34557884 | 33 | 2.00E-17 | Bacteroides fragilis YCH46 | DIGUANYLATE CYCLASE [Wolnella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolnella succinogenes] | | | 2.7.3.- |
| 1295, 1296 | 53712627 | 37 | 6.00E-26 | Bacteroides fragilis YCH46 | putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD48085.1 putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] | | | |
| 12951, 12952 | 48862623 | 22 | 2.00E-09 | Microbulifer degradans 2-40 | COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Microbulifer degradans 2-40] | | | 2.1.1.- |
| 12955, 12956 | 57237984 | 53 | 2.00E-47 | Campylobacter jejuni RM1221 | tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] gb AAW35567.1 tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] | | | 4.2.1.70 |
| 12957, 12958 | 34557269 | 58 | 7.00E-82 | Wolnella succinogenes DSM 1740 | ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolnella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolnella succinogenes] | | | 3.6.1.- |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|-------------|----------|
| 12959, 12960 | 57237231 | 53 | 2.00E-53 | Campylobacter jejuni RM1221 | DNA adenine methylase [Campylobacter jejuni RM1221] gb AAW34814.1 DNA adenine methylase [Campylobacter jejuni RM1221] | | | 2.1.1.72 |
| 12961, 12962 | 48846045 | 40 | 3.00E-42 | Geobacter metallireducens GS | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 12963, 12964 | 48891870 | 48 | 5.00E-56 | Trichodesmium erythraeum IMS101 | COG0566: rRNA methylases [Trichodesmium erythraeum IMS101] conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | 2.1.1.- |
| 12965, 12966 | 57169064 | 31 | 1.00E-25 | Campylobacter coli RM2228 | ATP-BINDING PROTEIN-ATPases involved in chromosome partitioning [Wolfinella succinogenes DSM 1740] emb CAE10672.1 ATP-BINDING PROTEIN-ATPases involved in chromosome partitioning [Wolfinella succinogenes] | | | |
| 12967, 12968 | 34557957 | 41 | 5.00E-37 | Wolfinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolfinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolfinella succinogenes] COG3279: Response regulator of the LysR/AIGR family [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 12969, 12970 | 34556560 | 35 | 5.00E-48 | Wolfinella succinogenes DSM 1740 | PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolfinella succinogenes DSM 1740] emb CAE09198.1 PUTATIVE UDP- GLUCURONIC ACID EPIMERASE [Wolfinella succinogenes] | | | 5.1.3.- |
| 12971, 12972 | 34556483 | 56 | 3.00E-38 | Wolfinella succinogenes DSM 1740 | 3'(2')5'-bisphosphate nucleotidase [Campylobacter coli RM2228] gb EAL56330.1 3'(2')5'-bisphosphate nucleotidase [Campylobacter coli RM2228] | Aquifex aeolicus VF5 section 16 of 109 of the complete genome | 87 4.00E-14 | 3.1.3.25 |
| 12973, 12974 | 57168975 | 63 | 6.00E-80 | Campylobacter coli RM2228 | PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolfinella succinogenes DSM 1740] emb CAE10693.1 PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolfinella succinogenes] | | | 2.3.2.- |
| 12975, 12976 | 34557978 | 46 | 5.00E-62 | Wolfinella succinogenes DSM 1740 | succinylornithine transaminase [Alvinella pompejana epibiont 7G3] | | | 2.6.1.11 |
| 12979, 12980 | 34558829 | 44 | 2.00E-47 | Alvinella pompejana epibiont 7G3 | hypothetical protein WS0394 [Wolfinella succinogenes DSM 1740] emb CAE09540.1 conserved hypothetical protein [Wolfinella succinogenes] | | | |
| 12981, 12982 | 34556825 | 39 | 2.00E-35 | Wolfinella succinogenes DSM 1740 | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|---|----|-------------------|
| 12983, 12984 | 15678576 | 38 | 2.00E-18 | Methanothermobacter thermautotrophicus str. Delta H | sensory transduction regulatory protein [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85054.1 sensory transduction regulatory protein [Methanothermobacter thermotrophicus str. Delta H] p J D69172 sensory transduction regulatory protein - Methanobacterium thermautotrophicum (strain Delta H) | | | 2.7.3.- |
| 12985, 12986 | 34557975 | 57 | 1.00E-72 | Wolinella succinogenes DSM 1740 | AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes] | | | |
| 12987, 12988 | 34557975 | 67 | 9.00E-67 | Wolinella succinogenes DSM 1740 | AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes] | Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome | 93 | 1.00E-13 3.4.24.- |
| 12989, 12990 | 45658172 | 45 | 9.00E-44 | Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130 | serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] | | | 3.1.3.16 |
| 12991, 12992 | 46201501 | 28 | 7.00E-12 | Magnetospirillum magnetotacticum MS-1 | COG2208: Serine phosphatase RsbU, regulator of sigma subunit [Magnetospirillum magnetotacticum MS-1] | | | |
| 12993, 12994 | 37519590 | 31 | 3.00E-38 | Gloeobacter violaceus PCC 7421 | HlyB/MsbA family ABC transporter [Gloeobacter violaceus PCC 7421] db JBAC87962.1 HlyB/MsbA family ABC transporter [Gloeobacter violaceus PCC 7421] | | | 3.4.21.- |
| 12997, 12998 | 48856940 | 37 | 5.00E-19 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | |
| 12999, 13000 | 48478360 | 30 | 4.00E-12 | Picrophilus torridus DSM 9790 | thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790] gb AAT43873.1 thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790] | | | 2.5.1.3 |
| 13001, 13002 | 27804856 | 29 | 7.00E-10 | Myxococcus xanthus | putative histidine kinase [Myxococcus xanthus] | | | |
| 13003, 13004 | 46578599 | 30 | 2.00E-19 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | radical SAM domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94666.1 radical SAM domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 13007, 13008 | 48832299 | 43 | 7.00E-42 | Magnetococcus sp. MC-1 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] | | | |
| 13009, 13010 | 39988006 | 44 | 1.00E-23 | Geobacter sulfurreducens PCA | sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA] gb AAR36307.1 sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA] | | | 2.7.-:- |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|--|--|--|----------|
| 13011, | 57233639 | 45 | 7.00E-17 | Dehalococcoides | DNA internalization-related competence protein ComEC/Rec2 [Dehalococcoides ethenogenes 195] | | | | |
| 13012 | | | | | | | | | |
| 13013, | | | | | | | | | |
| 13014 | 46155955 | 38 | 6.00E-29 | Haemophilus somnus 2336 | COG2249: Putative NADPH-quinone reductase (modulator of drug activity) | | | | 1.6.99- |
| 13015, | | | | | | | | | |
| 13016 | 28211915 | 38 | 2.00E-08 | Clostridium tetani E88 | imidazolonepropionase [Clostridium tetani E88] | | | | 3.5.2.7 |
| 13019, | | | | | | | | | |
| 13020 | 15605808 | 37 | 1.00E-15 | Aquifex aeolicus VF5 | hypothetical protein aq_268 [Aquifex aeolicus VF5] gb AAC06590.1 | | | | |
| 13025, | | | | | | | | | |
| 13026 | 48788644 | 47 | 2.00E-43 | Burkholderia fungorum LB400 | hypothetical protein aq_268 - Aquifex aeolicus | | | | 2.3.2.6 |
| 13027, | | | | | | | | | |
| 13028 | 29347026 | 41 | 8.00E-41 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1616 [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 13029, | | | | | | | | | |
| 13030 | 28896908 | 41 | 1.00E-19 | Vibrio parahaemolyticus RIMD 2210633 | general secretion pathway protein E [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58397.1 general secretion pathway protein E [Vibrio parahaemolyticus] | | | | |
| 13033, | | | | | | | | | |
| 13034 | 51572906 | 60 | 2.00E-31 | Borrelia garinii PBI | peptide chain release factor 2 [Borrelia garinii PBI] ref YP_072523.1 peptide chain release factor 2 [Borrelia garinii PBI] | | | | |
| 13035, | | | | | | | | | |
| 13036 | 53714646 | 34 | 4.00E-23 | Bacteroides fragilis YCH46 | putative outer membrane protein [Bacteroides fragilis YCH46] | | | | |
| 13037, | | | | | | | | | |
| 13038 | 57505272 | 50 | 1.00E-27 | Campylobacter upsaliensis RM3195 | glyceraldehyde-3-phosphate dehydrogenase, type I [Campylobacter upsaliensis RM3195] | | | | 1.2.1.12 |
| 13039, | | | | | | | | | |
| 13040 | 53718408 | 29 | 7.00E-09 | Burkholderia pseudomallei K96243 | hypothetical protein BPSL0769 [Burkholderia pseudomallei K96243] | | | | |
| 13041, | | | | | | | | | |
| 13042 | 17231298 | 26 | 2.00E-15 | Nostoc sp. PCC 7120 | hypothetical protein air3806 [Nostoc sp. PCC 7120] pir AG2281 hypothetical protein air3806 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75505.1 | | | | |
| 13047, | | | | | | | | | |
| 13048 | 53714415 | 72 | 3.00E-80 | Bacteroides fragilis YCH46 | dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] | | | | 2.4.1.83 |
| 13049, | | | | | | | | | |
| 13050 | 34557635 | 47 | 1.00E-53 | Wolnella succinogenes DSM 1740 | RND PUMP PROTEIN [Wolnella succinogenes DSM 1740] | | | | |

| | | | | | | |
|-----------------|----------|----|----------|---|---|---------------|
| 13051, 13052 | 34558004 | 54 | 9.00E-85 | Wollinella succinogenes DSM 1740 | RNA POLYMERASE ALPHA SUBUNIT [Wollinella succinogenes DSM 1740] emb CAE10719.1 RNA POLYMERASE ALPHA SUBUNIT [Wollinella succinogenes] sp Q7M8F7 RPOA_WOLSU DNA-directed RNA polymerase alpha chain (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit) | 2.7.7.6 |
| 13053, 13054 | 29335929 | 28 | 5.00E-08 | Bacteroides thetaiotaomicron | Tram-like [Bacteroides thetaiotaomicron] ref NP_818968.1 Tram-like protein [Bacteroides thetaiotaomicron] | |
| 13055, 13056 | 34556523 | 55 | 3.00E-25 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0069 [Wollinella succinogenes DSM 1740] emb CAE09238.1 conserved hypothetical protein [Wollinella succinogenes] | |
| 13057, 13058 | 34556524 | 41 | 4.00E-18 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0070 [Wollinella succinogenes DSM 1740] emb CAE09239.1 hypothetical protein [Wollinella succinogenes] | 2.3.1.12 8 |
| 13059, 13060 | 34557782 | 38 | 3.00E-31 | Wollinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes] | 2.7.3.- |
| 13061, 13062 | 21229081 | 52 | 4.00E-66 | Methanosarcina mazei Go1 | hypothetical protein MM2979 [Methanosarcina mazei Go1] gb AAM32675.1 hypothetical protein [Methanosarcina mazei Go1] | |
| 13063, 13064 | 53712881 | 33 | 2.00E-22 | Bacteroides fragilis YCH46 | hypothetical protein BF1590 [Bacteroides fragilis YCH46] db BAD48339.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | |
| 13065, 13066 | 34556560 | 45 | 3.00E-21 | Wollinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes] | 2.7.3.- |
| 13069, 13070 | 32261726 | 60 | 4.00E-42 | Helicobacter hepaticus ATCC 51449 | acetylglutamate kinase [Helicobacter hepaticus ATCC 51449] ref NP_859710.1 acetylglutamate kinase [Helicobacter hepaticus ATCC 51449] sp Q7VJR4 ARGB_HELHP Acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-phosphotransferase) | 2.7.2.8 |
| 1307, 1308 | 48854748 | 55 | 4.00E-90 | Cytophaga hutchinsonii | COG1216: Predicted glycosyltransferases [Cytophaga hutchinsonii] | 2.4.1.- |
| 13071, 13072 | 34556517 | 47 | 5.00E-42 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0063 [Wollinella succinogenes DSM 1740] emb CAE09232.1 conserved hypothetical protein [Wollinella succinogenes] | |
| 13073, 13074 | 48764124 | 42 | 3.00E-25 | Rhodospirillum rubrum | COG3019: Predicted metal-binding protein [Rhodospirillum rubrum] hypothetical protein all7133 [Nostoc sp. PCC 7120] db BAE78217.1 all7133 [Nostoc sp. PCC 7120] pir AE2494 hypothetical protein all7133 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha | |
| 13075, 13076 | 17233149 | 36 | 3.00E-32 | Nostoc sp. PCC 7120 | | |
| 13077, 13078 | 23475535 | 53 | 5.00E-51 | Desulfovibrio desulfuricans G20 | COG0845: Membrane-fusion protein [Desulfovibrio desulfuricans G20] | |

| | | | | | | | | |
|-----------------|--------------|----|----------|---|---|--|--|---------------------|
| 13079, 13080 | 23466453 | 41 | 4.00E-30 | Haemophilus sommus 129PT | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Haemophilus somnus 129PT] | | | |
| 13085, 13086 | 45250013 | 67 | 3.00E-84 | Aneurinibacillus thermoaerophilus | dTDP-glucose 4,6-dehydratase [Aneurinibacillus thermoaerophilus] | | | 4.2.1.46 |
| 13087, 13088 | 53728940 | 33 | 1.00E-08 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | COG0561: Predicted hydrolases of the HAD superfamily [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | |
| 1309, 1310 | 29347685 | 65 | 3.00E-61 | Bacteroides thetaiotaomicron VPI-5482 | thymidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77382.1 thymidine kinase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.1.21 |
| 13095, 13096 | 48862944 | 42 | 3.00E-40 | Microbulbifer degradans 2-40 | COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Microbulbifer degradans 2-40] | | | |
| 13097, 13098 | AAU3592 8 | 60 | 8.00E-40 | | Desc:Helicobacter pylori cellular proliferation protein #241. Org:Helicobacter pylori | | | 4.6.1.4 |
| 13101, 13102 | 57241323 | 49 | 8.00E-21 | Campylobacter lari RM2100 | hypothetical protein CLA1225 [Campylobacter lari RM2100] gb EAL55019.1 hypothetical protein CLA1225 [Campylobacter lari RM2100] | | | |
| 13103, 13104 | 57241291 | 51 | 5.00E-41 | Campylobacter lari RM2100 | cell division protein (ftsK) [Campylobacter lari RM2100] gb EAL54987.1 cell division protein (ftsK) [Campylobacter lari RM2100] | | | |
| 13105, 13106 | 56419990 | 55 | 9.00E-53 | Geobacillus kaustophilus HTA426 | recombinase of Bh.Int-like element [Geobacillus kaustophilus HTA426] dbj BAD75740.1 recombinase of Bh.Int-like element [Geobacillus kaustophilus HTA426] | | | 2.7.7.49 |
| 13107, 13108 | 32262431 | 61 | 1.00E-84 | Helicobacter hepaticus ATCC 51449 | 3-dehydroquinase synthase [Helicobacter hepaticus ATCC 51449] ref NP_860413.1 3-dehydroquinase synthase [Helicobacter hepaticus ATCC 51449] sp Q7VHT1 AROB_HELHP 3-dehydroquinase synthase | | | 82 1.00E-11 4.2.3.4 |
| 13109, 13110 | 34557844 | 26 | 5.00E-22 | Wolinella succinogenes DSM 1740 | MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10559.1 MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes] | | | |
| 1311, 1312 | 18308986 | 31 | 2.00E-31 | Clostridium perfringens str. 13 | DNA repair and genetic recombination protein [Clostridium perfringens str. 13] dbj BAB79710.1 DNA repair and genetic recombination protein [Clostridium perfringens str. 13] sp Q8XPF9 RECF_CLOPE DNA replication and repair protein refC | | | |
| 13113, 13114 | 31239345 | 36 | 7.00E-17 | Anopheles gambiae | ENSANGP00000018355 [Anopheles gambiae] gb EAA14826.1 ENSANGP00000018355 [Anopheles gambiae str. PEST] ref XP_553245.1 ENSANGP00000018355 [Anopheles gambiae str. PEST] | | | 3.1.-.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|--|---------|
| 13115, 13116 | 12744764 | 33 | 7.00E-13 | Pichia pastoris Wollinella succinogenes DSM 1740 | PR-aminimidazole succinocarboxamide synthase [Pichia pastoris] sp Q9C1J4 PUR7_PICPA Phosphoribosylamidoimidazole- succinocarboxamide synthase (SAICAR synthetase) | | | | 6.3.2.6 |
| 13119, 13120 | 34557698 | 37 | 4.00E-24 | Wollinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10413.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes] | | | | |
| 13121, 13122 | 23014414 | 31 | 3.00E-21 | Magnetospirillum magnetotacticum MS-1 | COG0643: Chemotaxis protein histidine kinase and related kinases [Magnetospirillum magnetotacticum MS-1] | | | | |
| 13125, 13126 | 54309698 | 53 | 3.00E-49 | Photobacterium profundum SS9 | hypothetical deoxyguanosinetriphosphatetriphosphohydrolase [Photobacterium profundum SS9] emb CAG20916.1 hypothetical deoxyguanosinetriphosphatetriphosphohydrolase [Photobacterium profundum] | | | | 3.1.5.1 |
| 13127, 13128 | 11499442 | 40 | 4.00E-25 | Archaeoglobus fulgidus DSM 4304 | NADH oxidase (noxA-5) [Archaeoglobus fulgidus DSM 4304] gb AAB89398.1 NADH oxidase (noxA-5) [Archaeoglobus fulgidus DSM 4304] pir A69482 NADH oxidase (noxA-5) homolog - Archaeoglobus fulgidus | | | | 1.6.-.- |
| 13131, 13132 | 56708505 | 50 | 4.00E-77 | Francisella tularensis subsp. tularensis Schu 4 | dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46097.1 dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis] gb AAS60264.1 sugar dehydratase [Francisella tularensis subsp. tularensis] | | | | 4.2.1.- |
| 13135, 13136 | 46580167 | 23 | 5.00E-08 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96234.1 site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | |
| 13137, 13138 | 34557245 | 34 | 1.00E-35 | Wollinella succinogenes DSM 1740 | TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wollinella succinogenes DSM 1740] emb CAE09960.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wollinella succinogenes] | | | | 2.7.3.- |
| 13139, 13140 | 9655557 | 40 | 1.00E-29 | Vibrio cholerae O1 biovar eltor str. N16961 | periplasmic binding protein-related protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230734.1 periplasmic binding protein-related protein [Vibrio cholerae O1 biovar eltor str. N16961] pir A82245 periplasmic binding protein-related protein VC1089 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 13141, 13142 | 15607008 | 38 | 4.00E-22 | Aquifex aeolicus VF5 | hypothetical protein aq_2027 [Aquifex aeolicus VF5] gb AAC07788.1 hypothetical protein [Aquifex aeolicus VF5] pir A70474 conserved hypothetical protein aq_2027 - Aquifex aeolicus sp O67821 YK27_AQUAE Hypothetical protein AQ_2027 | | | | |
| 13143, 13144 | 51244727 | 38 | 8.00E-31 | Desulfotalea psychrophila LSV54 | hypothetical protein DP0875 [Desulfotalea psychrophila LSV54] emb CAG35604.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | | 4.-.-.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 13145, 13146 | 34556479 | 45 | 1.00E-55 | Wolinella succinogenes DSM 1740 | POSSIBLE NUCLEOTIDYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09194.1 POSSIBLE NUCLEOTIDYLTRANSFERASE [Wolinella succinogenes] | | | 2.7.7.59 |
| 13147, 13148 | 34556778 | 52 | 1.00E-32 | Wolinella succinogenes DSM 1740 | THIF, MOEB, HESA FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09493.1 THIF, MOEB, HESA FAMILY PROTEIN [Wolinella succinogenes] | | | |
| 13149, 13150 | 18309954 | 41 | 8.00E-28 | Clostridium perfringens str. 13 | probable histidinol phosphatase [Clostridium perfringens str. 13] dbj BAB80678.1 probable histidinol phosphatase [Clostridium perfringens str. 13] | | | |
| 13151, 13152 | 34557884 | 46 | 1.00E-28 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE [Wolinella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolinella succinogenes] | | | 2.7.3.- |
| 13153, 13154 | 45656100 | 41 | 1.00E-39 | Leptospira Interrogans serovar Copenhageni str. Floeruz L1-130 | photoproduct lyase [Leptospira Interrogans serovar Copenhageni str. Floeruz L1-130] gb AAS68823.1 photoproduct lyase [Leptospira Interrogans serovar Copenhageni str. Floeruz L1-130] | | | 4.1.99.- |
| 13155, 13156 | 34557419 | 47 | 5.00E-21 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | 2.7.3.- |
| 13157, 13158 | 57241192 | 37 | 3.00E-16 | Campylobacter lari RM2100 | fructose-1,6-bisphosphatase [Campylobacter lari RM2100] gb EAL54888.1 fructose-1,6-bisphosphatase [Campylobacter lari RM2100] | | | 3.1.3.11 |
| 13163, 13164 | 34556519 | 42 | 3.00E-37 | Wolinella succinogenes DSM 1740 | PUTATIVE DIMETHYLADENOSINE TRANSFERASE 16S RRNA DIMETHYLASEEC 2.1.1. [Wolinella succinogenes DSM 1740] emb CAE09234.1 PUTATIVE DIMETHYLADENOSINE TRANSFERASE 16S RRNA DIMETHYLASEEC 2.1.1. [Wolinella succinogenes] | | | 2.1.1.- |
| 1317, 1318 | 53736083 | 52 | 2.00E-59 | Crocospaera watsonii WH 8501 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Crocospaera watsonii WH 8501] | | | 2.4.1.83 |
| 13171, 13172 | 52425081 | 39 | 9.00E-30 | Mannheimia succiniciproducens MBEL55E | hypothetical protein MS1026 [Mannheimia succiniciproducens MBEL55E] gb AAU37633.1 unknown [Mannheimia succiniciproducens MBEL55E] | | | 2.1.1.72 |
| 13173, 13174 | 52425081 | 50 | 9.00E-45 | Mannheimia succiniciproducens MBEL55E | hypothetical protein MS1026 [Mannheimia succiniciproducens MBEL55E] gb AAU37633.1 unknown [Mannheimia succiniciproducens MBEL55E] (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase [Geobacter sulfurreducens PCA] gb AAR3564.1 (3R)-hydroxymyristoyl-(acyl-carrier- protein) dehydratase [Geobacter sulfurreducens PCA] sp P61453 FABZ_GEOSL (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase ((3R)-hydroxymyristoyl ACP dehydratase) | | | 2.1.1.72 |
| 13175, 13176 | 39997363 | 63 | 1.00E-35 | Geobacter sulfurreducens PCA | | | | 4.2.1.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 13177, 13178 | 45520556 | 30 | 4.00E-12 | Methylobacillus flagellatus KT | COG0835: Chemotaxis signal transduction protein [Methylobacillus flagellatus KT] | | | |
| 13179, 13180 | 15606118 | 43 | 6.00E-35 | Aquifex aolicus VF5 | glycogen synthase [Aquifex aolicus VF5] gb AAC06894.1 glycogen synthase [Aquifex aolicus VF5] pir C70363 glycogen synthase - Aquifex aolicus sp O66935 GLGA_AQUAE Glycogen synthase (Starch) [bacterial glycogen] synthase) | | | 2.4.1.21 |
| 13185, 13186 | 53711526 | 42 | 1.00E-30 | Bacteroides fragilis YCH46 | shikimate kinase [Bacteroides fragilis YCH46] dbj BAD46984.1 shikimate kinase [Bacteroides fragilis YCH46] | | | 2.7.1.71 |
| 13187, 13188 | 51573281 | 24 | 2.00E-09 | Borrelia garinii PBi | lipopolysaccharide biosynthesis-related protein [Borrelia garinii PBi] ref YP_072898.1 lipopolysaccharide biosynthesis-related protein [Borrelia garinii PBi] | | | 2.4.1.56 |
| 1319, 1320 | 48862770 | 46 | 3.00E-34 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02001866 [Microbulbifer degradans 2-40] | | | |
| 13193, 13194 | 34558362 | 45 | 2.00E-20 | Wolinella succinogenes DSM 1740 | PEPTIDYL-TRNA HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE11077.1 PEPTIDYL-TRNA HYDROLASE [Wolinella succinogenes] sp Q7M7U8 PTH_WOLSU Peptidyl-TRNA hydrolase (PTH) | | | 3.1.1.29 |
| 13199, 13200 | 34558118 | 30 | 1.00E-19 | Wolinella succinogenes DSM 1740 | HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10833.1 HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 13201, 13202 | 57168122 | 47 | 2.00E-34 | Campylobacter coli RM2228 | signal-transducing protein, histidine kinase [Campylobacter coli RM2228] gb EAL57165.1 signal-transducing protein, histidine kinase [Campylobacter coli RM2228] | | | 2.7.3.- |
| 13203, 13204 | 34558265 | 57 | 3.00E-25 | Wolinella succinogenes DSM 1740 | PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes] | | | |
| 13205, 13206 | 34558265 | 47 | 3.00E-62 | Wolinella succinogenes DSM 1740 | PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes] | | | |
| 13207, 13208 | 45524550 | 33 | 7.00E-25 | Crocospaera watsonii WH 8501 | hypothetical protein Cwat03005121 [Crocospaera watsonii WH 8501] | | | |
| 13209, 13210 | 34557184 | 50 | 4.00E-48 | Wolinella succinogenes DSM 1740 | BH0401 PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09899.1 BH0401 PROTEIN [Wolinella succinogenes] | | | |
| 1321, 1322 | 23471862 | 33 | 5.00E-15 | Pseudomonas syringae pv. syringae B728a | COG3172: Predicted ATPase/kinase involved in NAD metabolism [Pseudomonas syringae pv. syringae B728a] | | | |
| 13211, 13212 | 34556743 | 49 | 5.00E-54 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0307 [Wolinella succinogenes DSM 1740] emb CAE09458.1 hypothetical protein [Wolinella succinogenes] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|--|---------|
| 13213, 13214 | 16519917 | 39 | 6.00E-55 | Rhizobium sp. NGR234 | Y4qJ [Rhizobium sp. NGR234] gb AAB92465.1 Y4qJ [Rhizobium sp. NGR234] sp P55631 Y4QJ_RHISN Putative transposase Y4QJ | | | | |
| 13215, 13216 | 53762765 | 32 | 1.00E-23 | Ralstonia eutropha JMP134 | COG1073: Hydrolases of the alpha/beta superfamily [Ralstonia eutropha JMP134] | | | | |
| 13217, 13218 | 15602076 | 36 | 4.00E-18 | Pasteurella multocida subsp. multocida str. Pm70 | hypothetical protein PM0211 [Pasteurella multocida subsp. multocida str. Pm70] gb AAK02295.1 unknown [Pasteurella multocida subsp. multocida str. Pm70] sp Q9CP49 Y211_PASMU Hypothetical UPF0276 protein PM0211 | | | | |
| 13227, 13228 | 23114483 | 37 | 3.00E-34 | Desulfotobacterium hafnense DCB-2 | COG2931: RTX toxins and related Ca2+-binding proteins [Desulfotobacterium hafnense DCB-2] | | | | |
| 13231, 13232 | 29604946 | 34 | 2.00E-13 | Streptomyces avermitilis MA-4680 | putative esterase [Streptomyces avermitilis MA-4680] ref NP_822479.1 putative esterase [Streptomyces avermitilis MA-4680] | | | | |
| 13233, 13234 | 20808597 | 55 | 9.00E-57 | Thermoanaerobacter tengcongensis MB4 | Thioredoxin reductase [Thermoanaerobacter tengcongensis MB4] gb AAM25372.1 Thioredoxin reductase [Thermoanaerobacter tengcongensis MB4] | | | | 1.6.4.5 |
| 13235, 13236 | 34558248 | 24 | 8.00E-17 | Wolinella succinogenes DSM 1740 | METHYL-ACCEPTING CHEMOTAXIS PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10863.1 METHYL-ACCEPTING CHEMOTAXIS PROTEIN [Wolinella succinogenes] | | | | |
| 13237, 13238 | 34763541 | 52 | 6.00E-58 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | SWF/SNF family helicase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23925.1 SWF/SNF family helicase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | | 3.6.1.3 |
| 13239, 13240 | 48856112 | 38 | 4.00E-44 | Cytophaga hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 13241, 13242 | 48856112 | 40 | 3.00E-24 | Cytophaga hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 13243, 13244 | 13928880 | 35 | 3.00E-29 | Rattus norvegicus | plasma glutamate carboxypeptidase [Rattus norvegicus] gb AAC72384.1 hematopoietic lineage switch 2 related protein [Rattus norvegicus] | | | | |
| 13247, 13248 | 30250110 | 47 | 1.00E-46 | Nitrosomonas europaea ATCC 19718 | hypothetical protein NE2176 [Nitrosomonas europaea ATCC 19718] emb CAD86087.1 conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] | | | | |
| 1325, 1326 | 21232295 | 49 | 3.00E-36 | Xanthomonas campestris pv. campestris str. ATCC 33913 | monofunctional biosynthetic peptidoglycan transglycosylase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM42136.1 monofunctional biosynthetic peptidoglycan transglycosylase [Xanthomonas campestris pv. campestris str. ATCC 33913] sp Q8P6V1 MTGA_XANCP Monofunctional biosynthetic peptidoglycan transglycosylase (Monofunctional TGase) | | | | 2.4.2.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 13255, 13256 | 34556928 | 54 | 4.00E-66 | Wolnella succinogenes DSM 1740 | PUTATIVE GAMMA-GLUTAMYL KINASE [Wolnella succinogenes DSM 1740] emb CAE09643.1 PUTATIVE GAMMA-GLUTAMYL KINASE [Wolnella succinogenes] sp Q7MA27 PROB_WOLSU Glutamate 5-kinase (Gamma-glutamyl kinase) (GK) | | | 2.7.2.11 |
| 13257, 13258 | 57168109 | 38 | 8.00E-22 | Campylobacter coli RM2228 | signal-transducing protein, histidine kinase, putative [Campylobacter coli RM2228] gb EAL57152.1 signal-transducing protein, histidine kinase, putative [Campylobacter coli RM2228] | | | 2.7.3.- |
| 13261, 13262 | 48833864 | 46 | 6.00E-25 | Magnetococcus sp. MC-1 | COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 13265, 13266 | 53712431 | 37 | 5.00E-34 | Bacteroides fragilis YCH46 | hypothetical protein BF1139 [Bacteroides fragilis YCH46] dbj BAD47889.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 1327, 1328 | 42557748 | 61 | 1.00E-31 | uncultured crenarchaeote | putative threonine synthase [uncultured crenarchaeote] | | | 4.2.99.2 |
| 13271, 13272 | 20089001 | 40 | 7.00E-13 | Methanosarcina acetivorans C2A | nucleotidyltransferase [Methanosarcina acetivorans C2A] gb AAM03556.1 nucleotidyltransferase [Methanosarcina acetivorans str. C2A] | | | 2.7.7.- |
| 13273, 13274 | 20088978 | 26 | 2.00E-14 | Methanosarcina acetivorans C2A | hypothetical protein MA0079 [Methanosarcina acetivorans C2A] gb AAM03533.1 hypothetical protein (multi-domain) [Methanosarcina acetivorans str. C2A] | | | |
| 13275, 13276 | 37520689 | 23 | 3.00E-10 | Gloeobacter violaecus PCC 7421 | hypothetical protein glf1120 [Gloeobacter violaecus PCC 7421] dbj BAC89061.1 glf1120 [Gloeobacter violaecus PCC 7421] | | | |
| 13277, 13278 | 6967633 | 46 | 6.00E-29 | Campylobacter jejuni subsp. jejuni NCTC 11168 | putative endonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81431 probable endonuclease Cj0139 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281350.1 putative endonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] | | | 3.1.21.- |
| 13279, 13280 | 54303177 | 46 | 5.00E-26 | Photobacterium profundum SS9 | hypothetical protein PBPRB1504 [Photobacterium profundum SS9] emb CAG23370.1 hypothetical protein [Photobacterium profundum] putative zinc metallo protease [Bdellovibrio bacteriovorus HD100] | | | |
| 13281, 13282 | 42525039 | 31 | 3.00E-20 | Bdellovibrio bacteriovorus HD100 | emb CAE81073.1 putative zinc metallo protease [Bdellovibrio bacteriovorus HD100] | | | 3.4.24.- |
| 13285, 13286 | 54308855 | 26 | 8.00E-07 | Photobacterium profundum SS9 | putative EntE, Peptide arylatase [Photobacterium profundum SS9] emb CAG20073.1 putative EntE, Peptide arylatase [Photobacterium profundum] | | | 6.2.1.1 |
| 13287, 13288 | 34558396 | 33 | 1.00E-33 | Wolnella succinogenes DSM 1740 | hypothetical protein WS2113 [Wolnella succinogenes DSM 1740] emb CAE11111.1 hypothetical protein [Wolnella succinogenes] | | | 3.1.3.16 |
| 13289, 13290 | 48837872 | 44 | 4.00E-56 | Methanosarcina barkeri str. fusaro | COG1373: Predicted ATPase (AAA+ superfamily) [Methanosarcina barkeri str. fusaro] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 1329, 1330 | 57169027 | 34 | 9.00E-24 | Campylobacter coli RM2228 | type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] gb EAL56262.1 type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] | | | 2.1.1.72 |
| 13293, 13294 | 34557679 | 50 | 2.00E-25 | Wolfinella succinogenes DSM 1740 | hypothetical protein WS1318 [Wolfinella succinogenes DSM 1740] emb CAE10394.1 hypothetical protein [Wolfinella succinogenes] | | | 1.--- |
| 13297, 13298 | 48864174 | 32 | 3.00E-14 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02000547 [Microbulbifer degradans 2-40] | | | |
| 133, 134 | 21227241 | 30 | 4.00E-11 | Methanosarcina mazel Go1 | Dolichyl-phosphate mannosyl transferase related protein [Methanosarcina mazel Go1] gb AAM30835.1 Dolichyl-phosphate mannosyl transferase related protein [Methanosarcina mazel Go1] | | | 2.--- |
| 13301, 13302 | 57241730 | 36 | 5.00E-13 | Campylobacter lari RM2100 | hypothetical protein CLA0161 [Campylobacter lari RM2100] gb EAL54400.1 hypothetical protein CLA0161 [Campylobacter lari RM2100] | | | |
| 13303, 13304 | 57167861 | 27 | 7.00E-10 | Campylobacter coli RM2228 | membrane protein, putative [Campylobacter coli RM2228] gb EAL57647.1 membrane protein, putative [Campylobacter coli RM2228] | | | |
| 13305, 13306 | 53715232 | 39 | 1.00E-09 | Bacteroides fragilis YCH46 | putative secreted sulfatase ydeN precursor [Bacteroides fragilis YCH46] dbj BAD50690.1 putative secreted sulfatase ydeN precursor [Bacteroides fragilis YCH46] | | | |
| 13307, 13308 | 48856591 | 26 | 8.00E-08 | Cytophaga hutchinsonii | COG0823: Periplasmic component of the Tol biopolymer transport system [Cytophaga hutchinsonii] | | | |
| 13309, 13310 | 48855914 | 38 | 4.00E-20 | Cytophaga hutchinsonii | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii] | | | |
| 1331, 1332 | 57169027 | 36 | 2.00E-22 | Campylobacter coli RM2228 | type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] gb EAL56262.1 type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] | | | 2.1.1.72 |
| 13313, 13314 | 32261607 | 31 | 2.00E-08 | Helicobacter hepaticus ATCC 51449 | hypothetical protein HH0060 [Helicobacter hepaticus ATCC 51449] ref NP_859591.1 hypothetical protein HH0060 [Helicobacter hepaticus ATCC 51449] | | | |
| 13315, 13316 | 31195913 | 46 | 3.00E-47 | Anopheles gambiae | ENSANGP00000000411 [Anopheles gambiae] related to 5' to 3' DNA helicase [Desulfotalea psychrophila Lsv54] emb CAG36716.1 related to 5' to 3' DNA helicase [Desulfotalea psychrophila Lsv54] | | | |
| 13317, 13318 | 51245839 | 32 | 6.00E-21 | Desulfotalea psychrophila Lsv54 | glycosyl transferase [Rhodopirellula baltica SH 1] emb CAD72671.1 glycosyl transferase [Pirellula sp.] | | | 3.6.1.- |
| 13321, 13322 | 32471993 | 34 | 5.00E-21 | Rhodopirellula baltica SH 1 | CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolfinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolfinella succinogenes] | | | |
| 13323, 13324 | 34556616 | 37 | 7.00E-21 | Wolfinella succinogenes DSM 1740 | | | | |

| | | | | | | | | |
|--------|----------|----|----------|--|--|--|--|----------|
| 13325, | 34556616 | 42 | 1.00E-40 | Wolinnella succinogenes DSM 1740 | CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinnella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinnella succinogenes] | | | |
| 13326 | | | | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |
| 13327, | 48853894 | 40 | 7.00E-37 | Pediococcus pentosaceus ATCC 25745 | COG2344: AT-rich DNA-binding protein [Pediococcus pentosaceus ATCC 25745] | | | |
| 13329, | 48870017 | 33 | 5.00E-22 | | | | | 2.7.7.- |
| 13330 | | | | | | | | |
| 13331, | | | | | | | | |
| 13332 | | | | | | | | |
| 13333, | | | | Porphyromonas gingivalis W83 | cysteine peptidase, putative [Porphyromonas gingivalis W83] ref NP_905889.1 cysteine peptidase, putative [Porphyromonas gingivalis W83] | | | |
| 13334 | 34397727 | 40 | 2.00E-35 | | | | | |
| 13335, | | | | | | | | |
| 13336 | 15616566 | 51 | 6.00E-59 | Bacillus halodurans C-125 | modification methylase [Bacillus halodurans C-125] dbj BAB07723.1 modification methylase [Bacillus halodurans C-125] pir D84150 modification methylase BH4004 [imported] - Bacillus halodurans (strain C-125) | | | 2.1.1.72 |
| 13337, | | | | Lactococcus lactis subsp. lactis bv. diacetylactis | | | | |
| 13338 | 8489196 | 31 | 6.00E-24 | | restriction enzyme [Lactococcus lactis subsp. lactis bv. diacetylactis] gb AAC77902.1 LlaKR21 restriction enzyme [Lactococcus lactis] | | | 3.1.21.4 |
| 13339, | | | | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 13340 | 48832337 | 37 | 2.00E-42 | | | | | |
| 13341, | | | | Cytophaga hutchinsonii | COG1600: Uncharacterized Fe-S protein [Cytophaga hutchinsonii] | | | |
| 13342 | 48855815 | 53 | 2.00E-45 | | | | | |
| 13343, | | | | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | |
| 13344 | 48831001 | 24 | 6.00E-14 | | | | | |
| 13345, | | | | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | aspartate ammonia-lyase, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96243.1 aspartate ammonia-lyase, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | 4.3.1.1 |
| 13346 | 46580176 | 42 | 6.00E-33 | | DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221] | | | |
| 13347, | | | | Campylobacter jejuni RM1221 | | | | |
| 13348 | 57238514 | 30 | 3.00E-10 | | | | | |
| 13349, | | | | Wolinnella succinogenes DSM 1740 | hypothetical protein WS1256 [Wolinnella succinogenes DSM 1740] emb CAE10335.1 conserved hypothetical protein [Wolinnella succinogenes] | | | |
| 13350 | 34557620 | 58 | 6.00E-74 | | | | | |
| 1335, | | | | Cytophaga hutchinsonii | hypothetical protein Chut02001830 [Cytophaga hutchinsonii] | | | |
| 1336 | 48855491 | 44 | 2.00E-30 | | hypothetical protein PBPPA1826 [Photobacterium profundum SS9] | | | |
| 13351, | | | | Photobacterium profundum SS9 | hypothetical protein [Photobacterium profundum] | | | |
| 13352 | 54309012 | 30 | 2.00E-08 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|---|----|----------|----------|
| 13353, 13354 | 30020374 | 40 | 1.00E-27 | NADP+ | Succinate-semialdehyde dehydrogenase [NADP+] [Bacillus cereus ATCC 14579] gb AAP09206.1 Succinate-semialdehyde dehydrogenase [NADP+] [Bacillus cereus ATCC 14579] | | | | 1.2.1.3 |
| 13357, 13358 | 34557573 | 39 | 1.00E-55 | Wolinella succinogenes DSM 1740 | SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes] | Leptospira interrogans serovar lai str. 56601 chromosome I, section 229 of 397 of the complete sequence | 90 | 7.00E-07 | 2.7.3.- |
| 13359, 13360 | 34556471 | 36 | 3.00E-36 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09186.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | 2.7.3.- |
| 13361, 13362 | 53759644 | 29 | 7.00E-23 | Methylobacillus flagellatus KT | hypothetical protein Mflag03001521 [Methylobacillus flagellatus KT] | | | | |
| 13363, 13364 | 48856479 | 60 | 3.00E-69 | Cytophaga hutchinsonii | COG0179: 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) [Cytophaga hutchinsonii] | | | | 4.1.1.- |
| 13365, 13366 | 48855764 | 31 | 4.00E-22 | Cytophaga hutchinsonii | COG5316: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 13367, 13368 | 15605806 | 47 | 1.00E-28 | Aquifex aerolicus VF5 | hypothetical protein aq_265 [Aquifex aerolicus VF5] gb AAC06589.1 hypothetical protein [Aquifex aerolicus VF5] pir C70324 conserved hypothetical protein aq_265 - Aquifex aerolicus | | | | 2.7.3.- |
| 13369, 13370 | 57505466 | 48 | 5.00E-49 | Campylobacter upsaliensis RM3195 | aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195] gb EAL53077.1 aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195] | | | | 3.4.13.3 |
| 1337, 1338 | 20803924 | 28 | 8.00E-15 | Mesorhizobium loti | HYPOTHETICAL PROTEIN [Mesorhizobium loti] | | | | |
| 13371, 13372 | 48833400 | 40 | 3.00E-22 | Magnetococcus sp. MC-1 | COG0500: SAM-dependent methyltransferases [Magnetococcus sp. MC-1] | | | | |
| 13373, 13374 | 21228207 | 29 | 1.00E-11 | Methanosarcina mazel Go1 | putative glycosyltransferase [Methanosarcina mazel Go1] gb AAM31801.1 putative glycosyltransferase [Methanosarcina mazel Go1] | | | | 2.4.1.- |
| 13375, 13376 | 34557966 | 55 | 1.00E-55 | Wolinella succinogenes DSM 1740 | ATP-DEPENDENT HELICASE [Wolinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wolinella succinogenes] Histidyl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] gb AAM24457.1 Histidyl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] sp Q8RA18 SYH_THETN Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS) | | | | 3.6.1.- |
| 13377, 13378 | 20807682 | 44 | 1.00E-60 | Thermoanaerobacter tengcongensis MB4 | | | | | 6.1.1.21 |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|---------|---------------|
| 13379, 13380 | 53715401 | 37 | 8.00E-20 | Bacteroides fragilis YCH46 | ribosomal large subunit pseudouridine synthase D [Bacteroides fragilis YCH46] dbj BAD50859.1 ribosomal large subunit pseudouridine synthase D [Bacteroides fragilis YCH46] | | | 4.2.1.70 |
| 13381, 13382 | 53756922 | 51 | 7.00E-74 | Methylococcus capsulatus str. Bath | heavy metal efflux pump, Czca family [Methylococcus capsulatus str. Bath] ref YP_115121.1 heavy metal efflux pump, Czca family [Methylococcus capsulatus str. Bath] | | | |
| 13383, 13384 | 9949348 | 56 | 2.00E-28 | Pseudomonas aeruginosa PAO1 | peptidyl-prolyl cis-trans isomerase A [Pseudomonas aeruginosa PAO1] ref NP_251917.1 peptidyl-prolyl cis-trans isomerase A [Pseudomonas aeruginosa PAO1] sp Q59641 PPIA_PSEAE Peptidyl-prolyl cis-trans isomerase A precursor (PPIase A) (Rotamase A) (Cyclophilin A) pir G83243 peptidyl-prolyl cis-trans isomerase A PA3227 [imported] - Pseudomonas aeruginosa (strain PAO1) | | 5.2.1.8 | |
| 13385, 13386 | 46580489 | 34 | 1.00E-21 | Desulfovibrio vulgaris subsp. vulgaris str. | oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96557.1 oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 13387, 13388 | 48833864 | 39 | 3.00E-35 | Magnetococcus sp. MC-1 | COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 13389, 13390 | 34556565 | 36 | 2.00E-26 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09280.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes] emb CAD23185.1 putative transcriptional regulator protein [Wolinella succinogenes] | | | |
| 1339, 1340 | 48853838 | 47 | 1.00E-28 | Cytophaga hutchinsonii | COG1522: Transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 13391, 13392 | 24373599 | 34 | 4.00E-09 | Shewanella oneidensis MR-1 | hypothetical protein SO2039 [Shewanella oneidensis MR-1] gb AAN55086.1 conserved domain protein [Shewanella oneidensis MR-1] | | | |
| 13393, 13394 | 34557297 | 53 | 8.00E-34 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSPORTER [Wolinella succinogenes DSM 1740] emb CAE10012.1 PUTATIVE TRANSPORTER [Wolinella succinogenes] | | | 1.8.- |
| 13395, 13396 | 53730423 | 45 | 1.00E-32 | Dechloromonas aromatica RCB | COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB] | | | |
| 13399, 13400 | 32451220 | 52 | 5.00E-21 | Bacteroides sp. 139 | putative dTDP-dehydrohamnose reductase [Bacteroides sp. 139] | | | 1.1.1.13 3 |
| 13401, 13402 | 19704339 | 32 | 2.00E-18 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Transcriptional regulator, TetR family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95200.1 Transcriptional regulator, TetR family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | |
| 13403, 13404 | 48853332 | 28 | 2.00E-10 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|--------------------------------------|--|--|----|----------|----------|
| 13405, 13406 | 56709007 | 30 | 2.00E-20 | Silicibacter pomeroyi DSS-3 | cytochrome cd1 nitrite reductase [Silicibacter pomeroyi DSS-3] gb AAV97357.1 cytochrome cd1 nitrite reductase [Silicibacter pomeroyi DSS-3] | | | | |
| 13407, 13408 | 34557573 | 54 | 8.00E-48 | Wolinella succinogenes DSM 1740 | SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF-FAMILY PROTEIN [Wolinella succinogenes] | | | | 2.7.3.- |
| 1341, 1342 | 20806566 | 53 | 2.00E-68 | Thermoanaerobacter tengcongensis MB4 | Seryl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] gb AAM2334.1 Seryl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] sp Q8RDJ5 SYS_THEIN Seryl-tRNA synthetase (Seryl-tRNA ligase) (SerRS) | | | | 6.1.1.11 |
| 13411, 13412 | 34556560 | 42 | 6.00E-73 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | |
| 13413, 13414 | 34557407 | 40 | 2.00E-51 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | | 2.7.3.- |
| 13415, 13416 | 48860860 | 59 | 1.00E-100 | Microbulbifer degradans 2-40 | COG0439: Biotin carboxylase [Microbulbifer degradans 2-40] | | | | 6.3.4.6 |
| 13417, 13418 | 34557494 | 60 | 1.00E-81 | Wolinella succinogenes DSM 1740 | PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes DSM 1740] emb CAE10209.1 PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes] | Wolinella succinogenes, complete genome; segment 4/7 | 84 | 4.00E-08 | 6.3.5.- |
| 13419, 13420 | 13508081 | 28 | 9.00E-20 | Mycoplasma pneumoniae M129 | type I restriction enzyme HsdM [Mycoplasma pneumoniae M129] gb AAB96142.1 type I restriction enzyme HsdM [Mycoplasma pneumoniae M129] pir S73820 type I restriction enzyme hsdM - Mycoplasma pneumoniae (strain ATCC 29342) sp P75436 T1MD_MYCPN Putative type I restriction enzyme MpnORFDP M protein (M.MpnORFDP) (H91_orf543) | | | | 2.1.1.72 |
| 13421, 13422 | AAU3570 | 1 | 2.00E-81 | pylori | Desc:Helicobacter pylori cellular proliferation protein #14. Org:Helicobacter pylori | | | | 2.7.9.2 |
| 13425, 13426 | 37678843 | 47 | 9.00E-53 | Vibrio vulnificus YJ016 | hypothetical protein VV0659 [Vibrio vulnificus YJ016] db BAC93423.1 conserved hypothetical protein [Vibrio vulnificus YJ016] | | | | |
| 13427, 13428 | 53714594 | 42 | 1.00E-29 | Bacteroides fragilis YCH46 | LacI family transcriptional regulator [Bacteroides fragilis YCH46] db BAD50052.1 LacI family transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 13429, 13430 | 34557684 | 51 | 2.00E-38 | Wolinella succinogenes DSM 1740 | PHOSPHOTYROSINE PROTEIN PHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE10399.1 PHOSPHOTYROSINE PROTEIN PHOSPHATASE [Wolinella succinogenes] | | | | 3.1.3.48 |
| 1343, 1344 | 48854902 | 41 | 5.00E-34 | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|---------|
| 13431, 13432 | 16078046 | 51 | 8.00E-67 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU09810 [Bacillus subtilis subsp. subtilis str. 168] emb CAA74443.1 hypothetical protein [Bacillus subtilis] emb CAB12820.1 yhaZ [Bacillus subtilis subsp. subtilis str. 168] pir D69820 hypothetical protein yhaZ - Bacillus subtilis | | | |
| 13433, 13434 | 20092636 | 40 | 7.00E-22 | Methanosarcina acetivorans C2A | hypothetical protein MA3840 [Methanosarcina acetivorans C2A] gb AAM07191.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | |
| 13437, 13438 | 48855764 | 39 | 3.00E-18 | Cytophaga hutchinsonii | COG5316: Uncharacterized conserved protein [Cytophaga hutchinsonii] putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO78416.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 13439, 13440 | 29348719 | 59 | 5.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | hydrogenase maturation protein HypF [Shewanella oneidensis MR-1] gb AAN55141.1 hydrogenase maturation protein HypF [Shewanella oneidensis MR-1] | | | |
| 13441, 13442 | 24373654 | 45 | 3.00E-57 | Shewanella oneidensis MR-1 | MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10559.1 MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes] | | | |
| 13445, 13446 | 34557844 | 25 | 2.00E-21 | Wolinella succinogenes DSM 1740 | SULFATE ADENYLYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10944.1 SULFATE ADENYLYLTRANSFERASE [Wolinella succinogenes] | | | 2.7.7.4 |
| 13447, 13448 | 34558229 | 46 | 4.00E-63 | Wolinella succinogenes DSM 1740 | DNA-binding response regulator RprY [Alvinella pompejana epibiont 6C6] transcriptional regulator, Crp family [Porphyromonas gingivalis W83] ref NP_905705.1 transcriptional regulator, Crp family [Porphyromonas gingivalis W83] | | | 2.7.3.- |
| 13449, 13450 | 34558806 | 31 | 6.00E-13 | Alvinella pompejana epibiont 6C6 | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii] | | | |
| 1345, 1346 | 34397542 | 33 | 1.00E-31 | Porphyromonas gingivalis W83 | hypothetical protein WS0587 [Wolinella succinogenes DSM 1740] emb CAE09719.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 13457, 13458 | 48855914 | 52 | 5.00E-21 | Cytophaga hutchinsonii | APOLIPOPROTEIN N-ACYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09249.1 APOLIPOPROTEIN N-ACYLTRANSFERASE [Wolinella succinogenes] sp Q7MAR3 LNT_WOLSU Apolipoprotein N- acyltransferase (ALP N-acyltransferase) | | | 2.3.1.- |
| 13459, 13460 | 34557004 | 52 | 5.00E-39 | Wolinella succinogenes DSM 1740 | hypothetical protein PBPR3401 [Photobacterium profundum SS9] emb CAG21685.1 conserved hypothetical protein [Photobacterium profundum] | | | |
| 13461, 13462 | 34556534 | 40 | 2.00E-51 | Wolinella succinogenes DSM 1740 | | | | |
| 13463, 13464 | 54310467 | 31 | 6.00E-14 | Photobacterium profundum SS9 | | | | |

| | | | | | | | | |
|--------|----------|----|-----------|---------------------------------------|---|--|----|------------------|
| 13465, | 48863717 | 26 | 2.00E-19 | Microbulbifer degradans 2-40 | COG2308: Uncharacterized conserved protein [Microbulbifer degradans 2-40] | | | |
| 13466 | | | | Microbulbifer degradans 2-40 | COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Microbulbifer degradans 2-40] | | | |
| 13467, | 48863716 | 40 | 1.00E-48 | Helicobacter hepaticus ATCC 51449 | hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449] | | | |
| 13468 | | | | Helicobacter hepaticus ATCC 51449 | ref NP_860480.1 hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449] | | | |
| 13469, | 32262499 | 50 | 5.00E-09 | Geobacter sulfurreducens PCA | hypothetical protein GSU0981 [Geobacter sulfurreducens PCA] | | | |
| 13470 | | | | Geobacter sulfurreducens PCA | gb AAR34308.1 conserved hypothetical protein [Geobacter sulfurreducens PCA] | | | |
| 1347, | 39996084 | 36 | 2.00E-22 | Campylobacter upsaliensis RM3195 | phosphoglucosamine mutase [Campylobacter upsaliensis RM3195] | Helicobacter pylori strain JF37 phosphoglucosamine mutase (glmM) gene, partial cds | 83 | 3.00E-15 5.4.2.- |
| 13471, | 57242727 | 65 | 1.00E-102 | Campylobacter leri RM2100 | probable transcription regulator Cj0571 [Campylobacter leri RM2100] | | | |
| 13472 | | | | Campylobacter leri RM2100 | gb EAL55392.1 probable transcription regulator Cj0571 [Campylobacter leri RM2100] | | | |
| 13473, | 57240278 | 42 | 1.00E-41 | Magnetococcus sp. MC-1 | COG2602: Beta-lactamase class D [Magnetococcus sp. MC-1] | | | 3.5.2.6 |
| 13474 | 48834051 | 49 | 2.00E-24 | Shewanella oneidensis MR-1 | hypothetical protein SO1851 [Shewanella oneidensis MR-1] gb AAN54903.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | Escherichia coli CFT073 section 4 of 18 of the complete genome | 89 | 3.00E-08 2.1.1.- |
| 13475, | 24373416 | 77 | 2.00E-81 | Desulfotalea psychrophila LSV54 | related to ATP-dependent helicase [Desulfotalea psychrophila LSV54] | | | |
| 13476 | 51245935 | 35 | 3.00E-41 | Nostoc sp. PCC 7120 | emb CAG36812.1 related to ATP-dependent helicase [Desulfotalea psychrophila LSV54] | | | 3.-.-.- |
| 13477, | | | | Nostoc sp. PCC 7120 | two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] | Pirellula sp. strain 1 complete genome; segment 6/24 | 95 | 1.00E-07 2.7.3.- |
| 13478 | 17231253 | 36 | 9.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | histidinol-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75309.1 histidinol-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8ABA8 HIS8_BACTN Histidinol-phosphate aminotransferase [imidazole acetol-phosphate transaminase] | Bacteroides thetaiotaomicron VPI-5482, section 1 of 21 of the complete genome | 87 | 5.00E-08 2.6.1.9 |
| 13479, | 29345612 | 48 | 6.00E-83 | Desulfotalea psychrophila LSV54 | hypothetical protein DP1553 [Desulfotalea psychrophila LSV54] | | | |
| 13480, | 51245405 | 41 | 2.00E-30 | Desulfotalea psychrophila LSV54 | emb CAG36282.1 unknown protein [Desulfotalea psychrophila LSV54] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--------------------------------------|--|---|--|--|----------|
| 13495, 13496 | 34332886 | 28 | 4.00E-19 | 12472 | Chromobacterium violaceum ATCC | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_903131.1 hypothetical protein CV3461 [Chromobacterium violaceum ATCC 12472] | | | 2.7.3.- |
| 13497, 13498 | 34558788 | 33 | 4.00E-35 | 6C6 | Alvinella pompejana epibiont | TPR domain protein [Alvinella pompejana epibiont 6C6] | | | |
| 135, 136 | 48855435 | 48 | 3.00E-24 | hutchinsonii | Cytophaga hutchinsonii | COG0777: Acetyl-CoA carboxylase beta subunit [Cytophaga hutchinsonii] | | | 6.4.1.2 |
| 13503, 13504 | 3511126 | 37 | 1.00E-37 | aegyptius | Haemophilus aegyptius | HaeIV restriction/modification system [Haemophilus aegyptius] | | | |
| 13505, 13506 | 23130584 | 36 | 6.00E-19 | PCC 73102 | Nostoc punctiforme PCC 73102 | COG0816: Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. subtilis) [Nostoc punctiforme PCC 73102] | | | |
| 13507, 13508 | 15606156 | 38 | 6.00E-38 | VF5 | Aquifex aeolicus VF5 | hypothetical protein aq_775 [Aquifex aeolicus VF5] gb AAC06941.1 hypothetical protein [Aquifex aeolicus VF5] pir A70368 conserved hypothetical protein aq_775 - Aquifex aeolicus | | | 4.-.-.- |
| 13509, 13510 | 24373682 | 35 | 1.00E-25 | Shewanella oneidensis MR-1 | Shewanella oneidensis MR-1 | purine-binding chemotaxis protein CheW [Shewanella oneidensis MR-1] gb AAN55169.1 purine-binding chemotaxis protein CheW [Shewanella oneidensis MR-1] | | | 2.7.3.- |
| 1351, 1352 | 23112865 | 41 | 1.00E-35 | Desulfotobacterium hafnense DCB-2 | Desulfotobacterium hafnense DCB-2 | COG4636: Uncharacterized protein conserved in cyanobacteria [Desulfotobacterium hafnense DCB-2] | | | |
| 13511, 13512 | 13357672 | 38 | 5.00E-13 | str. ATCC 700970 | Ureaplasma parvum serovar 3 str. ATCC 700970 | phosphoglycolate phosphatase [Ureaplasma parvum serovar 3 str. ATCC 700970] gb AAF30521.1 phosphoglycolate phosphatase [Ureaplasma parvum serovar 3 str. ATCC 700970] pir F82931 phosphoglycolate phosphatase UU115 [imported] - Ureaplasma urealyticum | | | 3.1.3.18 |
| 13513, 13514 | 32261701 | 51 | 1.00E-38 | 51449 | Helicobacter hepaticus ATCC 51449 | transcription elongation factor GreA [Helicobacter hepaticus ATCC 51449] ref NP_859685.1 transcription elongation factor GreA [Helicobacter hepaticus ATCC 51449] | | | |
| 13515, 13516 | 48846821 | 30 | 2.00E-17 | 15 | Geobacter metallireducens GS 15 | COG0639: Diadenosine tetraphosphatase and related serine/threonine protein phosphatases [Geobacter metallireducens GS-15] | | | 3.1.3.16 |
| 13521, 13522 | 52550386 | 43 | 9.00E-20 | GZfos3D4 | uncultured archaeon GZfos3D4 | putative glycerate kinase [uncultured archaeon GZfos3D4] | | | 1.1.1.81 |
| 13523, 13524 | 48863830 | 47 | 7.00E-30 | degradans 2-40 | Microbulbifer degradans 2-40 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Microbulbifer degradans 2-40] | | | |
| 13525, 13526 | 34557111 | 35 | 1.00E-08 | 1740 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0700 [Wolinella succinogenes DSM 1740] emb CAE09826.1 hypothetical protein [Wolinella succinogenes] | | | |

| | | | | | | | | |
|--|---|----------------------|--|---|---|--|---------|---------------------|
| 13529, 13530 | 29142624 | 28 | 2.00E-20 | Salmonella enterica subsp. enterica serovar Typhi Ty2 | putative aminotransferase CobD [Salmonella enterica subsp. enterica serovar Typhi Ty2] ref NP_455220.1 putative aminotransferase CobD [Salmonella enterica subsp. enterica serovar Typhi str. CT18] gb AAO69826.1 putative aminotransferase CobD [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD05121.1 putative aminotransferase CobD [Salmonella enterica subsp. enterica serovar Typhi] pir AG0581 probable aminotransferase CobD cobD [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) sp Q8Z8H8 COBD_SALT1 Threonine-phosphate decarboxylase (L-threonine-O-3-phosphate decarboxylase) | | | 2.6,1.9 |
| 13533, 13534 13535, 13536 | 29348161 53691857 | 53 39 | 1.00E-87 3.00E-43 | Bacteroides thetaiotaomicron VPI-5482 Desulfovibrio desulfuricans G20 | primosomal protein N' (replication factor Y) [Bacteroides thetaiotaomicron VPI-5482] gb AAO77858.1 primosomal protein N' (replication factor Y) [Bacteroides thetaiotaomicron VPI-5482] COG1876: D-alanyl-D-alanine carboxypeptidase [Desulfovibrio desulfuricans G20] | | | |
| 13537, 13538 | 32469350 | 53 | 4.00E-25 | Francisella tularensis subsp. novicida | unknown [Francisella tularensis subsp. novicida] GUANYLATE KINASE [Wolinella succinogenes DSM 1740] | | | |
| 13539, 13540 13541, 13542 | 34556634 48856940 | 53 33 | 4.00E-57 1.00E-15 | Wolinella succinogenes DSM 1740 Cytophaga hutchinsonii | emb CAE09349.1 GUANYLATE KINASE [Wolinella succinogenes] sp Q7MAK5 KGUA_WOLSU Guanylate kinase (GMP kinase) COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] DNA polymerase III, alpha subunit [Porphyromonas gingivalis W83] ref NP_904390.1 DNA polymerase III, alpha subunit [Porphyromonas gingivalis W83] | | 2.7.4.8 | |
| 13545, 13546 | 34396222 | 60 | 1.00E-102 | Porphyromonas gingivalis W83 | 2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE09579.1 2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes] D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes DSM 1740] emb CAE09578.1 D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes] COG4191: Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Magnetococcus sp. MC-1] | | | 2.7.7.7 |
| 13549, 13550 13551, 13552 13553, 13554 13555, 13556 | 34556864 34556863 48833776 5360168 | 48 48 36 32 | 8.00E-46 1.00E-22 3.00E-33 9.00E-37 | Wolinella succinogenes DSM 1740 Wolinella succinogenes DSM 1740 Magnetococcus sp. MC-1 Flavobacterium johnsoniae | | | | 6.3.2.15 2.7.3.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 13559, 13560 | 57237231 | 52 | 2.00E-65 | Campylobacter jejuni RM1221 | DNA adenine methylase [Campylobacter jejuni RM1221] gb AAW34814.1 DNA adenine methylase [Campylobacter jejuni RM1221] | | | 2.1.1.72 |
| 13561, 13562 | 48856760 | 45 | 3.00E-33 | Cytophaga hutchinsonii | COG2062: Phosphohistidine phosphatase SixA [Cytophaga hutchinsonii] | | | 3.1.3.- |
| 13563, 13564 | 52550557 | 39 | 7.00E-55 | uncultured archaeon GZfos9E5 | predicted P-loop ATPase [uncultured archaeon GZfos9E5] | | | |
| 13565, 13566 | 34557232 | 37 | 8.00E-16 | Wolinella succinogenes DSM 1740 | NIFS PROTEIN (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE09947.1 NIFS PROTEIN (FRAGMENT) [Wolinella succinogenes] | | | 4.4.1.- |
| 13567, 13568 | 57169090 | 35 | 3.00E-12 | Campylobacter coli RM2228 | N-terminal HTH domain of molybdenum-binding protein family [Campylobacter coli RM2228] gb EAL56239.1 N-terminal HTH domain of molybdenum-binding protein family [Campylobacter coli RM2228] | | | |
| 13569, 13570 | 21673339 | 26 | 5.00E-14 | Chlorobium tepidum TLS | hypothetical protein CT0504 [Chlorobium tepidum TLS] gb AAM71746.1 hypothetical protein [Chlorobium tepidum TLS] | | | |
| 1357, 1358 | 47569655 | 62 | 3.00E-09 | Bacillus cereus G9241 | prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241] gb EAL12072.1 prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241] | | | |
| 13573, 13574 | 34556738 | 52 | 9.00E-87 | Wolinella succinogenes DSM 1740 | SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes DSM 1740] emb CAE09453.1 SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes] sp Q7MAE6 ARGD_WOLSU Acetylornithine aminotransferase (ACOAT) | | | 2.6.1.11 |
| 13575, 13576 | 34556738 | 53 | 9.00E-57 | Wolinella succinogenes DSM 1740 | SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes DSM 1740] emb CAE09453.1 SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes] sp Q7MAE6 ARGD_WOLSU Acetylornithine aminotransferase (ACOAT) | | | 2.6.1.11 |
| 13577, 13578 | 48853920 | 49 | 2.00E-30 | Cytophaga hutchinsonii | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii] | | | |
| 13579, 13580 | 34558448 | 56 | 2.00E-25 | Wolinella succinogenes DSM 1740 | ANTHRANILATE SYNTHASE COMPONENT II [Wolinella succinogenes DSM 1740] emb CAE11163.1 ANTHRANILATE SYNTHASE COMPONENT II [Wolinella succinogenes] | | | 4.1.3.27 |
| 13583, 13584 | 15893748 | 27 | 9.00E-10 | Clostridium acetobutylicum ATCC 824 | Transcriptional regulator, AcrR family [Clostridium acetobutylicum ATCC 824] gb AAK78437.1 Transcriptional regulator, AcrR family [Clostridium acetobutylicum ATCC 824] pir B96956 transcription regulator, AcrR family [Imported] - Clostridium acetobutylicum | | | |
| 13585, 13586 | 34557295 | 24 | 1.00E-13 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0905 [Wolinella succinogenes DSM 1740] emb CAE10010.1 hypothetical protein [Wolinella succinogenes] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|----------|
| 13587, 13588 | 19705009 | 30 | 1.00E-30 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Oxidoreductase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93803.1 Oxidoreductase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | 1.1.1.- |
| 13589, 13590 | 57238414 | 50 | 3.00E-40 | Campylobacter jejuni RM1221 | nucleotide phosphoribosyltransferase, putative [Campylobacter jejuni RM1221] gb AAW35997.1 nucleotide phosphoribosyltransferase, putative [Campylobacter jejuni RM1221] emb CAB73797.1 putative nucleotide phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir G81281 probable nucleotide phosphoribosyltransferase C 1370 [Imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282516.1 putative nucleotide phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] | | | 2.4.2.22 |
| 1359, 1360 | 47569655 | 39 | 4.00E-13 | Bacillus cereus G9241 | prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241] gb EAL12072.1 prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241] | | | |
| 13591, 13592 | 48893877 | 30 | 7.00E-12 | Trichodesmium erythraeum IMS101 | COG0642: Signal transduction histidine kinase [Trichodesmium erythraeum IMS101] | | | 2.7.3.- |
| 13593, 13594 | 34557246 | 57 | 3.00E-61 | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | | | 2.7.3.- |
| 13597, 13598 | 45528155 | 59 | 9.00E-23 | Crocospaera watsonii WH 8501 | COG0662: Mannose-6-phosphate isomerase [Crocospaera watsonii WH 8501] | | | |
| 13599, 13600 | 53731618 | 68 | 4.00E-61 | Methanococcoides burtonii DSM 6242 | COG0577: ABC-type antimicrobial peptide transport system, permease component [Methanococcoides burtonii DSM 6242] | | | |
| 13601, 13602 | 53731618 | 75 | 3.00E-88 | Methanococcoides burtonii DSM 6242 | COG0577: ABC-type antimicrobial peptide transport system, permease component [Methanococcoides burtonii DSM 6242] | | | |
| 13603, 13604 | 27366052 | 37 | 2.00E-40 | Vibrio vulnificus CMCP6 | ABC-type amino acid transport, signal transduction systems, periplasmic component/domain [Vibrio vulnificus CMCP6] gb AAO11107.1 ABC-type amino acid transport, signal transduction systems, periplasmic component/domain [Vibrio vulnificus CMCP6] | | | |
| 13605, 13606 | 17545857 | 43 | 4.00E-31 | Ralstonia solanacearum GMI1000 | PUTATIVE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GMI1000] emb CAD14840.1 PUTATIVE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] | | | |
| 13607, 13608 | 32261983 | 41 | 3.00E-08 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859966.1 hypothetical protein HH0435 [Helicobacter hepaticus ATCC 51449] gb AAD30109.1 membrane-associated protein map18 [Helicobacter hepaticus] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|---------------|
| 13609, 13610 | 23126603 | 34 | 9.00E-38 | Nostoc punctiforme PCC 73102 | COG0834: ABC-type amino acid transport/signal transduction systems, periplasmic component/domain [Nostoc punctiforme PCC 73102] | | | |
| 1361, 1362 | 48856375 | 37 | 3.00E-27 | Cytophaga hutchinsonii | COG0568: DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32) [Cytophaga hutchinsonii] | | | |
| 13611, 13612 | 46578435 | 29 | 7.00E-42 | Desulfovibrio vulgaris subsp. vulgaris str. | methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gblAA594502.1 methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | 2.7.3.- |
| 13613, 13614 | 21226648 | 30 | 6.00E-11 | Methanosarcina mazel Go1 | hypothetical protein MM0546 [Methanosarcina mazel Go1] gblAAM30242.1] conserved protein [Methanosarcina mazel Go1] | | | |
| 13615, 13616 | 54024734 | 40 | 8.00E-38 | Nocardia farcinica IFM 10152 | putative restriction-modification system endonuclease [Nocardia farcinica IFM 10152] dbjBAD57612.1] putative restriction-modification system endonuclease [Nocardia farcinica IFM 10152] | | | 3.1.21.3 |
| 13619, 13620 | 48855496 | 42 | 1.00E-64 | Cytophaga hutchinsonii | COG0514: Superfamily II DNA helicase [Cytophaga hutchinsonii] | | | 3.6.1.- |
| 13621, 13622 | 57238514 | 34 | 4.00E-21 | Campylobacter jejuni RM1221 | DNA-binding response regulator [Campylobacter jejuni RM1221] | | | 2.7.3.- |
| 13623, 13624 | 42522455 | 41 | 5.00E-27 | Bdellovibrio bacteriovorus HD100 | cell wall surface anchor family protein [Bdellovibrio bacteriovorus HD100] embICA78828.1] cell wall surface anchor family protein [Bdellovibrio bacteriovorus HD100] | | | |
| 13629, 13630 | 46019826 | 40 | 2.00E-46 | Streptococcus thermophilus | putative cytosine-specific methyltransferase [Streptococcus thermophilus] | | | 2.1.1.73 |
| 1363, 1364 | 48853840 | 32 | 9.00E-25 | Cytophaga hutchinsonii | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | |
| 13631, 13632 | 57240720 | 47 | 3.00E-48 | Campylobacter lari RM2100 | biotin--acetyl-CoA-carboxylase ligase [Campylobacter lari RM2100] gblEAL55113.1] biotin--acetyl-CoA-carboxylase ligase [Campylobacter lari RM2100] | | | 6.3.4.15 |
| 13635, 13636 | 53765153 | 35 | 4.00E-16 | Anabaena variabilis ATCC 29413 | COG1975: Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family [Anabaena variabilis ATCC 29413] | | | |
| 13637, 13638 | 57241988 | 42 | 4.00E-19 | Campylobacter upsaliensis RM3195 | folypolyglutamate synthase (folC) [Campylobacter upsaliensis RM3195] gblEAL53961.1] folypolyglutamate synthase (folC) [Campylobacter upsaliensis RM3195] | | | 6.3.2.17 |
| 13641, 13642 | 54302389 | 55 | 6.00E-88 | Photobacterium profundum SS9 | hypothetical protein PBPRB0710 [Photobacterium profundum SS9] embICAG22582.1] hypothetical protein [Photobacterium profundum SS9] | | | 6.3.2.3 |
| 13643, 13644 | 54302390 | 56 | 3.00E-46 | Photobacterium profundum SS9 | hypothetical carboxypeptidase G2 [Photobacterium profundum SS9] embICAG22583.1] hypothetical carboxypeptidase G2 [Photobacterium profundum] | | | 3.4.17.1 1 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|---------------------|---------|
| 13645, 13646 | 29347044 | 39 | 4.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1634 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76741.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 13647, 13648 | 31291 | 59 | 8.00E-74 | Homo sapiens | unnamed protein product [Homo sapiens] emb CAD97795.1 hypothetical protein [Homo sapiens] | | | | 3.7.1.2 |
| 13651, 13652 | 57168696 | 42 | 1.00E-23 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56657.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 13653, 13654 | 56750182 | 33 | 2.00E-08 | Synechococcus elongatus PCC 6301 | hypothetical protein syc0173_c [Synechococcus elongatus PCC 6301] dbj BAD78363.1 hypothetical protein [Synechococcus elongatus PCC 6301] probable membrane protein Cj0152c [Campylobacter lari RM2100] | | | | 2.7.3.- |
| 13655, 13656 | 57241387 | 30 | 2.00E-18 | Campylobacter lari RM2100 | gb EAL54499.1 probable membrane protein Cj0152c [Campylobacter lari RM2100] conserved hypothetical protein; putative sensory transduction histidine kinase [Acinetobacter sp. ADP1] emb CAG69864.1 conserved hypothetical protein; putative sensory transduction histidine kinase [Acinetobacter sp. ADP1] | | | | 2.7.3.- |
| 13659, 13660 | 50086176 | 25 | 3.00E-14 | Acinetobacter sp. ADP1 | putative membrane protein [Staphylococcus aureus subsp. aureus MRSA252] emb CAG40924.1 putative membrane protein [Staphylococcus aureus subsp. aureus MRSA252] | | | | |
| 13663, 13664 | 49484088 | 22 | 1.00E-07 | Staphylococcus aureus subsp. aureus MRSA252 | DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW35678.1 DNA-binding response regulator [Campylobacter jejuni RM1221] emb CAB73477.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282370.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81329 probable two-component regulator Cj1223c [imported] - Campylobacter jejuni (strain NCTC 11168) | | | | |
| 13667, 13668 | 57238095 | 49 | 6.00E-35 | Campylobacter jejuni RM1221 | COG0265: Trypsin-like serine proteases, typically periplasmic, contain C- terminal PDZ domain [Cytophaga hutchinsonii] | | | 87 6.00E-12 2.7.3.- | |
| 1367, 1368 | 48853600 | 36 | 4.00E-31 | Cytophaga hutchinsonii | Highly conserved protein containing a domain related to cellulase catalytic domain and a thioredoxin domain [Clostridium acetobutylicum ATCC 824] gb AAK81471.1 Highly conserved protein containing a domain related to cellulase catalytic domain and a thioredoxin domain [Clostridium acetobutylicum ATCC 824] pir D97335 hypothetical protein CAC3546 [imported] - Clostridium acetobutylicum | | | 3.4.21.- | |
| 13673, 13674 | 15896782 | 37 | 2.00E-45 | Clostridium acetobutylicum ATCC 824 | PUTATIVE TWO 2-COMPONENT RECEIVER DOMAINS PROTEIN [Sinorhizobium meliloti 1021] emb CAC46578.1 PUTATIVE TWO 2- COMPONENT RECEIVER DOMAINS PROTEIN [Sinorhizobium meliloti] | | | | 2.7.4.9 |
| 13675, 13676 | 15965752 | 32 | 5.00E-17 | Sinorhizobium meliloti 1021 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|--|---|---|----|----------|----------|
| 13677, 13678 | 34556483 | 61 | 1.00E-105 | Wollinella succinogenes DSM 1740 | PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wollinella succinogenes DSM 1740] emb CAE09198.1 PUTATIVE UDP- GLUCURONIC ACID EPIMERASE [Wollinella succinogenes] | B.thuringiensis PK1 & cap genes, putative | 85 | 3.00E-18 | 5.1.3.- |
| 13683, 13684 | 3122989 | 70 | 5.00E-52 | Escherichia coli | UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) gb AAC45829.1 hypothetical uridine-5'-diphosphoglucose dehydrogenase [Escherichia coli] | Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150 | 88 | 5.00E-09 | 1.1.1.22 |
| 13685, 13686 | 57240662 | 39 | 7.00E-33 | Campylobacter lari RM2100 | response regulator [Campylobacter lari RM2100] gb EAL55055.1 response regulator [Campylobacter lari RM2100] | | | | 2.7.3.- |
| 13689, 13690 | 57240337 | 55 | 2.00E-46 | Campylobacter lari RM2100 | HIT family protein [Campylobacter lari RM2100] gb EAL55451.1 HIT family protein [Campylobacter lari RM2100] | | | | 3.6.1.17 |
| 1369, 1370 | 53797583 | 49 | 9.00E-52 | Chloroflexus aurantiacus | COG1200: RecG-like helicase [Chloroflexus aurantiacus] | | | | 3.6.1.- |
| 13693, 13694 | 42525039 | 34 | 9.00E-20 | Bdellovibrio bacteriovorus HD100 | putative zinc metallo protease [Bdellovibrio bacteriovorus HD100] emb CAE81073.1 putative zinc metallo protease [Bdellovibrio bacteriovorus HD100] | | | | 3.4.24.- |
| 13695, 13696 | 52548588 | 28 | 1.00E-11 | uncultured archaeon GZfos17F1 | FOG TPR repeat [uncultured archaeon GZfos17F1] | | | | |
| 137, 138 | 39997183 | 41 | 3.00E-42 | Geobacter sulfurreducens PCA | ADP-heptose synthase [Geobacter sulfurreducens PCA] gb AAR35461.1 ADP-heptose synthase [Geobacter sulfurreducens PCA] sp Q74BF6 HLDE_GEOSL Bifunctional protein hldE [Includes: D-beta-D- heptose 7-phosphate kinase (D-beta-D-heptose 7-phosphotransferase); D- beta-D-heptose 1-phosphate adenosyltransferase] | | | | 2.7.-.- |
| 13703, 13704 | 34557665 | 47 | 5.00E-27 | Wollinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes] | | | | 2.7.3.- |
| 13705, 13706 | 34556560 | 52 | 1.00E-31 | Wollinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes] | | | | |
| 13707, 13708 | 23123945 | 27 | 3.00E-24 | Nostoc punctiforme PCC 73102 | COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 1371, 1372 | 48853483 | 45 | 3.00E-29 | Cytophaga hutchinsonii | COG0566: rRNA methylases [Cytophaga hutchinsonii] | | | | 2.1.1.34 |
| 13713, 13714 | 48854978 | 52 | 3.00E-68 | Cytophaga hutchinsonii | COG1410: Methionine synthase 1, cobalamin-binding domain [Cytophaga hutchinsonii] | | | | 2.1.1.13 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|----------|
| 13715, 13716 | 13472325 | 32 | 6.00E-23 | Mesorhizobium loti MAFF303099 | endo-1,3-1,4-beta-glycanase [Mesorhizobium loti MAFF303099] dbj BAB49678.1 endo-1,3-1,4-beta-glycanase [Mesorhizobium loti MAFF303099] | | | | 3.2.1.- |
| 13717, 13718 | 34557931 | 67 | 3.00E-73 | Wollinella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTION REGULATOR [Wollinella succinogenes DSM 1740] emb CAE10846.1 PUTATIVE TRANSCRIPTION REGULATOR [Wollinella succinogenes] | | | | 2.1.1.63 |
| 13719, 13720 | 48846313 | 38 | 7.00E-11 | Geobacter metallireducens GS-15 | COG1450: Type II secretory pathway, component PulD [Geobacter metallireducens GS-15] | | | | |
| 13721, 13722 | 15606636 | 27 | 4.00E-10 | Aquifex aeolicus VF5 | hypothetical protein aq_1473 [Aquifex aeolicus VF5] gb AAC07420.1 putative protein [Aquifex aeolicus VF5] pir A70428 hypothetical protein aq_1473 - Aquifex aeolicus | | | | |
| 13725, 13726 | 46201088 | 66 | 1.00E-97 | Magnetospirillum magnetotacticum MS-1 | COG2192: Predicted carbamoyl transferase, NodU family [Magnetospirillum magnetotacticum MS-1] | Prochlorococcus marinus MED4 complete genome; segment 4/5 | 86 | 2.00E-10 | 2.7.3.- |
| 13729, 13730 | 34555660 | 30 | 1.00E-27 | Wollinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes] | | | | 2.7.3.- |
| 1373, 1374 | 48855091 | 36 | 2.00E-31 | Cytophaga hutchinsonii | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 13731, 13732 | 29347060 | 37 | 4.00E-17 | Bacteroides thetataoamicron VPI-5482 | putative teichoic acid biosynthesis protein F [Bacteroides thetataoamicron VPI-5482] gb AAO76757.1 putative teichoic acid biosynthesis protein F [Bacteroides thetataoamicron VPI-5482] | | | | |
| 13733, 13734 | 48853891 | 58 | 8.00E-40 | Cytophaga hutchinsonii | COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Cytophaga hutchinsonii] | | | | |
| 13735, 13736 | 32262912 | 55 | 1.00E-44 | Helicobacter hepaticus ATCC 51449 | lipopolysaccharid core biosynthesis protein [Helicobacter hepaticus ATCC 51449] ref NP_860892.1 lipopolysaccharid core biosynthesis protein [Helicobacter hepaticus ATCC 51449] | | | | 2.7.7.3 |
| 13737, 13738 | 39896754 | 36 | 6.00E-45 | Geobacter sulfurreducens PCA | response regulator, putative [Geobacter sulfurreducens PCA] gb AAR35028.1 response regulator, putative [Geobacter sulfurreducens PCA] | | | | 2.7.3.- |
| 13739, 13740 | 54302806 | 45 | 3.00E-40 | Photobacterium profundum SS9 | hypothetical protein PBPRB1127 [Photobacterium profundum SS9] emb CAG22999.1 conserved hypothetical protein [Photobacterium profundum] | | | | |

| | | | | | | | | | |
|--|--|----------------------|---|--|--|--|--|----|-------------------|
| 13741, 13742 | 6968536 | 54 | 2.00E-66 | Campylobacter jejuni subsp. jejuni NCTC 11168 | tRNA pseudouridine synthase B [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81314 pseudouridylylase synthase (EC 4.2.1.70) tRNA-specific Cj1102 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282250.1 tRNA pseudouridine synthase B [Campylobacter jejuni subsp. jejuni NCTC 11168] sp Q8PNJ2 TRUB_CAMJE tRNA pseudouridine synthase B (tRNA pseudouridine 55 synthase) (Psf55 synthase) (Pseudouridylylase synthase) (Uracil hydrolyase) | | | | 4.2.1.70 |
| 13747, 13748 1375, 1376 | 57242478 | 32 | 2.00E-15 | Campylobacter upsallensis RM3195 | type I restriction-modification system, M subunit, putative [Campylobacter upsallensis RM3195] gb EAL53546.1 type I restriction-modification system, M subunit, putative [Campylobacter upsallensis RM3195] | | | | |
| | 46486686 | 26 | 1.00E-17 | Lyngbya majuscula | JamP [Lyngbya majuscula] | | | | 2.3.1.38 |
| 13751, 13752 13757, 13758 13759, 13760 13765, 13766 | 51244502 ABU0094 8 48836151 57168617 | 71 32 46 25 | 1.00E-107 5.00E-30 1.00E-63 2.00E-09 | Desulfotalea psychrophila LSV54 Thermobifida fusca Campylobacter coli RM2228 | probable DNA gyrase, subunit A [Desulfotalea psychrophila LSV54] emb CAG35379.1 probable DNA gyrase, subunit A [Desulfotalea psychrophila LSV54] Desc:S. pneumoniae type 4 strain protein from coding region #517. Org:Streptococcus pneumoniae type 4 strain COG0210: Superfamily I DNA and RNA helicases [Thermobifida fusca] HsdM [Campylobacter coli RM2228] gb EAL56578.1 HsdM [Campylobacter coli RM2228] conserved hypothetical protein [Streptomyces coelicolor A3(2)] ref NP_627953.1 hypothetical protein SCO3763 [Streptomyces coelicolor A3(2)] | | | 95 | 6.00E-07 5.99.1.3 |
| 13769, 13770 13775, 13776 | 10432467 4234793 | 26 40 | 7.00E-13 5.00E-38 | Streptomyces coelicolor A3(2) Leptospira borgpetersenii | ref NP_627953.1 hypothetical protein SCO3763 [Streptomyces coelicolor A3(2)] unknown [Leptospira borgpetersenii] | | | | |
| 13779, 13780 13783, 13784 | 33347983 53712412 | 32 48 | 6.00E-07 5.00E-35 | Enterobacteria phage RB49 Bacteroides fragilis YCH46 | gp2 DNA end protector protein [Enterobacteria phage RB49] ref NP_891702.1 gp2 DNA end protector protein [Enterobacteria phage RB49] adenylate kinase [Bacteroides fragilis YCH46] dbj BAD47870.1 adenylate kinase [Bacteroides fragilis YCH46] | | | | 2.7.4.3 |
| 13785, 13786 | 29347006 | 51 | 3.00E-45 | Bacteroides thetaiotaomicron VPI-5482 | putative sulfatase yidJ [Bacteroides thetaiotaomicron VPI-5482] gb AAO76703.1 putative sulfatase yidJ [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.1.6.6 |

| | | | | | | | | |
|-----------------|--------------|----|----------|---|--|--|----|----------|
| 13787, 13788 | 29347006 | 49 | 3.00E-44 | Bacteroides thetalaotomicron VPI-5482 | putative sulfatase yidJ [Bacteroides thetalaotomicron VPI-5482] gb AAO76703.1 putative sulfatase yidJ [Bacteroides thetalaotomicron VPI-5482] | | | 3.1.6.6 |
| 13789, 13790 | 57241143 | 57 | 7.00E-99 | Campylobacter lari RM2100 | DNA ligase, NAD-dependent [Campylobacter lari RM2100] gb EAL54839.1 DNA ligase, NAD-dependent [Campylobacter lari RM2100] | | | 6.5.1.2 |
| 13791, 13792 | 48853636 | 39 | 6.00E-33 | Cytophaga hutchinsonii | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 13795, 13796 | 48833622 | 23 | 3.00E-19 | Magnetococcus sp. MC-1 | COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1] hypothetical protein OB2759 [Oceanobacillus ihayensis HTE831] | | | |
| 13797, 13798 | 23100214 | 37 | 9.00E-08 | Oceanobacillus ihayensis HTE831 | hypothetical protein OB2759 [Oceanobacillus ihayensis HTE831] dbj BAC14715.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831] | | | 3.1.3.15 |
| 13799, 13800 | 34556616 | 40 | 9.00E-64 | Wolinella succinogenes DSM 1740 | CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes] | | | |
| 13801, 13802 | 34556616 | 38 | 4.00E-29 | Wolinella succinogenes DSM 1740 | CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes] | | | |
| 13805, 13806 | 32170824 | 52 | 2.00E-24 | Sphingomonas elodea | dTDP-D-glucose-4,6-dehydratase [Sphingomonas elodea] | | | 4.2.1.46 |
| 13807, 13808 | 56783471 | 69 | 3.00E-61 | Campylobacter jejuni | sugar-1-phosphate nucleotidyltransferase [Campylobacter jejuni] | Nostoc sp. PCC 7120 DNA, complete genome | 93 | 3.00E-07 |
| 13813, 13814 | 23475504 | 33 | 3.00E-33 | Desulfovibrio desulfuricans G20 | COG2348: Uncharacterized protein involved in methicillin resistance [Desulfovibrio desulfuricans G20] | | | |
| 13819, 13820 | ABB8477 1 | 42 | 1.00E-35 | | DescDNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org.Cytophaga hutchinsonii | | | |
| 13821, 13822 | 34557329 | 35 | 4.00E-23 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0940 [Wolinella succinogenes DSM 1740] emb CAE10044.1 conserved hypothetical protein [Wolinella succinogenes] | | | 2.7.3.- |
| 13823, 13824 | 37677003 | 22 | 7.00E-11 | Vibrio vulnificus YJ016 | hypothetical protein VVA1343 [Vibrio vulnificus YJ016] dbj BAC97369.1 conserved hypothetical protein [Vibrio vulnificus YJ016] | | | |
| 13827, 13828 | 48854305 | 51 | 6.00E-22 | Cytophaga hutchinsonii | COG0026: Phosphoribosylaminimidazole carboxylase (NCAIR synthetase) [Cytophaga hutchinsonii] | | | 4.1.1.21 |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|-------------------|----------|
| 1383, 1384 | 29349052 | 41 | 2.00E-45 | Bacteroides thetaiotaomicron VPI-5482 | UDP-N-acetylmuramoylalanyl-D-glutaryl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides thetaiotaomicron VPI-5482] gblAAO78749.1 UDP-N-acetylmuramoylalanyl-D-glutaryl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides thetaiotaomicron VPI-5482] | | | 6.3.2.15 |
| 13831, 13832 | 48856007 | 42 | 1.00E-34 | Cytophaga hutchinsonii | COG0308: Aminopeptidase N [Cytophaga hutchinsonii] | | | 3.4.11.- |
| 13833, 13834 | 46164951 | 32 | 3.00E-37 | Pseudomonas aeruginosa UCBPP PA14 | COG2831: Hemolysin activation/secretion protein [Pseudomonas aeruginosa UCBPP-PA14] | | | |
| 13835, 13836 | 53765608 | 47 | 7.00E-68 | Anabaena variabilis ATCC 29413 | COG4096: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Anabaena variabilis ATCC 29413] | | | 3.1.21.3 |
| 13837, 13838 | 57241290 | 57 | 3.00E-46 | Campylobacter lari RM2100 | Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100] gblEAL54986.1 Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 97 3.00E-11 4.--- | |
| 13839, 13840 | 6967998 | 25 | 9.00E-08 | Campylobacter jejuni subsp. jejuni NCTC 11168 | putative periplasmic protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir B81399 probable periplasmic protein Cj0530 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281714.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni NCTC 11168] | | | |
| 13841, 13842 | 28210082 | 31 | 6.00E-14 | Clostridium tetani E88 | exodeoxyribonuclease V alpha chain [Clostridium tetani E88] gblAAO34963.1 exodeoxyribonuclease V alpha chain [Clostridium tetani E88] | | | 3.1.11.5 |
| 13843, 13844 | 53713270 | 53 | 5.00E-84 | Bacteroides fragilis YCH46 | helicase domain protein [Bacteroides fragilis YCH46] dbj BAD48728.1 helicase domain protein [Bacteroides fragilis YCH46] | | | |
| 13847, 13848 | 15965752 | 33 | 7.00E-17 | Sinorhizobium meliloti 1021 | PUTATIVE TWO 2-COMPONENT RECEIVER DOMAINS PROTEIN [Sinorhizobium meliloti 1021] emb CAC46578.1 PUTATIVE TWO 2-COMPONENT RECEIVER DOMAINS PROTEIN [Sinorhizobium meliloti] | | | |
| 1385, 1386 | 53799051 | 41 | 5.00E-15 | Chloroflexus aurantiacus | COG0500: SAM-dependent methyltransferases [Chloroflexus aurantiacus] | | | |
| 13851, 13852 | 3183059 | 44 | 4.00E-55 | Anthopleura japonica | Arginine kinase (AK) dbj BAA22888.1 arginine kinase [Anthopleura japonica] | | | 2.7.3.3 |
| 13857, 13858 | 11692716 | 28 | 2.00E-14 | Methanothermobacter ther woolfeii prophage psiM100 | unknown [Methanothermobacter woolfeii prophage psiM100] ref NP_071813.1 unknown [Methanothermobacter woolfeii prophage psiM100] | | | |
| 13859, 13860 | 11497405 | 38 | 6.00E-55 | Borrelia burgdorferi B31 | adenine specific DNA methyltransferase [Borrelia burgdorferi B31] gblAAF07736.1 adenine specific DNA methyltransferase [Borrelia burgdorferi B31] | | | |

| | | | | | | | | | |
|---|----------------------------------|----------------|----------------------------------|--|--|--|----|----------|----------|
| 13861, 13862, 13863, 13864 | 29349444 34396491 | 38 53 | 8.00E-25 2.00E-54 | Bacteroides thetaiotaomicron VPI-5482 Porphyromonas gingivalis W83 | hypothetical protein BT4036 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79141.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] GTP-binding protein [Porphyromonas gingivalis W83] ref NP_904658.1 GTP-binding protein [Porphyromonas gingivalis W83] | | | | |
| 13865, 13866, 13867, 13868, 13869, 13870 | 28170140 48854120 48854120 | 83 39 52 | 1.00E-84 3.00E-19 3.00E-68 | Vibrio vulnificus Cytophaga hutchinsonii Cytophaga hutchinsonii | dTDP-6-deoxy-D-xylo-4-hexulose-3,5-epimerase [Vibrio vulnificus] COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] | Vibrio vulnificus strain 1003 glucose-1-phosphate thymidyltransferase (mliA) gene, partial cds; dTDP-4-keto-L-rhamnose reductase (mliD), dTDP-6-deoxy-D-xylo-4-hexulose-3,5-epimerase (mliC), WcvE protein (wcvE), rhamnosyl transferase (wcvF), flippase (wzx), and glycosyl transferase (wcvG) genes, complete cds; and polymerase (wzy) gene, partial cds | 80 | 6.00E-37 | 5.1.3.13 |
| 1387, 1388 | 53715621 | 59 | 1.00E-34 | Bacteroides fragilis YCH46 Wolinella succinogenes DSM 1740 | hypothetical protein BF4341 [Bacteroides fragilis YCH46] dbj BAD51079.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | 6.2.1.3 |
| 13871, 13872 | 34558477 | 47 | 5.00E-10 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2202 [Wolinella succinogenes DSM 1740] emb CAE11192.1 hypothetical protein [Wolinella succinogenes] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|---------------|
| 13873, 13874 | 15678369 | 31 | 8.00E-26 | Methanothermobacter thermautotrophicus str. Delta H | coenzyme F420-reducing hydrogenase, beta subunit homolog [Methanothermobacter thermautotrophicus str. Delta H] gb AAB84847.1 coenzyme F420-reducing hydrogenase, beta subunit homolog [Methanothermobacter thermautotrophicus str. Delta H] pir H69143 coenzyme F420-reducing hydrogenase, beta subunit homolog - Methanobacterium thermoautotrophicum (strain Delta H) | | | | 1.12.99. 1 |
| 13875, 13876 | 23111747 | 42 | 9.00E-65 | Desulfotobacterium hafniense DCB-2 | COG1032: Fe-S oxidoreductase [Desulfotobacterium hafniense DCB-2] ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221] gb AAW36203.1 ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221] | | | | 1.97.1.4 |
| 13877, 13878 | 57238620 | 47 | 3.00E-49 | Campylobacter jejuni RM1221 | | | | | 2.7.7.60 |
| 13879, 13880 | | | | | | | | Desulfotalea psychrophila Lsv54 chromosome | 82 6.00E-15 |
| 13881, 13882 | 26987128 | 38 | 1.00E-29 | Pseudomonas putida KT2440 | sensory box protein [Pseudomonas putida KT2440] gb AAN66017.1 sensory box protein [Pseudomonas putida KT2440] | | | | 2.7.3.- |
| 13887, 13888 | 57240449 | 55 | 1.00E-35 | Campylobacter lari RM2100 | transcription-repair coupling factor [Campylobacter lari RM2100] gb EAL55563.1 transcription-repair coupling factor [Campylobacter lari RM2100] | | | | |
| 1389, 1390 | 48853834 | 69 | 2.00E-68 | Cytophaga hutchinsonii | COG0536: Predicted GTPase [Cytophaga hutchinsonii] | | | | |
| 13891, 13892 | 56420320 | 60 | 1.00E-51 | Geobacillus kaustophilus HTA426 | glutathione peroxidase [Geobacillus kaustophilus HTA426] dbj BAD76070.1 glutathione peroxidase [Geobacillus kaustophilus HTA426] | | | | 1.11.1.9 |
| 13893, 13894 | 34557957 | 35 | 2.00E-40 | Wolinella succinogenes DSM 1740 | ATP-BINDING PROTEIN-ATPases involved in chromosome partitioning [Wolinella succinogenes DSM 1740] emb CAE10672.1 ATP-BINDING PROTEIN-ATPases involved in chromosome partitioning [Wolinella succinogenes] | | | | |
| 13895, 13896 | 48832078 | 47 | 3.00E-56 | Magnetococcus sp. MC-1 | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Magnetococcus sp. MC-1] | | | | 2.7.3.- |
| 13897, 13898 | 53712612 | 39 | 3.00E-38 | Bacteroides fragilis YCH46 | O-succinylbenzoic acid-CoA ligase [Bacteroides fragilis YCH46] dbj BAD48070.1 O-succinylbenzoic acid-CoA ligase [Bacteroides fragilis YCH46] | | | | 6.2.1.26 |
| 13899, 13900 | 1197006 | 46 | 2.00E-54 | Bacteroides fragilis | unknown protein [Bacteroides fragilis] gb AA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551) | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|-------------|----------|
| 13903, 13904 | 29350114 | 32 | 2.00E-13 | Bacteroides thetaiotaomicron VPI-5482 | putative anti-sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79811.1 putative anti-sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 13905, 13906 | 53712242 | 39 | 1.00E-29 | Bacteroides fragilis YCH46 | RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] db BAD47700.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] | | | | |
| 13907, 13908 | 52548364 | 54 | 7.00E-67 | uncultured archaeon GZfos11H11 | pyruvate-formate lyase-activating enzyme [uncultured archaeon GZfos11H11] | | | | 1.97.1.4 |
| 13909, 13910 | 16077588 | 66 | 3.00E-42 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU05210 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12328.1 ydel [Bacillus subtilis subsp. subtilis str. 168] pir C69778 hypothetical protein ydel - Bacillus subtilis db BAA19356.1 FUNCTION UNKNOWN. [Bacillus subtilis] | | | 91 1.00E-06 | |
| 1391, 1392 | 15896321 | 28 | 2.00E-20 | Clostridium acetobutylicum ATCC 824 | Glycosyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK81010.1 Glycosyltransferase [Clostridium acetobutylicum ATCC 824] pir G97277 glycosyltransferase [imported] - Clostridium acetobutylicum | | | | 2.4.1.- |
| 13913, 13914 | 21232334 | 47 | 2.00E-21 | Xanthomonas campestris pv. campestris str. ATCC 33913 | DNA-damage-inducible protein d [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM42175.1 DNA-damage-inducible protein d [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | | |
| 13915, 13916 | 52009462 | 45 | 2.00E-26 | Silicibacter sp. TM1040 | COG0834: ABC-type amino acid transport/signal transduction systems, periplasmic component/domain [Silicibacter sp. TM1040] | | | | |
| 13917, 13918 | 34556541 | 42 | 5.00E-36 | Wolinella succinogenes DSM 1740 | ANTHRANILATE SYNTHASE COMPONENT I [Wolinella succinogenes DSM 1740] emb CAE09256.1 ANTHRANILATE SYNTHASE COMPONENT I [Wolinella succinogenes] | | | | 4.1.3.27 |
| 13919, 13920 | 57236934 | 41 | 4.00E-47 | Campylobacter jejuni RM1221 | RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221] gb AAW34517.1 RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221] | | | | 4.2.1.70 |
| 13921, 13922 | 34557444 | 39 | 2.00E-44 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1061 [Wolinella succinogenes DSM 1740] emb CAE10159.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 13923, 13924 | 21673510 | 31 | 6.00E-26 | Chlorobium tepidum TLS | type I restriction system specificity protein [Chlorobium tepidum TLS] gb AAM71917.1 type I restriction system specificity protein [Chlorobium tepidum TLS] | | | | 3.1.21.3 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|----|----------|---------|
| 13927, 13928 | 46580432 | 27 | 6.00E-30 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | hypothetical protein DVU2025 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96500.1 conserved hypothetical protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] ribosomal protein L5 [Campylobacter jejuni RM1221] gb AAW36285.1 ribosomal protein L5 [Campylobacter jejuni RM1221] emb CAB73681.1 50S ribosomal protein L5 [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282821.1 50S ribosomal protein L5 [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81267 50S ribosomal protein L5 Cj1695c [imported] - Campylobacter jejuni (strain NCTC 11168) sp Q9PLY3 RL5_CAMJE 50S ribosomal protein L5 | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 6/8 | 78 | 5.00E-16 | |
| 13929, 13930 | 57238702 | 71 | 1.00E-66 | Campylobacter jejuni RM1221 | COG1959: Predicted transcriptional regulator [Thiobacillus denitrificans ATCC 25259] | | | | |
| 1393, 1394 | 52007674 | 34 | 2.00E-10 | Thiobacillus denitrificans ATCC | | | | | |
| 13931, 13932 | 34558795 | 43 | 4.00E-68 | Alvinella pompejana epibiont | TonB-dependent receptor [Alvinella pompejana epibiont 6C6] | | | | |
| 13933, 13934 | 54302657 | 29 | 3.00E-11 | Photobacterium profundum SS9 | hypothetical outer membrane receptor protein [Photobacterium profundum SS9] emb CAG22850.1 hypothetical outer membrane receptor protein [Photobacterium profundum] | | | | |
| 13935, 13936 | 32262400 | 47 | 4.00E-32 | Helicobacter hepaticus ATCC | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860382.1 hypothetical protein HH0851 [Helicobacter hepaticus ATCC 51449] | | | | |
| 13937, 13938 | 34556481 | 46 | 4.00E-57 | Wolinella succinogenes DSM | hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 13939, 13940 | 34104648 | 54 | 3.00E-51 | Chromobacterium violaceum ATCC | probable sensory transduction protein [Chromobacterium violaceum ATCC 12472] ref NP_903011.1 probable sensory transduction protein [Chromobacterium violaceum ATCC 12472] | | | | |
| 13943, 13944 | 57240289 | 56 | 1.00E-59 | Campylobacter lari | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55403.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 13945, 13946 | 57240288 | 46 | 6.00E-60 | Campylobacter lari | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55402.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 13947, 13948 | 34557884 | 29 | 5.00E-29 | Wolinella succinogenes DSM | DIGUANYLATE CYCLASE [Wolinella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolinella succinogenes] | | | | 2.7.3.- |
| 13949, 13950 | 34557771 | 35 | 3.00E-13 | Wolinella succinogenes DSM | hypothetical protein WS1424 [Wolinella succinogenes DSM 1740] emb CAE10486.1 hypothetical protein [Wolinella succinogenes] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|--|----|----------------|
| 1395, 1396 | 48853997 | 27 | 9.00E-11 | Cytophaga hutchinsonii | COG2825: Outer membrane protein [Cytophaga hutchinsonii] DNA-binding response regulator [Campylobacter jejuni RM1221] | | | | |
| 13953, 13954 | 57238514 | 26 | 1.00E-07 | Campylobacter jejuni RM1221 | gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221] | | | | |
| 13955, 13956 | 34557410 | 52 | 3.00E-30 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1024 [Wolinella succinogenes DSM 1740] emb CAE1025.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 13957, 13958 | 48831642 | 48 | 4.00E-54 | Magnetococcus sp. MC-1 | COG1876: D-alanyl-D-alanine carboxypeptidase [Magnetococcus sp. MC-1] hydrogenase isoenzymes formation protein [Helicobacter hepaticus ATCC 51449] ref NP_859853.1 hydrogenase isoenzymes formation protein [Helicobacter hepaticus ATCC 51449] | | | | |
| 13959, 13960 | 32261870 | 59 | 6.00E-91 | Helicobacter hepaticus ATCC 51449 | COG1876: D-alanyl-D-alanine carboxypeptidase [Magnetococcus sp. MC-1] hydrogenase isoenzymes formation protein [Helicobacter hepaticus ATCC 51449] ref NP_859853.1 hydrogenase isoenzymes formation protein [Helicobacter hepaticus ATCC 51449] | | | | |
| 13963, 13964 | 34558493 | 72 | 1.00E-105 | Wolinella succinogenes DSM 1740 | PUTATIVE ZINC PROTEASE [Wolinella succinogenes DSM 1740] emb CAE11208.1 PUTATIVE ZINC PROTEASE [Wolinella succinogenes] | | | 81 | 5.00E-20 3.4.- |
| 13965, 13966 | 34557072 | 34 | 5.00E-10 | Wolinella succinogenes DSM 1740 | TWO COMPONENT RESPONSE REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09787.1 TWO COMPONENT RESPONSE REGULATOR [Wolinella succinogenes] | | | | |
| 13967, 13968 | 21229067 | 42 | 2.00E-15 | Methanosarcina mazel Go1 | hypothetical sensory transduction histidine kinase [Methanosarcina mazel Go1] gb AAM32661.1 hypothetical sensory transduction histidine kinase [Methanosarcina mazel Go1] | | | | 2.7.3.- |
| 13969, 13970 | 46142558 | 55 | 1.00E-29 | Methanococcoides burtonii DSM 6242 | COG0784: FOG: CheY-like receiver [Methanococcoides burtonii DSM 6242] | | | | 2.7.3.- |
| 13971, 13972 | 15898132 | 28 | 2.00E-11 | Sulfolobus solfataricus P2 | hypothetical protein SSO1289 [Sulfolobus solfataricus P2] gb AAK41527.1 Conserved hypothetical protein [Sulfolobus solfataricus P2] pir H90283 conserved hypothetical protein [imported] - Sulfolobus solfataricus | | | | |
| 13973, 13974 | 32263234 | 59 | 1.00E-46 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861213.1 hypothetical protein HH1682 [Helicobacter hepaticus ATCC 51449] | | | | 2.7.3.- |
| 13977, 13978 | 34557252 | 43 | 2.00E-17 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0858 [Wolinella succinogenes DSM 1740] emb CAE09967.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 13979, 13980 | 29346175 | 31 | 6.00E-28 | Bacteroides thetaiotaomicron VPI-5482 | putative protease [Bacteroides thetaiotaomicron VPI-5482] gb AAO75872.1 putative protease [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.4.21.- |

| | | | | | | | | |
|-----------------|--------------|----|----------|---|--|----|----------|----------|
| 13983, 13984 | 51246876 | 61 | 2.00E-76 | Desulfotalea psychrophila Lsv54 | related to pseudouridine synthase [Desulfotalea psychrophila Lsv54] emb CAG37753.1 related to pseudouridine synthase [Desulfotalea psychrophila Lsv54] | | | 4.2.1.70 |
| 13985, 13986 | ABG9157 1 | 39 | 7.00E-55 | | Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus | | | 2.7.7.13 |
| 13987, 13988 | 51246976 | 50 | 5.00E-61 | Desulfotalea psychrophila Lsv54 | probable reverse transcriptase/maturase family protein [Desulfotalea psychrophila Lsv54] emb CAG37869.1 probable reverse transcriptase/maturase family protein [Desulfotalea psychrophila Lsv54] transcription termination factor NusA [Campylobacter upsaliensis RM3195] gb EAL53769.1 transcription termination factor NusA [Campylobacter upsaliensis RM3195] | 89 | 6.00E-07 | 2.7.7.49 |
| 13989, 13990 | 57242307 | 47 | 8.00E-44 | Campylobacter upsaliensis RM3195 | | | | |
| 1399, 1400 | 53713469 | 50 | 2.00E-66 | Bacteroides fragilis YCH46 | putative helicase [Bacteroides fragilis YCH46] db BAD48927.1 putative helicase [Bacteroides fragilis YCH46] | | | |
| 13991, 13992 | 39936986 | 43 | 5.00E-45 | Rhodopseudomonas palustris CGA009 | putative dTDP-glucose 4,6-dehydratase [Rhodopseudomonas palustris CGA009] emb CAE29366.1 putative dTDP-glucose 4,6-dehydratase [Rhodopseudomonas palustris CGA009] | | | 4.2.1.46 |
| 13993, 13994 | 15897644 | 50 | 2.00E-73 | Sulfolobus solfataricus P2 | GTP binding protein [Sulfolobus solfataricus P2] emb CAB57559.1 gtp- binding protein [Sulfolobus solfataricus] gb AAK41039.1 GTP binding protein [Sulfolobus solfataricus P2] p H90222 GTP binding protein [Imported] - Sulfolobus solfataricus | | | |
| 13997, 13998 | 45658464 | 38 | 2.00E-19 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711217.1 two-component hybrid sensor and regulator [Leptospira interrogans serovar Lai str. 56601] gb AAK48235.1 two-component hybrid sensor and regulator [Leptospira interrogans serovar lai str. 56601] gb AAST1187.1 histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.7.3.- |
| 13999, 14000 | 34556470 | 52 | 2.00E-58 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09185.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes] | | | 2.7.- |
| 14001, 14002 | 34556469 | 33 | 6.00E-25 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0010 [Wolinella succinogenes DSM 1740] emb CAE09184.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 14003, 14004 | 45547576 | 46 | 8.00E-53 | Rubrobacter xylanophilus DSM 8941 | COG0539: Ribosomal protein S1 [Rubrobacter xylanophilus DSM 8941] | 91 | 6.00E-07 | 2.7.7.8 |

| | | | | | | | | |
|--------|----------|----|----------|--|--|--|--|----------|
| 14005, | 57241144 | 51 | 2.00E-49 | Campylobacter lari RM2100 | hemolysin A [Campylobacter lari RM2100] gb EAL54840.1 hemolysin A [Campylobacter lari RM2100] | | | |
| 14006 | | | | | helicase/SNF2 family domain protein [Bacillus cereus G9241] gb EAL13804.1 helicase/SNF2 family domain protein [Bacillus cereus G9241] | | | 2.7.7.- |
| 14007, | 47567784 | 37 | 4.00E-34 | Bacillus cereus G9241 | | | | |
| 14008 | | | | Wolnella succinogenes DSM 1740 | ATP-DEPENDENT HELICASE [Wolnella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wolnella succinogenes] | | | 3.6.1.- |
| 14009, | 34557966 | 53 | 4.00E-77 | Bacteroides fragilis YCH46 | putative lipoprotein [Bacteroides fragilis YCH46] db BAD47765.1 putative lipoprotein [Bacteroides fragilis YCH46] | | | |
| 14010 | 53712307 | 46 | 1.00E-26 | Gloeobacter violaceus PCC 7421 | hypothetical protein gl11889 [Gloeobacter violaceus PCC 7421] db BAC98830.1 gl11889 [Gloeobacter violaceus PCC 7421] | | | |
| 14011, | 37521458 | 33 | 7.00E-13 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | universal stress protein family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94744.1 universal stress protein family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 14012 | | | | Cytophaga hutchinsonii | hypothetical protein Chut02000132 [Cytophaga hutchinsonii] | | | |
| 14015, | 46578677 | 32 | 8.00E-16 | Campylobacter lari RM2100 | proline dipeptidase TC0863 [Campylobacter lari RM2100] gb EAL55157.1 proline dipeptidase TC0863 [Campylobacter lari RM2100] | | | 3.4.11.9 |
| 14016 | | | | Bacteroides thetaiotaomicron VPI-5482 | putative membrane transport protein [Bacteroides thetaiotaomicron VPI- 5482] gb AAO79158.1 putative membrane transport protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 14017, | 29349461 | 53 | 1.00E-77 | Desulfovibrio desulfuricans G20 | COG0840: Methyl-accepting chemotaxis protein [Desulfovibrio desulfuricans G20] | | | |
| 14018 | 23474422 | 29 | 2.00E-25 | Campylobacter lari RM2100 | response regulator (ompR) [Campylobacter lari RM2100] gb EAL54947.1 response regulator (ompR) [Campylobacter lari RM2100] | | | 2.7.3.- |
| 14019, | 57241251 | 53 | 1.00E-63 | Campylobacter lari RM2100 | signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54948.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100] | | | 2.7.3.- |
| 14020 | | | | Cytophaga hutchinsonii | COG2912: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 14021, | 48856174 | 40 | 4.00E-49 | Mesorhizobium loti MAFF303099 | hypothetical protein mlr1881 [Mesorhizobium loti MAFF303099] db BAB49143.1 mlr1881 [Mesorhizobium loti MAFF303099] | | | |
| 14022 | 13471790 | 52 | 3.00E-39 | Cytophaga hutchinsonii | hypothetical protein Chut02000101 [Cytophaga hutchinsonii] | | | |
| 14023, | 48856384 | 46 | 1.00E-20 | | | | | |
| 14024 | | | | | | | | |
| 14025, | | | | | | | | |
| 14026 | | | | | | | | |
| 14027, | | | | | | | | |
| 14028 | | | | | | | | |
| 14029, | | | | | | | | |
| 14030 | | | | | | | | |
| 1403, | | | | | | | | |
| 1404 | | | | | | | | |
| 14033, | | | | | | | | |
| 14034 | | | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|---------------|
| 14035, 14036 | 30249663 | 38 | 4.00E-40 | Nitrosomonas europaea ATCC 19718 | possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718] | | | 1.8.4.6 |
| 14037, 14038 | 29349974 | 37 | 4.00E-46 | Bacteroides thetaiotaomicron VPI-5482 | two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482] | | | 3.1.1.61 |
| 14039, 14040 | 34558828 | 27 | 5.00E-27 | Alvinella pompejana epibiont 7G3 | KIAA1005 protein [Alvinella pompejana epibiont 7G3] hypothetical protein MA4540 [Methanosarcina acetivorans C2A] gb AAM07879.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | |
| 14041, 14042 | 20093324 | 42 | 1.00E-26 | Methanosarcina acetivorans C2A | type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath] ref YP_114328.1 type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath] | | | 3.4.24.- |
| 14043, 14044 | 53757541 | 49 | 4.00E-65 | Methylococcus capsulatus str. Bath | | | | 3.1.21.3 |
| 14045, 14046 | 15668834 | 38 | 2.00E-16 | Methanocaldococ- cus jannaschii DSM 2661 | Inosine-5'-monophosphate dehydrogenase (guaB) [Methanocaldococcus jannaschii DSM 2661] gb AAB98648.1 inosine-5'-monophosphate dehydrogenase (guaB) [Methanocaldococcus jannaschii DSM 2661] pir E64381 conserved hypothetical protein MJ0653 - Methanococcus jannaschii sp Q58069 Y653_METJA Hypothetical protein MJ0653 hypothetical protein BT3247 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78353.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | 1.1.1.20 5 |
| 14047, 14048 | 29348656 | 38 | 6.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | | | | |
| 14049, 14050 | 45681961 | 25 | 6.00E-09 | Mesorhizobium sp. BNC1 | COG3919: Predicted ATP-grasp enzyme [Mesorhizobium sp. BNC1] | | | |
| 1405, 1406 | 46142700 | 35 | 1.00E-29 | Methanococcoides burtonii DSM 6242 | COG0642: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242] | | | 2.7.3.- |
| 14051, 14052 | 48832299 | 46 | 1.00E-46 | Magnetococcus sp. MC-1 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] | | | |
| 14053, 14054 | 48832299 | 44 | 2.00E-44 | Magnetococcus sp. MC-1 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] | | | |
| 14057, 14058 | 29654169 | 40 | 4.00E-37 | Coxiella burnetii RSA 493 | glycosyl transferase, group 1 family protein [Coxiella burnetii RSA 493] gb AAO90375.1 glycosyl transferase, group 1 family protein [Coxiella burnetii RSA 493] | | | |
| 14061, 14062 | 20806796 | 27 | 1.00E-13 | Thermoanaerobact- er tengcongensis MB4 | predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4] gb AAM23571.1 predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4] | | | 2.4.1.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|----------|
| 14063, 14064 | 29610237 | 28 | 4.00E-18 | Streptomyces avermitilis MA-4680 | putative glycosyltransferase [Streptomyces avermitilis MA-4680] ref NP_827749.1 putative glycosyltransferase [Streptomyces avermitilis MA-4680] | | | | 2.4.1.83 |
| 14065, 14066 | 48854768 | 37 | 2.00E-20 | Cytophaga hutchinsonii | COG2319: FOG: WD40 repeat [Cytophaga hutchinsonii] | | | | |
| 14067, 14068 | 6968471 | 43 | 5.00E-57 | Campylobacter jejuni subsp. jejuni NCTC 11168 | possible transferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir H81305 probable transferase Cj1035c [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282185.1 possible transferase [Campylobacter jejuni subsp. jejuni NCTC 11168] sp Q9PNQ6 ATE_CAMJE Putative arginyl- tRNA-protein transferase (R-transferase) (Arginyltransferase) | | | 2.3.2.8 | |
| 14069, 14070 | 34558373 | 56 | 8.00E-64 | Wolinella succinogenes DSM 1740 | UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE GLMU [Wolinella succinogenes DSM 1740] emb CAE11088.1 UDP-N- ACETYLGLUCOSAMINE PYROPHOSPHORYLASE GLMU [Wolinella succinogenes] | | | 2.7.7.23 | |
| 1407, 1408 | 53731556 | 33 | 5.00E-27 | Methanococcoides burtonii DSM 6242 | COG0642: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242] | | | 2.7.3.- | |
| 14071, 14072 | 34556560 | 54 | 5.00E-65 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | |
| 14073, 14074 | 32262189 | 42 | 3.00E-35 | Helicobacter hepaticus ATCC 51449 | 3-Deoxy-D-manno-octulosonic-acid transferase [Helicobacter hepaticus ATCC 51449] ref NP_860171.1 3-Deoxy-D-manno-octulosonic-acid transferase [Helicobacter hepaticus ATCC 51449] | | | 2.4.99.- | |
| 14081, 14082 | 48862648 | 34 | 1.00E-10 | Microbulifer degradans 2-40 | COG0705: Uncharacterized membrane protein (homolog of Drosophila rhomboid) [Microbulifer degradans 2-40] | | | | |
| 14085, 14086 | 23474440 | 28 | 9.00E-17 | Desulfovibrio desulfuricans G20 | COG0714: MoxR-like ATPases [Desulfovibrio desulfuricans G20] | | | | |
| 14087, 14088 | 33861847 | 44 | 2.00E-43 | Prochlorococcus marinus subsp. pastoris str. CCMP1986 | tRNA methyl transferase:tRNA (5-methylaminomethyl)-2-thiouridy... [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19750.1 tRNA methyl transferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] | | | 2.1.1.61 | |
| 14089, 14090 | 49236207 | 47 | 2.00E-35 | Moorella thermoacetica ATCC 39073 | COG0301: Thiamine biosynthesis ATP pyrophosphatase [Moorella thermoacetica ATCC 39073] | | | | |
| 1409, 1410 | 45658173 | 32 | 2.00E-14 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein L1C12325 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711602.1 hypothetical protein LA1421 [Leptospira interrogans serovar Lai str. 56601] gb AA48620.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AA570896.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|--|--|----|----------|----------|
| 14091, | 23125625 | 28 | 6.00E-09 | Nostoc punctiforme PCC 73102 | COG0514: Superfamily II DNA helicase [Nostoc punctiforme PCC 73102] | | | | 3.1.21.3 |
| 14092, | 46140259 | 52 | 3.00E-31 | Dechloromonas aromatica RCB | COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB] | | | | 2.7.3.- |
| 14095, | 53713780 | 37 | 2.00E-41 | Bacteroides fragilis YCH46 | cobalamin biosynthesis protein CobD [Bacteroides fragilis YCH46] | | | | |
| 14096, | 46201931 | 46 | 5.00E-24 | Magnetospirillum magnetotacticum MS-1 | COG2199: FOG: GGDEF domain [Magnetospirillum magnetotacticum MS-1] | | | | 2.7.3.- |
| 14097, | 558266 | 66 | 8.00E-74 | Wolinella succinogenes | orf [Wolinella succinogenes] pir[S50154 hypothetical protein 2 - Wolinella succinogenes] | | | | |
| 14098, | 24375871 | 34 | 5.00E-16 | Shewanella oneidensis MR-1 | hypothetical protein SO4391 [Shewanella oneidensis MR-1] gb AA57358.1 | | | | |
| 14099, | 16077106 | 46 | 1.00E-60 | Bacillus subtilis subsp. subtilis str. 168 | methionyl-tRNA synthetase [Bacillus subtilis subsp. subtilis str. 168] emb CAB11814.1 methionyl-tRNA synthetase [Bacillus subtilis subsp. subtilis str. 168] sp P37465 SYM_BACSU Methionyl-tRNA synthetase (Methionine-tRNA ligase) (MetRS) pir S86067 methionine-tRNA ligase (EC 6.1.1.10) metS - Bacillus subtilis db BAA05273.1 methionyl-tRNA synthetase [Bacillus subtilis] | | | | 6.1.1.10 |
| 14101, | 48855475 | 64 | 2.00E-35 | Cytophaga hutchinsonii | COG5557: Polysulphide reductase [Cytophaga hutchinsonii] | | | | |
| 14102, | 57168693 | 55 | 6.00E-67 | Campylobacter coli RM2228 | translation initiation factor IF-2 [Campylobacter coli RM2228] gb EAL56654.1 translation initiation factor IF-2 [Campylobacter coli RM2228] | Ureaplasma parvum serovar 3 str. ATCC 700970 section 30 of 59 of the complete genome | 94 | 4.00E-11 | 3.6.1.48 |
| 14103, | 20809124 | 49 | 6.00E-34 | Thermoanaerobacter tengcongensis MB4 | NAD/FAD-utilizing enzyme apparently involved in cell division [Thermoanaerobacter tengcongensis MB4] gb AAM25899.1 NAD/FAD-utilizing enzyme apparently involved in cell division [Thermoanaerobacter tengcongensis MB4] sp Q8R6K9 GIA2_THETN Glucose inhibited division protein A 2 | | | | |
| 14104, | 57241681 | 63 | 4.00E-97 | Campylobacter lari RM2100 | DNA gyrase, B subunit [Campylobacter lari RM2100] gb EAL54351.1 DNA gyrase, B subunit [Campylobacter lari RM2100] | Campylobacter lari serotype T64 DNA gyrase subunit B (gyrB) gene, partial cds | 87 | 2.00E-13 | 5.99.1.3 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|----------|---------------|
| 1411, 1412 | 45658174 | 42 | 1.00E-09 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC12326 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70897.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 14113, 14114 | 53729993 | 29 | 2.00E-08 | Dechloromonas aromatica RCB | COG3038: Cytochrome B561 [Dechloromonas aromatica RCB] | | | | |
| 14115, 14116 | 57242136 | 27 | 7.00E-25 | Campylobacter upsallensis RM3195 | signal-transducing protein, histidine kinase [Campylobacter upsallensis RM3195] gb EAL54109.1 signal-transducing protein, histidine kinase [Campylobacter upsallensis RM3195] | | | | 2.7.3.- |
| 14117, 14118 | 34557558 | 53 | 2.00E-55 | Wolinella succinogenes DSM 1740 | PUTATIVE AMINOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10273.1 PUTATIVE AMINOTRANSFERASE [Wolinella succinogenes] | | | | 4.4.1.- |
| 14119, 14120 | 16264212 | 44 | 1.00E-22 | Sinorhizobium melloti 1021 | hypothetical protein Smb20482 [Sinorhizobium melloti 1021] pir H95899 hypothetical protein [imported] - Sinorhizobium melloti (strain 1021) magaplasmid pSymB emb CAC48864.1 HYPOTHETICAL PROTEIN [Sinorhizobium melloti 1021] | | | | |
| 14121, 14122 | 56478430 | 43 | 9.00E-56 | Azoarcus sp. Ebn1 | putative acetyltransferase [Azoarcus sp. Ebn1] emb CAI09118.1 putative acetyltransferase [Azoarcus sp. Ebn1] | | | | 6.-.-.- |
| 14123, 14124 | 2118361 | 61 | 1.00E-53 | Haemophilus influenzae R2846 | formate-tetrahydrofolate ligase (EC 6.3.4.3) - Clostridium cylindrosporium sp Q07064 FTHS_CLOCY Formate-tetrahydrofolate ligase (Formyltetrahydrofolate synthetase) (FHS) (FTHFS) gb AAA23239.1 N10- CHO-H4folate synthetase | Clostridium perfringens str. 13 DNA, complete genome | 89 | 4.00E-19 | 6.3.4.3 |
| 14125, 14126 | 42629381 | 43 | 3.00E-25 | Helicobacter hepaticus ATCC 51449 | hypothetical protein Hfl103001140 [Haemophilus influenzae R2846] lipid A biosynthesis protein LpxK [Helicobacter hepaticus ATCC 51449] ref NP_860540.1 lipid A biosynthesis protein LpxK [Helicobacter hepaticus ATCC 51449] | | | | 2.7.1.13 0 |
| 1413, 1414 | 24214122 | 45 | 2.00E-34 | Leptospira interrogans serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] | | | | |
| 14135, 14136 | 34558237 | 36 | 7.00E-39 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1946 [Wolinella succinogenes DSM 1740] emb CAE10952.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 14137, 14138 | 53684899 | 27 | 4.00E-12 | Desulfotobacterium hafniense DCB-2 | COG2234: Predicted aminopeptidases [Desulfotobacterium hafniense DCB- 2] | | | | 3.4.17.2 1 |
| 14139, 14140 | 15605874 | 22 | 2.00E-12 | Aquifex aerophilus VF5 | hypothetical protein aq_367 [Aquifex aerophilus VF5] gb AAC06656.1 hypothetical protein [Aquifex aerophilus VF5] pir G70332 conserved hypothetical protein aq_367 - Aquifex aerophilus | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|-------------------|----------------------------|---|--|--|----------|
| 14141, 14142 | 15611181 | 56 | 1.00E-103 | J99 | Helicobacter pylori | PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] gb AAD05690.1 PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] pir E71972 pyruvate, water dikinase (EC 2.7.9.2) - Helicobacter pylori (strain J99) spl Q9ZMV4 PPSA_HELPJ Phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase) | | | 2.7.9.2 |
| 14143, 14144 | 49237143 | 36 | 2.00E-12 | ATCC 39073 | Moorella thermoacetica | COG0701: Predicted permeases [Moorella thermoacetica ATCC 39073] | | | |
| 14147, 14148 | 17940062 | 40 | 9.00E-36 | Interrogans | Leptospira | unknown [Leptospira Interrogans] | | | 2.4.1.- |
| 14149, 14150 | 11499239 | 44 | 2.00E-07 | DSM 4304 | Archaeoglobus fulgidus | tungsten formylmethanofuran dehydrogenase, subunit G (fwdG) [Archaeoglobus fulgidus DSM 4304] gb AAB89607.1 tungsten formylmethanofuran dehydrogenase, subunit G (fwdG) [Archaeoglobus fulgidus DSM 4304] pir H69455 tungsten formylmethanofuran dehydrogenase, subunit G (fwdG) homolog - Archaeoglobus fulgidus thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861359.1 thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449] | | | 1.2.99.5 |
| 14153, 14154 | 32263380 | 46 | 5.00E-40 | 51449 | Helicobacter hepaticus | COG0761: Penicillin tolerance protein [Geobacter metallireducens GS-15] | | | 2.5.1.3 |
| 14155, 14156 | 48846794 | 48 | 4.00E-36 | 15 | Geobacter metallireducens | 2-acetylglucosaminidase [Aquifex aeolicus VF5] gb AAC07802.1 2-acetylglucosaminidase [Aquifex aeolicus VF5] [Aquifex aeolicus VF5] pir E70476 2-acetylglucosaminidase acyltransferase - Aquifex aeolicus | | | 6.2.1.20 |
| 14157, 14158 | 15607028 | 33 | 7.00E-10 | VF5 | Aquifex aeolicus | transcriptional regulator [Bacteroides fragilis YCH46] db BAD50861.1 | | | |
| 14159, 14160 | 53715403 | 26 | 4.00E-09 | YCH46 | Bacteroides fragilis | transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 14161, 14162 | 34557963 | 45 | 2.00E-36 | 1740 | Wolinella succinogenes | FLAVOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE10678.1 FLAVOPROTEIN [Wolinella succinogenes] | | | |
| 14163, 14164 | 37526735 | 57 | 6.00E-26 | TTO1 | Photobacterium luminescens | hypothetical protein plu2845 [Photobacterium luminescens subsp. laumondii TTO1] emb CAE15219.1 unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1] | | | |
| 14165, 14166 | 57505678 | 32 | 1.00E-07 | RM3195 | Campylobacter upsallensis | conserved hypothetical protein [Campylobacter upsallensis RM3195] gb EAL52739.1 conserved hypothetical protein [Campylobacter upsallensis RM3195] | | | |
| 1417, 1418 | 48728708 | 32 | 1.00E-16 | fluorescens Pfo-1 | Pseudomonas fluorescens | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Pseudomonas fluorescens Pfo-1] | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---|---|---|----|----------|----------|---------|
| 14171, 14172 | 52842621 | 31 | 3.00E-10 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | AMPC cephalosporinase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28473.1 AMPC cephalosporinase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56657.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | | |
| 14175, 14176 | 57168696 | 43 | 1.00E-26 | Campylobacter coli RM2228 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE10055.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | | | | | 2.7.3.- |
| 14177, 14178 | 34557340 | 39 | 6.00E-67 | Wolinella succinogenes DSM 1740 | COG1799: Uncharacterized protein conserved in bacteria [Desulfotobacterium hafnense DCB-2] | | | | | |
| 14181, 14182 | 53684633 | 25 | 2.00E-07 | Desulfotobacterium hafnense DCB-2 | PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolinella succinogenes DSM 1740] emb CAE09198.1 PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolinella succinogenes] | B.thuringiensis PK1 & cap genes, putative | 85 | 2.00E-18 | 5.1.3.- | |
| 14185, 14186 | 34556483 | 64 | 5.00E-84 | Wolinella succinogenes DSM 1740 | 3'(2'),5'-bisphosphate nucleotidase [Campylobacter coli RM2228] gb EAL56330.1 3'(2'),5'-bisphosphate nucleotidase [Campylobacter coli RM2228] | Aquifex aeolicus VF5 section 16 of 109 of the complete genome | 87 | 4.00E-14 | 3.1.3.25 | |
| 14187, 14188 | 57168975 | 62 | 3.00E-81 | Campylobacter coli RM2228 | DNA-directed RNA polymerase beta' chain [Bacteroides fragilis YCH46] db BAD50934.1 DNA-directed RNA polymerase beta' chain [Bacteroides fragilis YCH46] | Bacteroides fragilis YCH46 DNA, complete genome | 85 | 6.00E-10 | 2.7.7.6 | |
| 14189, 14190 | 53715476 | 56 | 4.00E-81 | Bacteroides fragilis YCH46 | hypothetical protein AF2325 [Archaeoglobus fulgidus DSM 4304] gb AAB88946.1 A. fulgidus predicted coding region AF2325 [Archaeoglobus fulgidus DSM 4304] pir E69540 hypothetical protein AF2325 - Archaeoglobus fulgidus | | | | | |
| 1419, 1420 | 11499906 | 27 | 2.00E-08 | Archaeoglobus fulgidus DSM 4304 | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | | |
| 14191, 14192 | 48854613 | 28 | 3.00E-24 | Cytophaga hutchinsonii | COG3129: Predicted SAM-dependent methyltransferase [Cytophaga hutchinsonii] | | | | | 2.7.3.- |
| 14193, 14194 | 48856096 | 52 | 5.00E-85 | Cytophaga hutchinsonii | hypothetical protein BT3112 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78218.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | | |
| 14195, 14196 | 29348521 | 48 | 3.00E-25 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3112 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78218.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | | |
| 14197, 14198 | 29348521 | 45 | 7.00E-38 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein [Staphylococcus aureus] | | | | | |
| 14199, 14200 | 57207874 | 32 | 4.00E-12 | Staphylococcus aureus | | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|--|---|--|--|--|----------|
| 14201, 14202 | 34557348 | 38 | 6.00E-18 | Wolnella succinogenes DSM 1740 | HECB PRECURSOR [Wolnella succinogenes DSM 1740] emb CAE10063.1 HECB PRECURSOR [Wolnella succinogenes] | | | | |
| 14203, 14204 | 53714768 | 31 | 5.00E-12 | Bacteroides fragilis YCH46 | hypothetical protein BF3483 [Bacteroides fragilis YCH46] dbj BAD50226.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 14205, 14206 | 20808521 | 30 | 3.00E-22 | Thermoanaerobact er tengcongensis MB4 | NADH:flavin oxidoreductases, Old Yellow Enzyme family [Thermoanaerobacter tengcongensis MB4] gb AAM25296.1 NADH:flavin oxidoreductases, Old Yellow Enzyme family [Thermoanaerobacter tengcongensis MB4] | | | | 1.6.-.- |
| 1421, 1422 | 21673804 | 38 | 9.00E-47 | Chlorobium tepidum TLS | carbohydrate kinase, PfkB family [Chlorobium tepidum TLS] gb AAM7221.1 carbohydrate kinase, PfkB family [Chlorobium tepidum TLS] | | | | 2.7.1.15 |
| 14211, 14212 | AAW9827 0 | 50 | 2.00E-67 | | Desc:H. pylori GHPO 442 protein. Org: Helicobacter pylori | | | | 1.4.99.1 |
| 14213, 14214 | 57159872 | 29 | 4.00E-17 | Thermococcus kodakaraensis | NADH:ubiquinone oxidoreductase, NADH-binding subunit F [Thermococcus kodakaraensis] ref YP_184026.1 NADH:ubiquinone oxidoreductase, NADH- binding subunit F [Thermococcus kodakaraensis] | | | | 1.6.5.3 |
| 14215, 14216 | 53691858 | 56 | 1.00E-86 | Desulfovibrio desulfuricans G20 | hypothetical protein Ddes02000066 [Desulfovibrio desulfuricans G20] | | | | |
| 14217, 14218 | 46581597 | 44 | 1.00E-23 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | lipoprotein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97665.1 lipoprotein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | |
| 14223, 14224 | 23130537 | 45 | 4.00E-17 | Nostoc punctiforme PCC 73102 | COG0778: Nitroreductase [Nostoc punctiforme PCC 73102] | | | | |
| 14227, 14228 | 34557966 | 57 | 8.00E-46 | Wolnella succinogenes DSM 1740 | ATP-DEPENDENT HELICASE [Wolnella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wolnella succinogenes] | | | | 3.6.1.- |
| 14231, 14232 | 28211368 | 28 | 1.00E-13 | Clostridium tetani E88 | hypothetical protein CTC01714 [Clostridium tetani E88] gb AAO36249.1 conserved protein [Clostridium tetani E88] | | | | |
| 14233, 14234 | 32263376 | 65 | 5.00E-72 | Helicobacter hepaticus ATCC 51449 | phosphoenolpyruvate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861355.1 phosphoenolpyruvate synthase [Helicobacter hepaticus ATCC 51449] | | | | 2.7.9.2 |
| 14235, 14236 | AAW8997 9 | 61 | 3.00E-53 | | Desc: Protein encoded by clone d11 ORF2. Org: Helicobacter pylori | | | | 1.2.7.3 |
| 14237, 14238 | 55733904 | 41 | 1.00E-36 | Oryza sativa (japonica cultivar- group) | putative glycosyltransferase [Oryza sativa (japonica cultivar-group)] ref XP_475798.1 putative glycosyltransferase [Oryza sativa (japonica cultivar-group)] | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|-------|--|---|--------------------------------|--|----|----------|
| 14239, 14240 | 48846045 | 37 | 4.00E-38 | 15 | Geobacter metallireducens GS- | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | | 2.7.3.- |
| 14241, 14242 | 30249663 | 34 | 2.00E-29 | 19718 | Nitrosomonas europaea ATCC | possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718] emb CAD85612.1 possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718] | | | | 1.8.4.6 |
| 14243, 14244 | 48855001 | 28 | 1.00E-19 | | Cytophaga hutchinsonii | COG2849: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | 2.7.1.68 |
| 14245, 14246 | 53713690 | 55 | 2.00E-51 | | Bacteroides fragilis YCH46 | dihydroorotate dehydrogenase electron transfer subunit [Bacteroides fragilis YCH46] dbj BAD49148.1 dihydroorotate dehydrogenase electron transfer subunit [Bacteroides fragilis YCH46] | Bacteroides thetataotamicon | VPI-5482, section 4 of 21 of the complete genome | 89 | 6.00E-09 |
| 14247, 14248 | 29346302 | 75 | 7.00E-56 | | Bacteroides thetataotamicon | dihydroorotate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75999.1 dihydroorotate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.3.3.1 |
| 14249, 14250 | 37680330 | 30 | 1.00E-26 | | Vibrio vulnificus YJ016 | predicted signal transduction protein [Vibrio vulnificus YJ016] dbj BAC94910.1 predicted signal transduction protein [Vibrio vulnificus YJ016] | | | | |
| 1425, 1426 | 53797181 | 34 | 8.00E-21 | | Chloroflexus aurantiacus | COG3427: Uncharacterized conserved protein [Chloroflexus aurantiacus] | | | | |
| 14251, 14252 | 20806595 | 61 | 7.00E-68 | | Thermoanaerobact er tengcongensis MB4 | predicted glycosylase [Thermoanaerobacter tengcongensis MB4] gb AAM23370.1 predicted glycosylase [Thermoanaerobacter tengcongensis MB4] | | | | |
| 14253, 14254 | 16077744 | 52 | 3.00E-70 | | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU06760 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12496.1 yeeA [Bacillus subtilis subsp. subtilis str. 168] pir E69792 conserved hypothetical protein yeeA - Bacillus subtilis | | | | |
| 14255, 14256 | 16077745 | 63 | 1.00E-97 | | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU06770 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12497.1 yeeB [Bacillus subtilis subsp. subtilis str. 168] gb AAB66475.1 YeeB [Bacillus subtilis] pir F69792 hypothetical protein yeeB - Bacillus subtilis | | | | |
| 14257, 14258 | 52548731 | 54 | 2.00E-88 | | uncultured archaeon GZfos18F2 | hypothetical protein GZ18F2_10 [uncultured archaeon GZfos18F2] | | | | |
| 14259, 14260 | 48856539 | 31 | 5.00E-14 | | Cytophaga hutchinsonii | COG0791: Cell wall-associated hydrolases (invasion-associated proteins) [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|-----------|--------------------|---|---|--|----|----------|---------|
| 14261, 14262 | 34556892 | 80 | 1.00E-132 | 1740 | Wollinella succinogenes DSM | DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes] sp Q7MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)] | Ehrlichia ruminantium RNA polymerase beta subunit (rpoB) gene, partial cds | 88 | 4.00E-45 | 2.7.7.6 |
| 14263, 14264 | 34557246 | 37 | 7.00E-59 | 1740 | Wollinella succinogenes DSM | SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes] | | | | |
| 14265, 14266 | 51245892 | 25 | 1.00E-06 | psychrophila LSV54 | Desulfotalea psychrophila LSV54 | related to integrase [Desulfotalea psychrophila LSV54] emb CAG36769.1 related to integrase [Desulfotalea psychrophila LSV54] | | | | |
| 1427, 1428 | 53711500 | 50 | 2.00E-39 | YCH46 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD46958.1 two-component system response regulator [Bacteroides fragilis YCH46] | | | | 2.7.3.- |
| 14271, 14272 | 34558386 | 48 | 8.00E-33 | 1740 | Wollinella succinogenes DSM | hypothetical protein WS2103 [Wollinella succinogenes DSM 1740] emb CAE11101.1 hypothetical protein [Wollinella succinogenes] | | | | |
| 14275, 14276 | 34558157 | 39 | 1.00E-12 | 1740 | Wollinella succinogenes DSM | SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wollinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wollinella succinogenes] | | | | |
| 14277, 14278 | 48853608 | 41 | 7.00E-53 | hutchinsonii | Cytophaga hutchinsonii | hypothetical protein Chu02003656 [Cytophaga hutchinsonii] | | | | |
| 14279, 14280 | 34556575 | 59 | 1.00E-104 | 1740 | Wollinella succinogenes DSM | PUTATIVE FORMATE DEHYDROGENASE, ALPHA SUBUNIT [Wollinella succinogenes DSM 1740] emb CAE09290.1 PUTATIVE FORMATE DEHYDROGENASE, ALPHA SUBUNIT [Wollinella succinogenes] | | | | 1.2.1.2 |
| 14281, 14282 | 32262777 | 48 | 3.00E-42 | 51449 | Helicobacter hepaticus ATCC | DNA processing protein DprA [Helicobacter hepaticus ATCC 51449] ref NP_860758.1 DNA processing protein DprA [Helicobacter hepaticus ATCC 51449] | | | | |
| 14283, 14284 | 29348441 | 41 | 2.00E-65 | VPI-5482 | Bacteroides thetaiotaomicron VPI-5482 | conserved hypothetical protein, with a weak acyltransferase domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO78138.1 conserved hypothetical protein, with a weak acyltransferase domain [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 14287, 14288 | 39995706 | 41 | 7.00E-35 | PCA | Geobacter sulfurreducens PCA | sensor histidine kinase [Geobacter sulfurreducens PCA] gb AAR33930.1 sensor histidine kinase [Geobacter sulfurreducens PCA] | | | | 2.7.3.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|-------|-------------------------------------|--|--|--|----------------------|
| 14293, 14294 | 48845470 | 48 | 6.00E-43 | 15 | Geobacter metallireducens GS | COG2353: Uncharacterized conserved protein [Geobacter metallireducens GS-15] | | | |
| 14295, 14296 | 34556624 | 40 | 3.00E-51 | 1740 | Wolinella succinogenes DSM | ISOLEUCYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE09339.1 ISOLEUCYL-TRNA SYNTHETASE [Wolinella succinogenes] | | | 6.1.1.5 |
| 143, 144 | 32476811 | 47 | 5.00E-27 | 1 | Rhodopirellula baltica SH 1 | hypothetical protein-signal peptide prediction [Rhodopirellula baltica SH 1] emb CAD77183.1 hypothetical protein-signal peptide prediction [Pirellula sp.] | | | |
| 14305, 14306 | 34558171 | 21 | 5.00E-08 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS1876 [Wolinella succinogenes DSM 1740] emb CAE10886.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 14307, 14308 | 34556981 | 30 | 4.00E-24 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS0562 [Wolinella succinogenes DSM 1740] emb CAE09696.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 14309, 14310 | 34556560 | 36 | 1.00E-34 | 1740 | Wolinella succinogenes DSM | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 1431, 1432 | 53711857 | 33 | 7.00E-24 | YCH46 | Bacteroides fragilis YCH46 | beta-N-acetylglucosaminidase [Bacteroides fragilis YCH46] dbj BAD47315.1 beta-N-acetylglucosaminidase [Bacteroides fragilis YCH46] | | | |
| 14311, 14312 | 10441471 | 25 | 7.00E-09 | | Lactococcus lactis subsp. lactis | abortive infection phage resistance protein abiU [Lactococcus lactis subsp. lactis] | | | |
| 14313, 14314 | 32262189 | 41 | 8.00E-38 | 51449 | Helicobacter hepaticus ATCC | 3-Deoxy-D-manno-octulosonic-acid transferase [Helicobacter hepaticus ATCC 51449] ref NP_860171.1 3-Deoxy-D-manno-octulosonic-acid transferase [Helicobacter hepaticus ATCC 51449] | | | 2.4.99.- 2.4.1.15 |
| 14315, 14316 | 48854183 | 50 | 2.00E-56 | | Cytophaga hutchinsonii | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | 1 |
| 14319, 14320 | 24376199 | 42 | 5.00E-19 | | Shewanella oneidensis MR-1 | hypothetical protein SO4727 [Shewanella oneidensis MR-1] gb AA57686.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | |
| 14323, 14324 | 34558118 | 39 | 5.00E-35 | 1740 | Wolinella succinogenes DSM | HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10833.1 HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 14325, 14326 | 57241714 | 34 | 5.00E-30 | | Campylobacter lari RM2100 | fibrinectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100] gb EAL54384.1 fibrinectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100] | | | |

| | | | | | | |
|-----------------|----------|----|-----------|--|---|----------|
| 14329, 14330 | 12512884 | 43 | 2.00E-27 | Escherichia coli O157:H7 | deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] ref NP_285856.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7 EDL933] ref NP_308191.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] sp Q8X8Y9 DGT_PECO57 Deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase) pir D85500 deoxyguanosine triphosphate triphosphohydrolase [Imported] - Escherichia coli (strain O157:H7, substrain EDL933) dbj BAB33587.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] pir D90649 deoxyguanosine triphosphate triphosphohydrolase [Imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) | 3.1.5.1 |
| 1433, 1434 | 53712575 | 30 | 9.00E-15 | Bacteroides fragilis YCH46 | tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] dbj BAD48033.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | |
| 14331, 14332 | 34557222 | 66 | 1.00E-114 | Wolfinella succinogenes DSM 1740 | PHOSPHOENOLPYRUVATE SYNTHASE [Wolfinella succinogenes DSM 1740] emb CAE09937.1 PHOSPHOENOLPYRUVATE SYNTHASE [Wolfinella succinogenes] | 2.7.9.2 |
| 14333, 14334 | 53795932 | 42 | 3.00E-29 | Chloroflexus aurantiacus | COG1941: Coenzyme F420-reducing hydrogenase, gamma subunit [Chloroflexus aurantiacus] | 1.12.-.- |
| 14335, 14336 | 46142296 | 63 | 1.00E-94 | Methanococcoides burtonii DSM 6242 | COG4804: Uncharacterized conserved protein [Methanococcoides burtonii DSM 6242] | |
| 14337, 14338 | 53713068 | 28 | 5.00E-13 | Bacteroides fragilis YCH46 | hypothetical protein BF1779 [Bacteroides fragilis YCH46] dbj BAD48526.1 hypothetical protein [Bacteroides fragilis YCH46] | |
| 14339, 14340 | 34557873 | 49 | 5.00E-64 | Wolfinella succinogenes DSM 1740 | hypothetical protein WS1545 [Wolfinella succinogenes DSM 1740] emb CAE10588.1 conserved hypothetical protein [Wolfinella succinogenes] | |
| 14343, 14344 | 42780097 | 28 | 1.00E-15 | Bacillus cereus ATCC 10987 | helicase, SNF2 family [Bacillus cereus ATCC 10987] emb CAB40614.1 SNF2-like helicase [Bacillus cereus] gb AAS39952.1 helicase, SNF2 family [Bacillus cereus ATCC 10987] | 3.6.1.3 |
| 14345, 14346 | 53714400 | 46 | 2.00E-41 | Bacteroides fragilis YCH46 | acyltransferase family protein [Bacteroides fragilis YCH46] dbj BAD49858.1 acyltransferase family protein [Bacteroides fragilis YCH46] | |
| 14349, 14350 | 34557247 | 60 | 6.00E-42 | Wolfinella succinogenes DSM 1740 | TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolfinella succinogenes DSM 1740] emb CAE09982.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolfinella succinogenes] | 2.7.3.- |
| 1435, 1436 | 48856980 | 50 | 5.00E-39 | Cytophaga hutchinsonii | COG1522: Transcriptional regulators [Cytophaga hutchinsonii] | |
| 14351, 14352 | 23467790 | 54 | 1.00E-67 | Haemophilus sommus 129PT | COG0147: Anthranilate/para-aminobenzoate synthases component I [Haemophilus sommus 129PT] | 4.1.3.- |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|----|----------|
| 14353, 14354 | 57240744 | 27 | 1.00E-24 | Campylobacter lari RM2100 | probable membrane protein Cj0124c [Campylobacter lari RM2100] gb EAL55137.1 probable membrane protein Cj0124c [Campylobacter lari RM2100] | | | |
| 14355, 14356 | 29349623 | 53 | 3.00E-66 | Bacteroides thetaiotaomicron VPI-5482 | shikimate 5-dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79320.1 shikimate 5-dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] | | | 1.1.1.25 |
| 14357, 14358 | 38099730 | 26 | 7.00E-09 | Magnaporthe grisea 70-15 | hypothetical protein MG10847.4 [Magnaporthe grisea 70-15] ref XP_360535.1 hypothetical protein MG10847.4 [Magnaporthe grisea 70-15] | | | |
| 14363, 14364 | 34396413 | 73 | 1.00E-136 | Porphyromonas gingivalis W83 | conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_904581.1 hypothetical protein PG0257 [Porphyromonas gingivalis W83] | Bartonella henselae strain Houston-1, complete genome | 79 | 6.00E-26 |
| 14365, 14366 | 29345762 | 57 | 6.00E-32 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0352 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75459.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 14367, 14368 | 57238514 | 28 | 4.00E-26 | Campylobacter jejuni RM1221 | DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221] | | | 2.7.3.- |
| 14369, 14370 | 34557182 | 52 | 1.00E-28 | Wolinella succinogenes DSM 1740 | PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09897.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] | | | |
| 14371, 14372 | 15894152 | 35 | 2.00E-15 | Clostridium acetobutylicum ATCC 824 | Two-component response regulator [Clostridium acetobutylicum ATCC 824] gb AAK78841.1 Two-component response regulator [Clostridium acetobutylicum ATCC 824] pir F97006 two-component response regulator [imported] - Clostridium acetobutylicum | | | 3.1.1.61 |
| 14375, 14376 | 48855045 | 36 | 1.00E-07 | Cytophaga hutchinsonii | COG2027: D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 4) [Cytophaga hutchinsonii] | | | 3.4.16.4 |
| 14377, 14378 | 15678845 | 33 | 3.00E-22 | Methanothermobacter thermautotrophicus str. Delta H | sensory transduction histidine kinase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85323.1 sensory transduction histidine kinase [Methanothermobacter thermautotrophicus str. Delta H] pir A69210 sensory transduction histidine kinase - Methanothermobacter thermautotrophicus (strain Delta H) | | | 2.7.3.- |
| 14379, 14380 | 32262842 | 47 | 1.00E-23 | Helicobacter hepaticus ATCC 51449 | ornithine acetyltransferase [Helicobacter hepaticus ATCC 51449] ref NP_860822.1 ornithine acetyltransferase [Helicobacter hepaticus ATCC 51449] sp Q93EJ3 ARGJ_HELHP Arginine biosynthesis bifunctional protein argJ [includes: Glutamate N-acetyltransferase (Ornithine acetyltransferase) (Ornithine transacetylase) (OATase); Amino-acid acetyltransferase (N-acetylglutamate synthase) (AGS)] [Contains: Arginine biosynthesis bifunctional protein argJ alpha chain; Arginine biosynthesis bifunctional protein argJ beta chain] | | | 2.3.1.1 |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|----------|----------|
| 14383, 14384 | 53713680 | 46 | 6.00E-67 | Bacteroides fragilis YCH46 | hypothetical protein BF2389 [Bacteroides fragilis YCH46] dbj BAD49138.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 14385, 14386 | 19705335 | 50 | 2.00E-36 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Ferric uptake regulation protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94129.1 Ferric uptake regulation protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | |
| 14389, 14390 | 39594604 | 30 | 4.00E-24 | Caenorhabditis briggsae | Hypothetical protein CBG19289 [Caenorhabditis briggsae] | | 6.2.1.26 | |
| 14391, 14392 | 34102684 | 46 | 9.00E-59 | Chromobacterium violaceum ATCC 12472 | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_901044.1 hypothetical protein CV1374 [Chromobacterium violaceum ATCC 12472] | | | |
| 14393, 14394 | 34557291 | 41 | 1.00E-36 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | 2.7.3.- | |
| 14395, 14396 | 34398055 | 70 | 5.00E-49 | Porphyromonas gingivalis W83 | glycyl-tRNA synthetase [Porphyromonas gingivalis W83] ref NP_906216.1 glycyl-tRNA synthetase [Porphyromonas gingivalis W83] | Myroides odoratimimus metallo-beta- lactamase (MUS-1) gene, complete cds | 88 | 2.00E-30 |
| 14397, 14398 | 29349019 | 73 | 4.00E-84 | Bacteroides thetaiotaomicron VPI-5482 | glycyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78716.1 glycyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI- 5482] | | | 6.1.1.14 |
| 14399, 14400 | 48766217 | 66 | 1.00E-35 | Rhodospirillum rubrum | COG0064: Asp-tRNAAsn/Glu-tRNA ^{Gln} amidotransferase B subunit (PET112 homolog) [Rhodospirillum rubrum] | | | 6.3.5.- |
| 14405, 14406 | 34558377 | 47 | 2.00E-47 | Wolinella succinogenes DSM 1740 | TRNA (URACIL-5-METHYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE11092.1 TRNA (URACIL-5-METHYLTRANSFERASE [Wolinella succinogenes]) | | | 2.1.1.35 |
| 14407, 14408 | 48854542 | 50 | 4.00E-25 | Cytophaga hutchinsonii | COG1748: Saccharopine dehydrogenase and related proteins [Cytophaga hutchinsonii] | | | 1.5.1.10 |
| 1441, 1442 | 47218152 | 49 | 1.00E-23 | Tetraodon nigrovirdis | unnamed protein product [Tetraodon nigrovirdis] | | | |
| 14413, 14414 | 34557661 | 60 | 1.00E-28 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1299 [Wolinella succinogenes DSM 1740] emb CAE10376.1 hypothetical protein [Wolinella succinogenes] probable ATP-dependent DNA helicase [Azoarcus sp. EbN1] emb CAI09453.1 probable ATP-dependent DNA helicase [Azoarcus sp. EbN1] | | | |
| 14419, 14420 | 56478765 | 51 | 1.00E-20 | Azoarcus sp. EbN1 | | | | 3.6.1.- |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|---|-------------|----------|
| 14421, 14422 | 57168001 | 27 | 5.00E-11 | Campylobacter coli RM2228 | phosphatidylserine decarboxylase-related protein [Campylobacter coli RM2228] gb EAL57044.1 phosphatidylserine decarboxylase-related protein [Campylobacter coli RM2228] | | | 4.1.1.65 |
| 14423, 14424 | 21673982 | 44 | 1.00E-34 | Chlorobium tepidum TLS | long-chain-fatty-acid-CoA ligase, putative [Chlorobium tepidum TLS] gb AAIM72389.1 long-chain-fatty-acid-CoA ligase, putative [Chlorobium tepidum TLS] | | | 6.2.1.3 |
| 14425, 14426 | 48855640 | 53 | 1.00E-21 | Cytophaga hutchinsonii | COG0714: MoxR-like ATPases [Cytophaga hutchinsonii] ABC transporter, nucleotide binding/ATPase protein [Agrobacterium tumefaciens str. C58] gb AAL41427.1 ABC transporter, nucleotide binding/ATPase protein [Agrobacterium tumefaciens str. C58] pir AE2626 hypothetical protein fbpA1 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) | | | |
| 14427, 14428 | 17934321 | 40 | 3.00E-10 | Agrobacterium tumefaciens str. C58 | COG0500: SAM-dependent methyltransferases [Nostoc punctiforme PCC 73102] | | | |
| 14429, 14430 | 53688795 | 40 | 1.00E-22 | Nostoc punctiforme PCC 73102 | excinuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD50064.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46] related to methyl-accepting chemotaxis protein [Desulfotalea psychrophila LSv54] emb CAG35707.1 related to methyl-accepting chemotaxis protein [Desulfotalea psychrophila LSV54] | Clostridium perfringens str. 13 DNA, complete genome | 88 2.00E-14 | |
| 14431, 14432 | 53714606 | 54 | 1.00E-26 | Bacteroides fragilis YCH46 | COG2062: Phosphohistidine phosphatase SixA [Cytophaga hutchinsonii] | | | 3.1.3.- |
| 14433, 14434 | 51244830 | 37 | 7.00E-07 | Desulfotalea psychrophila LSV54 | hypothetical protein WS1876 [Wolnella succinogenes DSM 1740] emb CAE10886.1 conserved hypothetical protein [Wolnella succinogenes] | | | |
| 14435, 14436 | 48856760 | 45 | 1.00E-32 | Cytophaga hutchinsonii | Carboxynorspermidine decarboxylase [Idiomarina loihiensis L2TR] gb AAV82832.1 Carboxynorspermidine decarboxylase [Idiomarina loihiensis L2TR] | | | 4.1.1.- |
| 14437, 14438 | 48856760 | 45 | 1.00E-32 | Wolnella succinogenes DSM 1740 | carboxynorspermidine decarboxylase [Campylobacter jejuni RM1221] gb AAW36121.1 carboxynorspermidine decarboxylase [Campylobacter jejuni RM1221] | | | 4.1.1.- |
| 14439, 14440 | 34558171 | 23 | 3.00E-07 | Idiomarina loihiensis L2TR | COG0676: Uncharacterized enzymes related to aldose 1-epimerase [Methylobacillus flagellatus KT] | | | |
| 14441, 14442 | 56461100 | 55 | 1.00E-32 | Campylobacter jejuni RM1221 | hypothetical protein Gmet02001892 [Geobacter metallireducens GS-15] | | | |
| 14443, 14444 | 57238538 | 59 | 3.00E-64 | Methylobacillus flagellatus KT | hypothetical protein Chut02002321 [Cytophaga hutchinsonii] | | | |
| 14445, 14446 | 53759813 | 39 | 2.00E-46 | Geobacter metallireducens GS-15 | | | | |
| 14447, 14448 | 48845647 | 43 | 1.00E-46 | Cytophaga hutchinsonii | | | | |
| 14449, 14450 | 48854655 | 34 | 1.00E-11 | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|---|----|----------|--|--|
| 14451, 14452 | 46156514 | 69 | 1.00E-45 | Haemophilus sommus 2336 | COG0582: Integrase [Haemophilus somnus 2336] Desc:Haemophilus influenzae cellular proliferation protein #135. Org:Haemophilus influenzae | 86 | 8.00E-11 | Desc:Bifidobacteriu m longum NCC2705 related nucleotide sequence SEQ ID:1106. Org:Bifidobacterium longumSynthetic | |
| 14453, 14454 | AAU3549 4 | 43 | 2.00E-41 | Ralstonia solanacearum GMI1000 | hypothetical protein RS01874 [Ralstonia solanacearum GMI1000] emb CAD13579.1 CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] | | 2.3.1.51 | | |
| 14455, 14456 | 17544770 | 33 | 1.00E-17 | Bacteroides fragilis YCH46 | hypothetical protein BF3486 [Bacteroides fragilis YCH46] dbj BAD50229.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | 2.1.1.- | | |
| 14457, 14458 | 53714771 | 27 | 2.00E-14 | Porphyromonas gingivalis W83 | sensor histidine kinase [Porphyromonas gingivalis W83] ref NP_905586.1 sensor histidine kinase [Porphyromonas gingivalis W83] | | | | |
| 14459, 14460 | 34397423 | 21 | 4.00E-12 | Chloroflexus aurantiacus | COG0110: Acetyltransferase (isoleucine patch superfamily) [Chloroflexus aurantiacus] | | 2.3.1.- | | |
| 14463, 14464 | 53795087 | 35 | 9.00E-18 | Desulfovibrio desulfuricans G20 | COG0451: Nucleoside-diphosphate-sugar epimerases [Desulfovibrio desulfuricans G20] | | 5.1.3.2 | | |
| 14465, 14466 | 53691528 | 35 | 1.00E-30 | Campylobacter lari RM2100 | probable transmembrane protein Cj0390 [Campylobacter lari RM2100] gb EAL54700.1 probable transmembrane protein Cj0390 [Campylobacter lari RM2100] | | | | |
| 14469, 14470 | 57241004 | 24 | 8.00E-10 | Bacteroides thetaiotaomicron VPI-5482 | beta-mannosidase precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO75565.1 beta-mannosidase precursor [Bacteroides thetaiotaomicron VPI-5482] | | 3.2.1.25 | | |
| 14471, 14472 | 29345868 | 28 | 7.00E-22 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | |
| 14475, 14476 | 45658172 | 42 | 3.00E-34 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | metallo-beta-lactamase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97276.1 metallo-beta-lactamase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | |
| 14477, 14478 | 46581208 | 38 | 2.00E-46 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|--|---|----|------------------|
| 14479, 14480 | 34557487 | 62 | 5.00E-82 | Wollinella succinogenes DSM 1740 | ABC TRANSPORTER, PERIPLASMIC SUBSTRATE-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10202.1 ABC TRANSPORTER, PERIPLASMIC SUBSTRATE-BINDING PROTEIN [Wollinella succinogenes] | | | |
| 14481, 14482 | 34557960 | 46 | 2.00E-72 | Wollinella succinogenes DSM 1740 | PROLINE AMINOPEPTIDASE [Wollinella succinogenes DSM 1740] emb CAE10675.1 PROLINE AMINOPEPTIDASE [Wollinella succinogenes] conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860475.1 hypothetical protein HH0944 [Helicobacter hepaticus ATCC 51449] | | | 3.4.11.9 |
| 14483, 14484 | 32262494 | 60 | 3.00E-69 | Helicobacter hepaticus ATCC 51449 | ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes DSM 1740] emb CAE0984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes] | | | 3.4.13.9 |
| 14485, 14486 | 34557269 | 59 | 1.00E-84 | Wollinella succinogenes DSM 1740 | [Wollinella succinogenes] fibronectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100] gb EAL54384.1 fibronectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100] | | | 3.6.1.- |
| 14487, 14488 | 57241714 | 33 | 3.00E-38 | Campylobacter lari RM2100 | membrane protein, putative [Treponema denticola ATCC 35405] gb AAS10964.1 membrane protein, putative [Treponema denticola ATCC 35405] | | | |
| 14489, 14490 | 42525985 | 29 | 8.00E-24 | Treponema denticola ATCC 35405 | hypothetical protein Tery02000770 [Trichodesmium erythraeum IMS101] hypothetical protein OB2886 [Oceanobacillus ihayensis HTE831] dbj BAC14842.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831] | | | 2.4.1.- |
| 14495, 14496 | 46578746 | 29 | 4.00E-19 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | response regulator [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94813.1 response regulator [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 14497, 14498 | 48763282 | 43 | 9.00E-57 | Rhodospirillum rubrum | COG0642: Signal transduction histidine kinase [Rhodospirillum rubrum] | | | 2.7.3.- |
| 14499, 14500 | 53711583 | 61 | 8.00E-47 | Bacteroides fragilis YCH46 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Bacteroides fragilis YCH46] dbj BAD47041.1 2,3-bisphosphoglycerate- independent phosphoglycerate mutase [Bacteroides fragilis YCH46] | | | 5.4.2.1 |
| 14501, 14502 | 29348828 | 63 | 1.00E-107 | Bacteroides thetaiotaomicron VPI-5482 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78525.1 2,3- bisphosphoglycerate-independent phosphoglycerate mutase [Bacteroides- thetaiotaomicron VPI-5482] sp Q8A287 GPMI_BACTN 2,3- bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM) | Legionella pneumophila str. Lens complete genome | 96 | 2.00E-13 5.4.2.1 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|----------|
| 14505, 14506 | 15896782 | 48 | 2.00E-69 | Clostridium acetobutylicum ATCC 824 | Highly conserved protein containing a domain related to cellulase catalytic domain and a thioredoxin domain [Clostridium acetobutylicum ATCC 824] gb AAK81471.1 Highly conserved protein containing a domain related to cellulase catalytic domain and a thioredoxin domain [Clostridium acetobutylicum ATCC 824] p D97335 hypothetical protein CAC3546 [imported] - Clostridium acetobutylicum | Methanosarcina acetivorans str. C2A, section 429 of 534 of the complete genome | 84 | 1.00E-11 | 2.7.4.9 |
| 14507, 14508 | 20809061 | 37 | 2.00E-38 | Thermoanaerobact er tengcongensis MB4 | ABC-type multidrug/protein/lipid transport system, ATPase component [Thermoanaerobacter tengcongensis MB4] gb AAM25836.1 ABC-type multidrug/protein/lipid transport system, ATPase component [Thermoanaerobacter tengcongensis MB4] | | | | 3.4.21.- |
| 1451, 1452 | 23113094 | 37 | 5.00E-07 | Desulfotobacterium hafnense DCB-2 | COG0438: Glycosyltransferase [Desulfotobacterium hafnense DCB-2] | | | | |
| 14511, 14512 | 34557571 | 53 | 1.00E-88 | Wolinella succinogenes DSM 1740 | GLUTAMATE SYNTHASE, LARGE SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10286.1 GLUTAMATE SYNTHASE, LARGE SUBUNIT [Wolinella succinogenes] | | | | 1.4.1.13 |
| 14515, 14516 | 48854339 | 59 | 2.00E-94 | Cytophaga hutchinsonii | COG0178: Exonuclease ATPase subunit [Cytophaga hutchinsonii] | | | | |
| 14517, 14518 | 53714606 | 50 | 4.00E-76 | Bacteroides fragilis YCH46 | exonuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD50064.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46] | | | | |
| 14519, 14520 | 34557665 | 49 | 4.00E-35 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | | 2.7.3.- |
| 14521, 14522 | 57167857 | 37 | 6.00E-14 | Campylobacter coli RM2228 | ferric uptake regulation protein, putative [Campylobacter coli RM2228] gb EAL57643.1 ferric uptake regulation protein, putative [Campylobacter coli RM2228] | | | | |
| 14525, 14526 | 21674678 | 32 | 1.00E-28 | Chlorobium tepidum TLS | hypothetical protein CT1866 [Chlorobium tepidum TLS] gb AAM73085.1 hypothetical protein [Chlorobium tepidum TLS] | | | | |
| 14527, 14528 | 53713068 | 37 | 3.00E-11 | Bacteroides fragilis YCH46 | hypothetical protein BF1779 [Bacteroides fragilis YCH46] db BAD48526.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 1453, 1454 | 53712397 | 43 | 6.00E-51 | Bacteroides fragilis YCH46 | putative glycosyltransferase [Bacteroides fragilis YCH46] gb AAD56741.1 putative glycosyltransferase [Bacteroides fragilis] db BAD47855.1 putative glycosyltransferase [Bacteroides fragilis YCH46] | | | | |
| 14531, 14532 | 26988742 | 44 | 1.00E-58 | Pseudomonas putida KT2440 | aminopeptidase N [Pseudomonas putida KT2440] gb AAN67631.1 aminopeptidase N [Pseudomonas putida KT2440] | | | | 3.4.11.2 |
| 14533, 14534 | 48855815 | 55 | 3.00E-52 | Cytophaga hutchinsonii | COG1600: Uncharacterized Fe-S protein [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|----------|
| 14535, 14536 | 15840961 | 37 | 7.00E-13 | Mycobacterium tuberculosis CDC1551 | methylintransferase [Mycobacterium tuberculosis CDC1551] gb AAK45812.1 methylintransferase [Mycobacterium tuberculosis CDC1551] | | | |
| 14537, 14538 | 42780401 | 54 | 5.00E-49 | Bacillus cereus ATCC 10987 | hypothetical protein BCE1327 [Bacillus cereus ATCC 10987] gb AAS40256.1 conserved hypothetical protein [Bacillus cereus ATCC 10987] | | | 2.1.1.- |
| 14539, 14540 | 15611096 | 44 | 1.00E-13 | Helicobacter pylori J99 | DETHIOBIOTIN SYNTHETASE [Helicobacter pylori J99] gb AAD05609.1 DETHIOBIOTIN SYNTHETASE [Helicobacter pylori J99] pir IG71982 dethiobiotin synthetase - Helicobacter pylori (strain J99) sp Q9ZN34 BIOD_HELPJ Dethiobiotin synthetase (Dethiobiotin synthase) (DTB synthetase) (DTBS) | | | 6.3.3.3 |
| 14541, 14542 | 53758942 | 46 | 5.00E-16 | Methylococcus capsulatus str. Bath | conserved domain protein [Methylococcus capsulatus str. Bath] ref YP_113621.1 hypothetical protein MCA1152 [Methylococcus capsulatus str. Bath] | | | |
| 14543, 14544 | 4234793 | 37 | 1.00E-43 | Leptospira borgpetersenii | unknown [Leptospira borgpetersenii] | | | |
| 14545, 14546 | 23114771 | 45 | 2.00E-57 | Desulfotobacterium hafniense DCB-2 | COG0451: Nucleoside-diphosphate-sugar epimerases [Desulfotobacterium hafniense DCB-2] | | | 4.2.1.- |
| 14547, 14548 | 48846045 | 32 | 5.00E-29 | Geobacter metallireducens GS-15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120] pir AC2091 serine/threonine kinase with two-component sensor domain all2282 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73981.1 serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120] | | | 2.7.3.- |
| 14549, 14550 | 17229774 | 23 | 3.00E-18 | Nostoc sp. PCC 7120 | hypothetical protein PA4369 [Pseudomonas aeruginosa PAO1] ref ZP_00137855.2 COG1704: Uncharacterized conserved protein [Pseudomonas aeruginosa UC8PP-PA14] pir H83100 hypothetical protein PA4369 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253059.1 hypothetical protein PA4369 [Pseudomonas aeruginosa PAO1] | | | |
| 14551, 14552 | 15920615 | 36 | 8.00E-24 | Sulfolobus tokodaii str. 7 | hypothetical adenylate kinase [Sulfolobus tokodaii str. 7] sp Q9757 KCY_SULTO Cytidylate kinase (CK) (Cytidine monophosphate kinase) (CMP kinase) dbj BAB55393.1 180aa long hypothetical adenylate kinase [Sulfolobus tokodaii str. 7] | | | 2.7.4.14 |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|---|--|----|-----------|----------|
| 14553, 14554 | 52424971 | 76 | 1.00E-48 | Mannheimia succiniciproducens MBEL55E | Nth protein [Mannheimia succiniciproducens MBEL55E] gb AAU37523.1 Nth protein [Mannheimia succiniciproducens MBEL55E] | Salmonella typhimurium LT2, section 67 of 220 of the complete genome | 84 | 4.00E-098 | 4.2.99.1 |
| 14555, 14556 | 28210429 | 44 | 5.00E-57 | Clostridium tetani E88 | transcriptional regulatory protein [Clostridium tetani E88] gb AAO35310.1 transcriptional regulatory protein [Clostridium tetani E88] | | | | |
| 14557, 14558 | 53715867 | 56 | 7.00E-57 | Bacteroides fragilis YCH46 | putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46] db BAD51325.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46] | | | 2.7.7.56 | |
| 14559, 14560 | 48856331 | 41 | 9.00E-47 | Cytophaga hutchinsonii | hypothetical protein Chut02000043 [Cytophaga hutchinsonii] | | | | |
| 14563, 14564 | 31194225 | 49 | 6.00E-28 | Anopheles gambiae | ENSANGP00000000349 [Anopheles gambiae] | | | | 1.5.1.3 |
| 14565, 14566 | ABP3846 9 | 44 | 4.00E-15 | | Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3314. Org:Staphylococcus epidermidis | | | | 2.7.6.3 |
| 14567, 14568 | 6968169 | 49 | 1.00E-37 | Campylobacter jejuni subsp. jejuni NCTC 11168 | putative 16S rRNA processing protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81342 probable 16S rRNA processing protein Cj0712 [Imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281884.1 putative 16S rRNA processing protein [Campylobacter jejuni subsp. jejuni NCTC 11168] sp Q9PPJ5 RIMM_CAMJE Probable 16S rRNA processing protein rlmM | | | | |
| 14569, 14570 | 38099730 | 27 | 9.00E-13 | Magnaporthe grisea 70-15 | hypothetical protein MG10847.4 [Magnaporthe grisea 70-15] ref XP_360535.1 hypothetical protein MG10847.4 [Magnaporthe grisea 70- 15] | | | | 3.1.26.- |
| 1457, 1458 | 32414055 | 30 | 4.00E-12 | Neurospora crassa | hypothetical protein [Neurospora crassa] gb EAA28210.1 hypothetical protein [Neurospora crassa] | | | | |
| 14571, 14572 | 15611744 | 54 | 1.00E-46 | Helicobacter pylori J99 | D-ALANYL-D-ALANINE-ADDING ENZYME [Helicobacter pylori J99] gb AAD06244.1 D-ALANYL-D-ALANINE-ADDING ENZYME [Helicobacter pylori J99] pir C71903 D-alanyl-D-alanine-adding enzyme - Helicobacter pylori (strain J99) | | | | 6.3.2.15 |
| 14573, 14574 | 39996271 | 35 | 2.00E-34 | Geobacter sulfurreducens PCA | hypothetical protein GSU1169 [Geobacter sulfurreducens PCA] gb AAR34545.1 hypothetical protein GSU1169 [Geobacter sulfurreducens PCA] | | | | |
| 14577, 14578 | 57240790 | 43 | 7.00E-39 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55183.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |

| | | | | | | | | | |
|-----------------|----------------------|----------|----------------------|---|--|--|----|----------|---------------|
| 14579, 14580 | 34556686 | 47 | 1.00E-29 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0245 [Wollinella succinogenes DSM 1740] emb CAE09401.1 conserved hypothetical protein [Wollinella succinogenes] | | | | |
| 14581, 14582 | AAW9878 3 | 37 | 7.00E-25 | | Desc:H. pylori GHPO 1210 protein. Org:Helicobacter pylori COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii] | | | | 2.7.1.11 2 |
| 14589, 14590 | 48854195 | 45 | 7.00E-26 | Cytophaga hutchinsonii | protoporphyrinogen IX and coproporphyrinogen III oxidase HemY [Legionella pneumophila str. Paris] emb CAH13947.1 protoporphyrinogen IX and coproporphyrinogen III oxidase HemY [Legionella pneumophila str. Paris] COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii] | | | | |
| 14593, 14594 | 54298730 48853737 | 40 25 | 7.00E-38 1.00E-20 | Legionella pneumophila str. Paris Cytophaga hutchinsonii | Low-affinity zinc transport protein [Bacillus cereus ATCC 14579] gb AAP08988.1 Low-affinity zinc transport protein [Bacillus cereus ATCC 14579] | | | | |
| 14595, 14596 | 30020156 34557246 | 26 39 | 3.00E-07 4.00E-32 | Bacillus cereus ATCC 14579 Wollinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes] | | | | 2.7.3.- |
| 14599, 14600 | 36955865 | 74 | 1.00E-106 | Polaribacter filamentus | NH(3)-dependent NAD(+) synthetase [Polaribacter filamentus] | Polaribacter filamentus NH(3)- dependent NAD(+) synthetase (nadE) gene, complete cds | 86 | 3.00E-15 | 6.3.5.1 |
| 14601, 14602 | 52841216 | 28 | 8.00E-18 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | hypothetical protein lpg0982 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27068.1 hypothetical protein lpg0982 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | |
| 14603, 14604 | 53711692 | 45 | 9.00E-61 | Bacteroides fragilis YCH46 | putative DNA-binding protein [Bacteroides fragilis YCH46] dbj BAD47150.1 putative DNA-binding protein [Bacteroides fragilis YCH46] | | | | |
| 14605, 14606 | 48765572 | 38 | 2.00E-32 | Rhodospirillum rubrum | COG2199: FOG: GGDEF domain [Rhodospirillum rubrum] | | | | |
| 14607, 14608 | 34557724 | 43 | 6.00E-51 | Wollinella succinogenes DSM 1740 | PUTATIVE ABC-TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10439.1 PUTATIVE ABC- TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wollinella succinogenes] | | | | 1.8.-:- |

| | | | | | | | | |
|-------------------------------------|----------|----|----------|---|---|--|--|----------|
| 14609, 14610, 1461, 1462 | 41718599 | 36 | 1.00E-26 | Methanococcoides burtonii DSM 6242 | COG0642: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242] | | | 2.7.3.- |
| 14611, 14612 | 48832069 | 36 | 1.00E-30 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | 3.4.21.- |
| 14613, 14614 | 52841303 | 41 | 8.00E-26 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | AbiD phage protein-like [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27155.1 AbiD phage protein-like [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | 2.7.3.- |
| 14615, 14616, 14619, 14620 | 48854366 | 38 | 6.00E-19 | Cytophaga hutchinsonii | COG4823: Abortive infection bacteriophage resistance protein [Cytophaga hutchinsonii] | | | |
| 14621, 14622 | 48832174 | 24 | 2.00E-10 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | |
| 14623, 14624 | 51245404 | 34 | 6.00E-09 | Desulfotalea psychrophila LSV54 | hypothetical protein DP1552 [Desulfotalea psychrophila LSV54] emb CAG36281.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 14625, 14626 | 15606614 | 21 | 5.00E-09 | Aquifex aeolicus VF5 | transporter (extracellular solute binding protein family 5) [Aquifex aeolicus VF5] gb AAC07389.1 transporter (extracellular solute binding protein family 5) [Aquifex aeolicus VF5] pir C70425 transporter (extracellular solute binding protein family 5) - Aquifex aeolicus | | | 2.4.1.- |
| 14627, 14628 | 18653297 | 35 | 2.00E-26 | Vibrio cholerae Bacteroides thetaiotaomicron VPI-5482 | putative glycosyl transferase [Vibrio cholerae] putative long-chain-fatty-acid-CoA ligase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78656.1 putative long-chain-fatty-acid-CoA ligase [Bacteroides thetaiotaomicron VPI-5482] | | | 6.2.1.3 |
| 14629, 14630, 1463, 1464 | 51247033 | 57 | 3.00E-29 | Desulfotalea psychrophila LSV54 | hypothetical protein DPPB82 [Desulfotalea psychrophila LSV54] emb CAG37926.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 14631, 14632 | 48861626 | 40 | 1.00E-40 | Microbulbifer degradans 2-40 | COG0842: Signal transduction histidine kinase [Microbulbifer degradans 2- 40] | | | |
| 14633, 14634 | 58459387 | 29 | 2.00E-15 | Idiomarina loihlensis L2TR | Acylaminoacyl-peptidase [Idiomarina loihlensis L2TR] gb AAV81119.1 Acylaminoacyl-peptidase [Idiomarina loihlensis L2TR] | | | 3.4.19.1 |
| 14635, 14636 | 34557309 | 42 | 5.00E-34 | Wolinella succinogenes DSM 1740 | IRON-SULFUR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10024.1 IRON-SULFUR PROTEIN [Wolinella succinogenes] | | | |
| | 53761737 | 45 | 4.00E-66 | Ralstonia eutropha JMP134 | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Ralstonia eutropha JMP134] | | | 2.7.3.- |

| | | | | | | | | |
|-------------------------------------|----------------------|----------|-----------------------|--|---|---------------------------|--|--|
| 14637, 14638, 14639, 14640 | 34557638 48855884 | 63 47 | 1.00E-111 2.00E-23 | Wolinella succinogenes DSM 1740 Cytophaga hutchinsonii | QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes] COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | |
| 14641, 14642 | 28899897 | 48 | 2.00E-42 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA0042 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61385.1 hypothetical protein [Vibrio parahaemolyticus] | | | |
| 14643, 14644 14645, 14646 | 49354332 23474904 | 34 45 | 8.00E-34 2.00E-57 | Mycoplasma fermentans Desulfovibrio desulfuricans G20 | putative ATP-dependent DNA helicase [Mycoplasma fermentans] COG2070: Dioxygenases related to 2-nitropropane dioxygenase [Desulfovibrio desulfuricans G20] | 3.6.1.- 1.13.11. 32 | | |
| 14647, 14648 | 34557603 | 54 | 5.00E-39 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1238 [Wolinella succinogenes DSM 1740] emb CAE10318.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 14649, 14650 | 34558157 | 44 | 3.00E-16 | Wolinella succinogenes DSM 1740 | SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes] | 2.7.3.- | | |
| 1465, 1466 | 59963015 | 42 | 3.00E-26 | Bacillus clausii KSM-K16 | hypothetical protein ABC1243 [Bacillus clausii KSM-K16] dbj BAD63781.1 conserved hypothetical protein [Bacillus clausii KSM-K16] | 3.4.11.5 | | |
| 14651, 14652 | 17545258 | 61 | 3.00E-74 | Ralstonia solanacearum GMI1000 | PROBABLE ATP-DEPENDENT RNA HELICASE PROTEIN [Ralstonia solanacearum GMI1000] emb CAD14067.1 PROBABLE ATP-DEPENDENT RNA HELICASE PROTEIN [Ralstonia solanacearum] | 2.7.7.- | | |
| 14653, 14654 | 46579094 | 35 | 2.00E-33 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | sensory box histidine kinase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS95161.1 sensory box histidine kinase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | 2.7.3.- | | |
| 14657, 14658 | 21673251 | 45 | 4.00E-48 | Chlorobium tepidum TLS | iron(III) ABC transporter, ATP-binding protein, putative [Chlorobium tepidum TLS] gb AAM71658.1 iron(III) ABC transporter, ATP-binding protein, putative [Chlorobium tepidum TLS] | 3.6.3.33 | | |
| 14659, 14660 | 19705009 | 39 | 2.00E-30 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Oxidoreductase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93803.1 Oxidoreductase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | 1.1.1.21 | | |
| 14661, 14662 | 34558468 | 44 | 2.00E-30 | Wolinella succinogenes DSM 1740 | PUTATIVE ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZ [Wolinella succinogenes DSM 1740] emb CAE11183.1 PUTATIVE ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZ [Wolinella succinogenes]) | 6.3.5.4 | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|----------|
| 14665, 14666 | 57242329 | 46 | 3.00E-42 | Campylobacter upsaliensis RM3195 | signal-transducing protein, histidine kinase [Campylobacter upsaliensis RM3195] gb EAL53791.1 signal-transducing protein, histidine kinase [Campylobacter upsaliensis RM3195] | | | 2.7.3.- |
| 14667, 14668 | 57241251 | 59 | 8.00E-67 | Campylobacter lari RM2100 | response regulator (ompR) [Campylobacter lari RM2100] gb EAL54947.1 response regulator (ompR) [Campylobacter lari RM2100] | | | 2.7.3.- |
| 14669, 14670 | 34557606 | 36 | 1.00E-48 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1241 [Wolinella succinogenes DSM 1740] emb CAE10321.1 conserved hypothetical protein [Wolinella succinogenes] | | | 3.5.1.- |
| 1467, 1468 | 39936696 | 49 | 6.00E-23 | Rhodopseudomonas palustris CGA009 | putative Transaldolase Phosphoglucose isomerase [Rhodopseudomonas palustris CGA009] emb CAE29075.1 putative Transaldolase Phosphoglucose isomerase [Rhodopseudomonas palustris CGA009] | | | 2.2.1.2 |
| 14671, 14672 | 48838846 | 50 | 3.00E-30 | Methanosarcina barkeri str. fusaro | COG0457: FOG: TPR repeat [Methanosarcina barkeri str. fusaro] putative phosphoesterase [Bordetella bronchiseptica RB50] | | | |
| 14673, 14674 | 33600223 | 29 | 3.00E-23 | Bordetella bronchiseptica RB50 | emb CAE31735.1 putative phosphoesterase [Bordetella bronchiseptica RB50] | | | |
| 14675, 14676 | 42522432 | 41 | 1.00E-40 | Bdellovibrio bacteriovorus HD100 | ABC-type phosphonate transport protein, ATP-binding [Bdellovibrio bacteriovorus HD100] emb CAE78805.1 ABC-type phosphonate transport protein, ATP-binding [Bdellovibrio bacteriovorus HD100] | | | 1.8.- |
| 14677, 14678 | 57242034 | 63 | 1.00E-68 | Campylobacter upsaliensis RM3195 | uroporphyrinogen decarboxylase [Campylobacter upsaliensis RM3195] gb EAL54007.1 uroporphyrinogen decarboxylase [Campylobacter upsaliensis RM3195] | | | 4.1.1.37 |
| 14679, 14680 | 28900746 | 38 | 7.00E-27 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA0891 [Vibrio parahaemolyticus RIMD 2210633] db BAC62234.1 hypothetical protein [Vibrio parahaemolyticus] | | | |
| 14683, 14684 | 51244370 | 43 | 2.00E-26 | Desulfotalea psychrophila LSV54 | hypothetical protein DP0518 [Desulfotalea psychrophila LSV54] emb CAG35247.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 14685, 14686 | 51246963 | 38 | 2.00E-14 | Desulfotalea psychrophila LSV54 | hypothetical protein DP3111 [Desulfotalea psychrophila LSV54] emb CAG37840.1 hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 14687, 14688 | 51246963 | 49 | 2.00E-36 | Desulfotalea psychrophila LSV54 | hypothetical protein DP3111 [Desulfotalea psychrophila LSV54] emb CAG37840.1 hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 14689, 14690 | 48858932 | 34 | 9.00E-26 | Clostridium thermocellum ATCC 27405 | COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | 2.7.3.- |

| | | | | | | | | | |
|-----------------|----------|----|-----------|----------|-------------------------------------|---|--|----|-------------------|
| 1469, 1470 | 52007674 | 36 | 6.00E-16 | 25259 | Thiobacillus denitrificans ATCC | COG1959: Predicted transcriptional regulator [Thiobacillus denitrificans ATCC 25259] | | | |
| 14691, 14692 | 20089988 | 36 | 5.00E-11 | | Methanosarcina acetivorans C2A | transcriptional regulator, MarR family [Methanosarcina acetivorans C2A] gb AA04543.1 transcriptional regulator, MarR family [Methanosarcina acetivorans str. C2A] | | | |
| 14693, 14694 | 34557604 | 44 | 4.00E-60 | 1740 | Wolinella succinogenes DSM | TRANSCRIPTION-REPAIR COUPLING FACTOR [Wolinella succinogenes DSM 1740] emb CAE10319.1 TRANSCRIPTION-REPAIR COUPLING FACTOR [Wolinella succinogenes] | | | |
| 14695, 14696 | 34557638 | 66 | 1.00E-106 | 1740 | Wolinella succinogenes DSM | QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes] excinuclease ABC, A subunit [Campylobacter jejuni RM1221] gb AAW34979.1 excinuclease ABC, A subunit [Campylobacter jejuni RM1221] | Rickettsia typhi str. Wilmington complete genome | 84 | 2.00E-12 |
| 14697, 14698 | 57237396 | 79 | 8.00E-77 | | Campylobacter jejuni RM1221 | hypothetical protein Magn03007449 [Magnetospirillum magnetotacticum MS- 1] | | | |
| 14699, 14700 | 46202599 | 33 | 6.00E-27 | MS-1 | Magnetospirillum magnetotacticum | putative UDP-glucose dehydrogenase [Photobacterium profundum SS9] emb CAG21035.1 putative UDP-glucose dehydrogenase [Photobacterium profundum] | Campylobacter jejuni | 96 | 7.00E-13 1.1.1.22 |
| 14701, 14702 | 54309817 | 71 | 1.00E-119 | | Photobacterium profundum SS9 | COG0845: Membrane-fusion protein [Microbulbifer degradans 2-40] COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Rubrivivax gelatinosus PM1] | | | 3.4.21.- |
| 14703, 14704 | 48862943 | 49 | 2.00E-59 | | Microbulbifer degradans 2-40 | hypothetical protein WS2202 [Wolinella succinogenes DSM 1740] emb CAE11192.1 hypothetical protein [Wolinella succinogenes] lipoprotein releasing system ATP-binding protein [Bacteroides thetataoomicron VPI-5482] gb AAO78745.1 lipoprotein releasing system ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] spiQ8A1M1 OLD_BACTN Lipoprotein releasing system ATP-binding protein fold | | | 1.8.- |
| 14705, 14706 | 47575513 | 47 | 1.00E-76 | | Rubrivivax gelatinosus PM1 | probable surface-associated protein cshA precursor [Rhodopirellula baltica SH 1] emb CAD71782.1 probable surface-associated protein cshA precursor [Pirellula sp.] | | | |
| 14707, 14708 | 34558477 | 35 | 5.00E-09 | 1740 | Wolinella succinogenes DSM | COG1066: Predicted ATP-dependent serine protease [Cytophaga hutchinsonii] | | | |
| 1471, 1472 | 29349048 | 57 | 4.00E-34 | VPI-5482 | Bacteroides thetataoomicron | related to ArsR-family transcription regulator [Desulfotalea psychrophila LSv54] emb CAG35673.1 related to ArsR-family transcription regulator [Desulfotalea psychrophila LSv54] | | | |
| 14711, 14712 | 32471112 | 30 | 2.00E-09 | | Rhodopirellula baltica SH 1 | | | | |
| 14713, 14714 | 48854139 | 57 | 1.00E-49 | | Cytophaga hutchinsonii | | | | |
| 14715, 14716 | 51244796 | 45 | 3.00E-18 | | Desulfotalea psychrophila LSv54 | | | | |

| | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|--|--|----------|
| 14717, | 48855926 | 35 | 1.00E-39 | Cytophaga hutchinsonii | COG1091: dTDP-4-dehydroharmannose reductase [Cytophaga hutchinsonii] | | | 1.1.1.13 |
| 14718 | | | | | Methyltransferase [Bacillus cereus ATCC 14579] gb AAP11449.1 | | | 3 |
| 14719, | 30022617 | 51 | 8.00E-42 | Bacillus cereus ATCC 14579 | Methyltransferase [Bacillus cereus ATCC 14579] | | | |
| 14720 | | | | | | | | |
| 14721, | | | | Clostridium thermocellum | COG0500: SAM-dependent methyltransferases [Clostridium thermocellum ATCC 27405] | | | 2.1.1.- |
| 14722 | 48859334 | 60 | 1.00E-49 | ATCC 27405 | | | | |
| 14725, | | | | Photobacterium profundum SS9 | hypothetical protein PBPRB0710 [Photobacterium profundum SS9] | | | |
| 14726 | 54302389 | 49 | 8.00E-42 | profundum SS9 | emb CAG22582.1 hypothetical protein [Photobacterium profundum] | | | |
| 14727, | | | | Cytophaga hutchinsonii | COG0747: ABC-type dipeptide transport system, periplasmic component [Cytophaga hutchinsonii] | | | |
| 14728 | 48854027 | 40 | 4.00E-48 | | hypothetical protein aq_737 [Aquifex aeolicus VF5] gb AAC06915.1 | | | |
| | | | | Aquifex aeolicus VF5 | hypothetical protein [Aquifex aeolicus VF5] pir G70364 conserved | | | |
| 14729, | | | | | hypothetical protein aq_737 - Aquifex aeolicus sp O66946 MRP_AQUAE | | | |
| 14730 | 15606130 | 50 | 4.00E-50 | | Mrp protein homolog | | | |
| | | | | Bacteroides thetaiotaomicron VPI-5482 | GTP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 1473, | | | | | gb AAO77365.1 GTP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 1474 | 29347668 | 39 | 5.00E-17 | | | | | |
| | | | | Bacillus anthracis str. 'Ames' | hypothetical protein GBAA0891 [Bacillus anthracis str. 'Ames Ancestor'] | | | |
| 14733, | | | | | ref NP_843402.1 hypothetical protein BA0891 [Bacillus anthracis str. 'Ames'] | | | |
| 14734 | 47526177 | 26 | 5.00E-24 | | ref NP_654834.1 hypothetical protein BA_1474 [Bacillus anthracis str. 'Ames'] | | | |
| | | | | ancestral | A2012] gb AAP24888.1 conserved hypothetical protein [Bacillus anthracis str. 'Ames'] | | | |
| | | | | ancestral | str. 'Ames'] gb AAT30001.1 conserved hypothetical protein [Bacillus anthracis str. 'Ames Ancestor'] | | | |
| 14735, | | | | Treponema denticola ATCC 35405 | cholinephosphate cytidyltransferase/choline kinase [Treponema denticola ATCC 35405] gb AAS11778.1 cholinephosphate cytidyltransferase/choline kinase [Treponema denticola ATCC 35405] | | | 2.7.1.32 |
| 14736 | 42526769 | 26 | 5.00E-12 | | | | | |
| 14737, | | | | Cytophaga hutchinsonii | COG0859: ADP-heptose:PS heptosyltransferase [Cytophaga hutchinsonii] | | | |
| 14738 | 48853824 | 48 | 1.00E-72 | | signal peptidase I [Porphyromonas gingivalis W83] ref NP_906073.1 signal | | | 3.4.21.8 |
| 14739, | | | | Porphyromonas gingivalis W83 | peptidase I [Porphyromonas gingivalis W83] | | | 9 |
| 14740 | 34397911 | 30 | 2.00E-29 | | signal peptidase I [Bacteroides fragilis YCH46] db BAD46930.1 signal | | | 3.4.21.8 |
| 14743, | | | | Bacteroides fragilis YCH46 | peptidase I [Bacteroides fragilis YCH46] | | | |
| 14744 | 53711472 | 52 | 2.00E-26 | | | | | |
| 14745, | | | | Enterococcus faecalis | TrsK-like protein [Enterococcus faecalis] | | | |
| 14746 | 33355837 | 54 | 1.00E-31 | | | | | |
| | | | | Dehalococcoides ethenogenes 195 | [SDet4, transposase [Dehalococcoides ethenogenes 195] gb AAW39508.1 | | | |
| 14747, | | | | | [SDet4, transposase [Dehalococcoides ethenogenes 195] | | | |
| 14748 | 57234003 | 60 | 7.00E-89 | | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|---------------|----------|
| 14749, 14750 | 34557966 | 58 | 9.00E-89 | Wollinella succinogenes DSM 1740 | ATP-DEPENDENT HELICASE [Wollinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wollinella succinogenes] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 92 | 7.00E-10 | 3.6.1.- | |
| 1475, 1476 | 56708105 | 33 | 4.00E-14 | Francisella tularensis subsp. tularensis Schu 4 | GDSL-like Lipase/Acyhydrolase family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45649.1 GDSL-like Lipase/Acyhydrolase family protein [Francisella tularensis subsp. tularensis] AsnC family transcriptional regulator [Bacteroides fragilis YCH46] db BAD48864.1 AsnC family transcriptional regulator [Bacteroides fragilis YCH46] | | | 3.1.2.- | | |
| 14751, 14752 | 53713406 | 46 | 3.00E-35 | Bacteroides fragilis YCH46 | COG0626: Cystathionine beta-lyases/cystathionine gamma-synthases [Chloroflexus aurantiacus] | | | | 4.4.1.11 | |
| 14753, 14754 | 53798453 | 78 | 2.00E-08 | Chloroflexus aurantiacus | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56275.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | | |
| 14757, 14758 | 57169040 | 22 | 1.00E-07 | Campylobacter coli RM2228 | hypothetical protein sil1308 [Synechocystis sp. PCC 6803] db BAA17635.1 sil1308 [Synechocystis sp. PCC 6803] pir S77301 hypothetical protein sil1308 - Synechocystis sp. (strain PCC 6803) | | | | 1.1.1.10 0 | |
| 14759, 14760 | 16330227 | 32 | 6.00E-14 | Synechocystis sp. PCC 6803 | hypothetical protein VPA0558 [Vibrio parahaemolyticus RIMD 2210633] db BAC61901.1 conserved hypothetical protein [Vibrio parahaemolyticus] COG1776: Chemotaxis protein CheC, inhibitor of MCP methylation [Magnetococcus sp. MC-1] | | | | | |
| 14765, 14766 | 28900413 | 42 | 9.00E-32 | parahaemolyticus RIMD 2210633 | conserved hypothetical protein [Silicibacter pomeroyi DSS-3] ref YP_165430.1 hypothetical protein SPO0160 [Silicibacter pomeroyi DSS- 3] | | | | | |
| 14767, 14768 | 48832346 | 25 | 5.00E-07 | Magnetococcus sp. MC-1 | unknown [Leptospira borgpetersenii] | | | | | |
| 14769, 14770 | 56676820 | 49 | 1.00E-50 | Silicibacter pomeroyi DSS-3 | hypothetical protein PP4291 [Pseudomonas putida KT2440] gb AAN6987.1 conserved hypothetical protein [Pseudomonas putida KT2440] | | | | | |
| 14771, 14772 | 4234793 | 36 | 1.00E-23 | Leptospira borgpetersenii | type I restriction modification enzyme protein S [Methanosarcina acetivorans C2A] gb AAM05801.1 type I restriction modification enzyme protein S [Methanosarcina acetivorans str. C2A] RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221] gb AAW34517.1 RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221] | | | | 3.1.21.3 | |
| 14775, 14776 | 26990982 | 28 | 1.00E-16 | Pseudomonas putida KT2440 | | | | | | 4.2.1.70 |
| 14779, 14780 | 20091246 | 46 | 3.00E-39 | Methanosarcina acetivorans C2A | | | | | | |
| 14783, 14784 | 57236934 | 42 | 8.00E-28 | Campylobacter jejuni RM1221 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|--|---|-------------|---------|
| 14785, 14786 | 46581495 | 35 | 2.00E-10 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | hypothetical protein DVU3092 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gblAAS97563.1] hypothetical protein DVU3092 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 14787, 14788 | 20807875 | 48 | 9.00E-18 | Thermoanaerobact er tengcongensis MB4 | CheY-like receiver domains [Thermoanaerobacter tengcongensis MB4] gblAAM24650.1] CheY-like receiver domains [Thermoanaerobacter tengcongensis MB4] | | 3.1.1.61 | |
| 14789, 14790 | 40741709 | 42 | 1.00E-16 | Aspergillus nidulans FGSC A4 | hypothetical protein AN4556.2 [Aspergillus nidulans FGSC A4] ref XP_408693.1] hypothetical protein AN4556.2 [Aspergillus nidulans FGSC A4] | | | |
| 14791, 14792 | 57238505 | 37 | 3.00E-35 | Campylobacter jejuni RM1221 | hypothetical protein CJE1655 [Campylobacter jejuni RM1221] gblAAW36088.1] conserved hypothetical protein [Campylobacter jejuni RM1221] | | | |
| 14793, 14794 | 53713554 | 52 | 3.00E-89 | Bacteroides fragilis YCH46 | putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46] dbj BAD49012.1] putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46] | | | |
| 14795, 14796 | 34557665 | 58 | 1.00E-38 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1] DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | 2.7.3.- | |
| 14801, 14802 | 37520430 | 29 | 2.00E-25 | Gloeobacter violaceus PCC 7421 | two-component sensor histidine kinase [Gloeobacter violaceus PCC 7421] dbj BAC88802.1] two-component sensor histidine kinase [Gloeobacter violaceus PCC 7421] | | 2.7.3.- | |
| 14803, 14804 | 53713488 | 37 | 6.00E-47 | Bacteroides fragilis YCH46 | two-component system sensor histidine kinase [Bacteroides fragilis YCH46] dbj BAD48946.1] two-component system sensor histidine kinase [Bacteroides fragilis YCH46] | | 2.7.3.- | |
| 14805, 14806 | 34397475 | 28 | 2.00E-13 | Porphyromonas gingivalis W83 | hypothetical protein PG1492 [Porphyromonas gingivalis W83] ref NP_905638.1] hypothetical protein PG1492 [Porphyromonas gingivalis W83] | | | |
| 14807, 14808 | 34397124 | 77 | 1.00E-109 | Porphyromonas gingivalis W83 | D-lysine 5,6-aminomutase, beta subunit [Porphyromonas gingivalis W83] ref NP_905289.1] D-lysine 5,6-aminomutase, beta subunit [Porphyromonas gingivalis W83] | Porphyromonas gingivalis W83 section 4 of 8 of the complete genome | 80 3.00E-18 | 5.4.3.3 |
| 14809, 14810 | 56460690 | 51 | 3.00E-63 | Idiomarina loihlensis L2TR | Zn-dependent hydrolases, glyoxylase family [Idiomarina loihlensis L2TR] gblAAV82422.1] Zn-dependent hydrolases, glyoxylase family [Idiomarina loihlensis L2TR] | | | |
| 1481, 1482 | 48838849 | 76 | 4.00E-96 | Methanosarcina barkeri str. fusaro | COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro] | Methanosarcina acetivorans str. C2A, section 22 of 534 of the complete genome | 81 3.00E-27 | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|-------------|
| 14813, 14814 | 57241396 | 61 | 1.00E-38 | Campylobacter lari RM2100 | amidophosphoribosyltransferase [Campylobacter lari RM2100] gb JEA154508.1 amidophosphoribosyltransferase [Campylobacter lari RM2100] | | | 2.4.2.14 |
| 14815, 14816 | 28974234 | 66 | 1.00E-47 | Campylobacter fetus | putative two-component regulator Cf0034 [Campylobacter fetus] | | Campylobacter fetus strain 23D sap gene locus, partial sequence | 83 8.00E-08 |
| 14817, 14818 | 28974235 | 32 | 2.00E-18 | Campylobacter fetus | putative putative two-component sensor Cf0035 [Campylobacter fetus] CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes] | | | |
| 14819, 14820 | 34556616 | 45 | 1.00E-66 | Wolinella succinogenes DSM 1740 | Hemolysin [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94497.1 Hemolysin [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | |
| 14821, 14822 | 19703636 | 33 | 3.00E-35 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | hypothetical protein MS1396 [Mannheimia succiniciproducens MBEL55E] gb AAU38003.1 unknown [Mannheimia succiniciproducens MBEL55E] | | | |
| 14823, 14824 | 52425451 | 36 | 6.00E-23 | Mannheimia succiniciproducens MBEL55E | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | |
| 14825, 14826 | 48856104 | 40 | 2.00E-38 | Cytophaga hutchinsonii | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860522.1 hypothetical protein HH0991 [Helicobacter hepaticus ATCC 51449] | | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 80 1.00E-16 |
| 14827, 14828 | 32262541 | 74 | 1.00E-71 | Helicobacter hepaticus ATCC 51449 | COG0370: Fe2+ transport system protein B [Geobacter metallireducens GS- 15] | | | |
| 1483, 1484 | 48845148 | 52 | 3.00E-19 | Geobacter metallireducens GS- 15 | putative methyltransferase CmuC [Bacteroides fragilis YCH46] dbj BAD49814.1 putative methyltransferase CmuC [Bacteroides fragilis YCH46] | | | |
| 14831, 14832 | 53714356 | 64 | 4.00E-80 | Bacteroides fragilis YCH46 | hypothetical protein WS0448 [Wolinella succinogenes DSM 1740] emb CAE09590.1 conserved hypothetical protein [Wolinella succinogenes] hypothetical protein, probably cold-shock inducible [Desulfotalea psychrophila LSV54] emb CAG34908.1 hypothetical protein, probably cold- shock inducible [Desulfotalea psychrophila LSV54] | | | |
| 14835, 14836 | 34556875 | 35 | 2.00E-24 | Wolinella succinogenes DSM 1740 | | | | |
| 14841, 14842 | 51244031 | 34 | 1.00E-06 | Desulfotalea psychrophila LSV54 | | | | |

| | | | | | | | | | |
|-------------------------------------|----------------------|----------|----------------------|---|--|--|--|-------------|----------|
| 14845, 14846, 14847, 14848 | 29347422 53691481 | 34 53 | 9.00E-26 1.00E-74 | Bacteroides thetaiotaomicron VPI-5482 Desulfovibrio desulfuricans G20 | conserved hypothetical protein, putative ATPase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77119.1 conserved hypothetical protein, putative ATPase [Bacteroides thetaiotaomicron VPI-5482] COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Desulfovibrio desulfuricans G20] hypothetical protein SMU.606 [Streptococcus mutans UA159] gb AAN58344.1 hypothetical protein SMU.606 [Streptococcus mutans UA159] | | | | |
| 14849, 14850 | 24379083 | 33 | 8.00E-16 | Streptococcus mutans UA159 | | | | | 2.7.1.- |
| 1485, 1486 | 37523515 | 77 | 8.00E-77 | Gloeobacter violaceus PCC 7421 | rifampin ADP-ribosyl transferase [Gloeobacter violaceus PCC 7421] dbj BAC91887.1 rifampin ADP-ribosyl transferase [Gloeobacter violaceus PCC 7421] | | | 82 6.00E-81 | |
| 14851, 14852 | 29346615 | 67 | 3.00E-91 | Bacteroides thetaiotaomicron VPI-5482 | putative ATPase, AAA family [Bacteroides thetaiotaomicron VPI-5482] gb AAO76312.1 putative ATPase, AAA family [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.4.24.- |
| 14853, 14854 | 16273482 | 54 | 3.00E-56 | Haemophilus influenzae Rd KW20 | formyltetrahydrofolate deformylase [Haemophilus influenzae Rd KW20] gb AAC23236.1 formyltetrahydrofolate deformylase (purU) [Haemophilus influenzae Rd KW20] sp Q03432 PURU_HAEIN Formyltetrahydrofolate deformylase (Formyl-FH(4) hydrolase) pir E64131 formyltetrahydrofolate deformylase (EC 3.5.1.10) - Haemophilus influenzae (strain Rd KW20) | | | | 3.5.1.10 |
| 14855, 14856 | 14518364 | 32 | 1.00E-19 | Microscilla sp. PRE1 | putative transposase [Microscilla sp. PRE1] gb AAK62881.1 MS159, putative transposase [Microscilla sp. PRE1] | | | | |
| 14859, 14860 | 56707780 | 57 | 2.00E-73 | Francisella tularensis subsp. tularensis Schu 4 | DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45292.1 DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis] | | | | |
| 14861, 14862, 14863, 14864 | 12512884 48553652 | 39 26 | 7.00E-31 3.00E-13 | Escherichia coli O157:H7 Cytophaga hutchinsonii | deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] ref NP_285856.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7 EDL933] ref NP_308191.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] sp Q8X8Y9 DGT_P_ECO57 Deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase) pir D85500 deoxyguanosine triphosphate triphosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain EDL933) dbj BAB33587.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] pir D90649 deoxyguanosine triphosphate triphosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | 3.1.5.1 |

| | | | | | | | | |
|-------------------------------------|----------------------|----------|----------------------|--|---|--|--|----------|
| 14865, 14866, 14867, 14868 | 34557782 48855616 | 27 27 | 8.00E-21 2.00E-13 | Wollinella succinogenes DSM 1740 Cytophaga hutchinsonii | PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes] COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 14869, 14870, 1487, 1488 | 20090843 48855191 | 43 50 | 6.00E-31 3.00E-51 | Methanosarcina acetivorans C2A Cytophaga hutchinsonii | hypothetical protein MA1995 [Methanosarcina acetivorans C2A] gb AAM05398.1 predicted protein [Methanosarcina acetivorans str. C2A] COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | |
| 14871, 14872 | 45250017 | 35 | 8.00E-40 | Aneurinibacillus thermoaerophilus | putative glycosyl transferase [Aneurinibacillus thermoaerophilus] hypothetical protein PA3762 [Pseudomonas aeruginosa PAO1] ref ZP_00137160.2 COG3323: Uncharacterized protein conserved in bacteria [Pseudomonas aeruginosa UCBPP-PA14] pir A83175 hypothetical protein PA3762 [Imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_252451.1 hypothetical protein PA3762 [Pseudomonas aeruginosa PAO1] | | | 2.4.1.- |
| 14873, 14874 | 9949932 | 48 | 3.00E-23 | Pseudomonas aeruginosa PAO1 | hypothetical protein WS0457 [Wollinella succinogenes DSM 1740] emb CAE09599.1 conserved hypothetical protein [Wollinella succinogenes] | | | 1.-.-.- |
| 14881, 14882, 14883, 14884 | 15375096 53711775 | 44 57 | 6.00E-18 1.00E-62 | Geobacillus stearothermophilus Bacteroides fragilis YCH46 | alpha-cyclodextrinase [Geobacillus stearothermophilus] glycosyltransferase [Bacteroides fragilis YCH46] db BAD47233.1 glycosyltransferase [Bacteroides fragilis YCH46] | | | 3.2.1.20 |
| 14885, 14886, 14887, 14888 | 45658172 48833325 | 38 28 | 7.00E-31 5.00E-32 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 Magnetococcus sp. MC-1 | serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AA570895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes] | | | 2.7.3.- |
| 14889, 14890, 14891, 14892 | 34557246 34557509 | 42 64 | 7.00E-35 6.00E-38 | Wollinella succinogenes DSM 1740 Wollinella succinogenes DSM 1740 | hypothetical protein WS1135 [Wollinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wollinella succinogenes] | | | 2.7.3.- |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|----|------------------|
| 14895, 14896 | 34556516 | 62 | 3.00E-53 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0062 [Wollinella succinogenes DSM 1740] emb CAE09231.1 conserved hypothetical protein [Wollinella succinogenes] emb AAL44087.1 glycosyltransferase [Agrobacterium tumefaciens str. C58] gb AAL44087.1 glycosyltransferase [Agrobacterium tumefaciens str. C58] pir A12958 glycosyltransferase Atu3271 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont) | | | |
| 14897, 14898 | 17936982 | 53 | 8.00E-51 | Agrobacterium tumefaciens str. C58 | ABC transporter (ATP-binding protein) [Clostridium acetobutylicum ATCC 824] gb AAK78152.1 ABC transporter (ATP-binding protein) [Clostridium acetobutylicum ATCC 824] pir E96920 ABC transporter (ATP-binding protein) CAC0168 [Imported] - Clostridium acetobutylicum | | | 2.4.1.- |
| 14901, 14902 | 15893463 | 47 | 5.00E-27 | Clostridium acetobutylicum ATCC 824 | putative long-chain-fatty-acid-CoA ligase [Bacteroides fragilis YCH46] dbj BAD50599.1 putative long-chain-fatty-acid-CoA ligase [Bacteroides fragilis YCH46] | | | 1.8.-.- |
| 14903, 14904 | 53715141 | 59 | 1.00E-47 | Bacteroides fragilis YCH46 | PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes] | Bacteroides thetaiotaomicron VPI-5482, section 10 of 21 of the complete genome | 93 | 2.00E-08 6.2.1.3 |
| 14905, 14906 | 34557782 | 43 | 2.00E-43 | Wollinella succinogenes DSM 1740 | BH0401 PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09899.1 BH0401 PROTEIN [Wollinella succinogenes] possible helicase [Rhodopseudomonas palustris CGA009] emb CAE27655.1 possible helicase [Rhodopseudomonas palustris CGA009] | | | 2.7.3.- |
| 14909, 14910 | 34557184 | 50 | 2.00E-55 | Wollinella succinogenes DSM 1740 | Hemolysin [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94497.1 Hemolysin [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | |
| 1491, 1492 | 39935283 | 30 | 1.00E-12 | Rhodopseudomonas palustris CGA009 | COG2072: Predicted flavoprotein involved in K+ transport [Enterococcus faecium] | | | |
| 14911, 14912 | 19703636 | 27 | 4.00E-21 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | hypothetical protein PG1236 [Porphyromonas gingivalis W83] ref NP_905423.1 hypothetical protein PG1236 [Porphyromonas gingivalis W83] | | | |
| 14915, 14916 | 48826153 | 32 | 3.00E-09 | Enterococcus faecium | galactose-1-phosphate transferase [Lactococcus lactis subsp. cremoris] omega-3 polyunsaturated fatty acid synthase Pf1C [Photobacterium profundum SS9] emb CAG19869.1 omega-3 polyunsaturated fatty acid synthase Pf1C [Photobacterium profundum] | | | 2.-.-.- |
| 14917, 14918 | 34397259 | 33 | 9.00E-29 | Porphyromonas gingivalis W83 | | | | |
| 14919, 14920 | 4557150 | 33 | 3.00E-15 | Lactococcus lactis subsp. cremoris | | | | |
| 14921, 14922 | 54308651 | 44 | 8.00E-56 | Photobacterium profundum SS9 | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 14923, 14924 | 34557931 | 68 | 2.00E-74 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10646.1 PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes] | | | 2.1.1.63 |
| 14925, 14926 | 34557780 | 43 | 5.00E-21 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10495.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes] | | | 2.7.-.- |
| 14927, 14928 | 46142672 | 41 | 6.00E-19 | Methanococcoides burtonii DSM 6242 | COG3769: Predicted hydrolase (HAD superfamily) [Methanococcoides burtonii DSM 6242] | | | |
| 14929, 14930 | 46142672 | 34 | 3.00E-35 | Methanococcoides burtonii DSM 6242 | COG3769: Predicted hydrolase (HAD superfamily) [Methanococcoides burtonii DSM 6242] | | | |
| 14931, 14932 | 34556616 | 43 | 1.00E-49 | Wolinella succinogenes DSM 1740 | CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes] | | | |
| 14933, 14934 | 20806595 | 61 | 4.00E-69 | Thermoanaerobact er tengcongensis MB4 | predicted glycosylase [Thermoanaerobacter tengcongensis MB4] gb AAM23370.1 predicted glycosylase [Thermoanaerobacter tengcongensis MB4] | | | |
| 14937, 14938 | 48853894 | 32 | 1.00E-10 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |
| 14939, 14940 | 48855730 | 36 | 1.00E-27 | Cytophaga hutchinsonii | hypothetical protein Chut02000936 [Cytophaga hutchinsonii] | | | |
| 14941, 14942 | 20092002 | 35 | 4.00E-12 | Methanosarcina acetivorans C2A | moaA/nifB/pqqE family protein [Methanosarcina acetivorans C2A] gb AAM06557.1 moaA/nifB/pqqE family protein [Methanosarcina acetivorans str. C2A] | | | |
| 14943, 14944 | 34557385 | 39 | 3.00E-35 | Wolinella succinogenes DSM 1740 | SELENOPHOSPHATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10100.1 SELENOPHOSPHATE SYNTHETASE [Wolinella succinogenes] | | | 2.7.9.3 |
| 14945, 14946 | 53713487 | 37 | 2.00E-17 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD48945.1 two-component system response regulator [Bacteroides fragilis YCH46] | | | |
| 14947, 14948 | 48855423 | 28 | 1.00E-13 | Cytophaga hutchinsonii | COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] | | | 5.2.1.8 |
| 14951, 14952 | 34556738 | 54 | 2.00E-59 | Wolinella succinogenes DSM 1740 | SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes DSM 1740] emb CAE09453.1 SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes] sp Q7MAE6 ARGD_WOLSU Acetylornithine aminotransferase (ACOAT) | | | 2.6.1.11 |
| 14953, 14954 | 34557931 | 75 | 2.00E-65 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10646.1 PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes] | | | 2.1.1.63 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 14955, 14956 | 28210060 | 58 | 8.00E-30 | Clostridium tetani E88 | thymidine kinase [Clostridium tetani E88] | | | 2.7.1.21 |
| 14959, 14960 | 32263380 | 44 | 1.00E-29 | Helicobacter hepaticus ATCC 51449 | thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861359.1 thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449] | | | 2.5.1.3 |
| 14961, 14962 | 15791002 | 37 | 1.00E-11 | Halobacterium salinarum NRC-1 | hypothetical protein VNG2170H [Halobacterium salinarum NRC-1] gb AAG20306.1 Vng2170h [Halobacterium sp. NRC-1] pir F84367 | | | |
| 14965, 14966 | 50084270 | 34 | 3.00E-22 | Acinetobacter sp. ADP1 | hypothetical protein Vng2170h [imported] - Halobacterium sp. NRC-1 cobyric acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyric acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyric acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyric acid synthase | | | |
| 14967, 14968 | 34557550 | 35 | 1.00E-16 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1180 [Wolinella succinogenes DSM 1740] emb CAE10265.1 hypothetical protein [Wolinella succinogenes] | | | |
| 14975, 14976 | 57168891 | 39 | 2.00E-43 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56346.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | |
| 14979, 14980 | 34557672 | 44 | 1.00E-42 | Wolinella succinogenes DSM 1740 | 30S RIBOSOMAL PROTEIN S1 [Wolinella succinogenes DSM 1740] emb CAE10387.1 30S RIBOSOMAL PROTEIN S1 [Wolinella succinogenes] | | | |
| 14981, 14982 | 57504658 | 49 | 5.00E-64 | Campylobacter coli RM2228 | methionyl-tRNA formyltransferase [Campylobacter coli RM2228] gb EAL56122.1 methionyl-tRNA formyltransferase [Campylobacter coli RM2228] | | | 2.1.2.9 |
| 14983, 14984 | 29347846 | 45 | 5.00E-65 | Bacteroides thetaiotaomicron VPI-5482 | putative secreted tripeptidyl aminopeptidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77543.1 putative secreted tripeptidyl aminopeptidase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 14985, 14986 | 48845271 | 42 | 7.00E-25 | Geobacter metallireducens GS 15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 14989, 14990 | 34557665 | 44 | 1.00E-30 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | 2.7.3.- |
| 14991, 14992 | 29346503 | 23 | 2.00E-13 | Bacteroides thetaiotaomicron VPI-5482 | conserved hypothetical protein, putative TonB-dependent outer membrane receptor protein [Bacteroides thetaiotaomicron VPI-5482] conserved hypothetical protein, putative TonB-dependent outer membrane receptor protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 14995, 14996 | 57168163 | 46 | 2.00E-38 | Campylobacter coli RM2228 | probable periplasmic protein Cj0599 [Campylobacter coli RM2228] gb EAL57206.1 probable periplasmic protein Cj0599 [Campylobacter coli RM2228] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 14997, 14998 | 34396942 | 61 | 1.00E-31 | Porphyrionomas gingivalis W83 | conserved hypothetical protein [Porphyrionomas gingivalis W83] ref NP_905107.1 hypothetical protein PG0858 [Porphyrionomas gingivalis W83] | | | |
| 14999, 15000 | 34558164 | 30 | 9.00E-33 | Wolinella succinogenes DSM 1740 | CHEMOTAXIS PROTEIN CHEV-CheY like receiver domain [Wolinella succinogenes DSM 1740] emb CAE10879.1 CHEMOTAXIS PROTEIN CHEV-CheY like receiver domain [Wolinella succinogenes] | | | 2.7.3.- |
| 15, 16 | 46119894 | 30 | 3.00E-19 | Crocospaera watsonii WH 8501 | COG1106: Predicted ATPases [Crocospaera watsonii WH 8501] oxygen-independent coproporphyrinogen III oxidase, putative [Shewanella oneidensis MR-1] gb AAAN57484.1 oxygen-independent coproporphyrinogen III oxidase, putative [Shewanella oneidensis MR-1] | | | 1.-.-.- |
| 15007, 15008 | 24375997 | 46 | 3.00E-15 | Shewanella oneidensis MR-1 | glycogen synthase [Aquifex aeolicus VF5] gb AAC06894.1 glycogen synthase [Aquifex aeolicus VF5] pir C70363 glycogen synthase - Aquifex aeolicus sp O66935 GLCA_AQUAE Glycogen synthase (Starch [bacterial glycogen] synthase) | | | 2.4.1.21 |
| 15009, 15010 | 15606118 | 47 | 2.00E-60 | Aquifex aeolicus VF5 | hypothetical protein BT3341 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78447.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 1501, 1502 | 29348750 | 33 | 3.00E-16 | Bacteroides thetaiotaomicron VPI-5482 | COG0841: Cation/multidrug efflux pump [Cytophaga hutchinsonii] | | | |
| 15011, 15012 | 48856922 | 38 | 9.00E-39 | Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Methanococcus burtonii DSM 6242] COG2265: SAM-dependent methyltransferases related to tRNA (uracil-5- γ) methyltransferase [Microbulifer degradans 2-40] | | | 2.7.3.- |
| 15013, 15014 | 46142049 | 45 | 2.00E-30 | Methanococcus burtonii DSM 6242 | ISPg3, transposase [Porphyrionomas gingivalis W83] ref NP_905059.1 ISPg3, transposase [Porphyrionomas gingivalis W83] | | | 2.1.1.35 |
| 15015, 15016 | 48860700 | 53 | 6.00E-82 | Microbulifer degradans 2-40 | N-ACETYLGLUCOSAMINE TRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09473.1 N-ACETYLGLUCOSAMINE TRANSFERASE [Wolinella succinogenes] | | | |
| 15017, 15018 | 34396893 | 57 | 1.00E-57 | Porphyrionomas gingivalis W83 | COG2303: Choline dehydrogenase and related flavoproteins [Crocospaera watsonii WH 8501] | | | 2.4.1.- |
| 15019, 15020 | 34556758 | 56 | 4.00E-60 | Wolinella succinogenes DSM 1740 | COG1600: Uncharacterized Fe-S protein [Cytophaga hutchinsonii] hypothetical membrane protein (BatD) [Desulfotalea psychrophila Lsv54] emb CAG35369.1 hypothetical membrane protein (BatD) [Desulfotalea psychrophila Lsv54] | | | 1.-.-.- |
| 15025, 15026 | 53735985 | 29 | 5.00E-15 | Crocospaera watsonii WH 8501 | PUTATIVE HISTIDINOL PHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE09611.1 PUTATIVE HISTIDINOL PHOSPHATASE [Wolinella succinogenes] | | | 3.1.3.15 |
| 15027, 15028 | 48855815 | 49 | 5.00E-36 | Cytophaga hutchinsonii | | | | |
| 15031, 15032 | 51244492 | 28 | 1.00E-06 | Desulfotalea psychrophila Lsv54 | | | | |
| 15033, 15034 | 34556896 | 49 | 3.00E-36 | Wolinella succinogenes DSM 1740 | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|---|----|------------------|
| 15035, 15036 | 34558037 | 30 | 2.00E-34 | Wolnella succinogenes DSM 1740 | SENSOR/RESPONSE REGULATOR HYBRID [Wolnella succinogenes DSM 1740] emb CAE10752.1 SENSOR/RESPONSE REGULATOR HYBRID [Wolnella succinogenes] | | | 2.7.3.- |
| 15037, 15038 | 53713953 | 31 | 5.00E-15 | Bacteroides fragilis YCH46 | putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD49411.1 putative glycosyltransferase [Bacteroides fragilis YCH46] | | | 2.7.8.6 |
| 15039, 15040 | 34558090 | 41 | 5.00E-50 | Wolnella succinogenes DSM 1740 | CINA-RELATED PROTEIN [Wolnella succinogenes DSM 1740] emb CAE10805.1 CINA-RELATED PROTEIN [Wolnella succinogenes] SENSORY BOX/GGDEF FAMILY PROTEIN [Wolnella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolnella succinogenes] | | | 2.7.3.- |
| 15041, 15042 | 34557573 | 40 | 7.00E-40 | Wolnella succinogenes DSM 1740 | COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Methylobacillus flagellatus KT] | | | |
| 15043, 15044 | 45521816 | 32 | 2.00E-34 | Wolnella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wolnella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolnella succinogenes] | | | 2.7.- |
| 15047, 15048 | 34557665 | 25 | 2.00E-21 | Wolnella succinogenes DSM 1740 | FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolnella succinogenes DSM 1740] emb CAE09765.1 FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolnella succinogenes] | | | |
| 15049, 15050 | 34557050 | 54 | 1.00E-83 | Streptomyces avermitilis MA-4680 | putative ATPase [Streptomyces avermitilis MA-4680] ref NP_827744.1 putative ATPase [Streptomyces avermitilis MA-4680] | | | 2.7.1.- |
| 15051, 15052 | 48846878 | 56 | 4.00E-95 | Geobacter metallireducens GS- 15 | COG0495: Leucyl-tRNA synthetase [Geobacter metallireducens GS-15] probable type IV pilus assembly protein (TapB) [Desulfotalea psychrophila LSv54] emb CAG36955.1 probable type IV pilus assembly protein (TapB) [Desulfotalea psychrophila LSv54] | Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 2 of 197 of the complete genome | 83 | 7.00E-10 6.1.1.4 |
| 15053, 15054 | 51246078 | 44 | 1.00E-30 | Desulfotalea psychrophila LSv54 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] hypothetical protein WS2057 [Wolnella succinogenes DSM 1740] emb CAE11057.1 hypothetical protein [Wolnella succinogenes] sp Q7MQS0 HISZ_WOLSU ATP phosphoribosyltransferase regulatory subunit | | | |
| 15055, 15056 | 48831584 | 42 | 3.00E-53 | Magnetococcus sp. MC-1 | | | | |
| 15063, 15064 | 34558342 | 36 | 3.00E-24 | Wolnella succinogenes DSM 1740 | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|----------|
| 15069, 15070 | 45658014 | 25 | 5.00E-18 | Leptospira interrogans serovar Copenhagen str. Flocruz L1-130 | putative molybdenum cofactor biosynthesis protein [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] ref NP_711798.1 Putative molybdopterin cofactor synthesis protein A [Leptospira interrogans serovar Lai str. 56601] gb AA048816.1 Putative molybdopterin cofactor synthesis protein A [Leptospira interrogans serovar lai str. 56601] gb AAS70737.1 putative molybdenum cofactor biosynthesis protein [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] | | | |
| 1507, 1508 | 32472461 | 32 | 6.00E-19 | Rhodopirellula baltica SH 1 | conserved hypothetical protein-putative sodium:solute symporter [Rhodopirellula baltica SH 1] emb CAD73139.1 conserved hypothetical protein-putative sodium:solute symporter [Pirellula sp.] | | | |
| 15071, 15072 | 57168968 | 40 | 3.00E-35 | Campylobacter coli RM2228 | hypothetical protein CCO1536 [Campylobacter coli gb EAL56323.1 hypothetical protein CCO1536 [Campylobacter coli RM2228] | | | |
| 15075, 15076 | 32262242 | 38 | 1.00E-26 | Helicobacter hepaticus ATCC 51449 | tRNA (uracil-5-)-methyltransferase TmA [Helicobacter hepaticus ATCC 51449] ref NP_860224.1 tRNA (uracil-5-)-methyltransferase TmA [Helicobacter hepaticus ATCC 51449] sp Q7U326 Y693_HELHP Hypothetical RNA methyltransferase HH0693 | | | 2.1.1.35 |
| 15077, 15078 | 46113312 | 40 | 2.00E-32 | Exiguobacterium sp. 255-15 | COG0324: RNA delta(2)-isopentenylpyrophosphate transferase [Exiguobacterium sp. 255-15] | | | 2.5.1.8 |
| 15079, 15080 | 29347555 | 64 | 5.00E-92 | Bacteroides thetaiotaomicron VPI-5482 | ribonucleoside-diphosphate reductase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO77252.1 ribonucleoside-diphosphate reductase alpha chain [Bacteroides thetaiotaomicron VPI-5482] | | | 1.17.4.1 |
| 15081, 15082 | 57241263 | 50 | 7.00E-48 | NiFe | [NiFe] hydrogenase maturation protein HypF [Campylobacter lai RM2100] [Campylobacter lai RM2100] | | | 3.6.1.7 |
| 15083, 15084 | 34397810 | 44 | 7.00E-50 | Porphyromonas gingivalis W83 | rhodanese-like domain protein [Porphyromonas gingivalis W83] ref NP_905972.1 rhodanese-like domain protein [Porphyromonas gingivalis W83] | | | |
| 15087, 15088 | 34558828 | 33 | 1.00E-31 | Alvinella pompejana epibiont 7G3 | KIAA1005 protein [Alvinella pompejana epibiont 7G3] | | | |
| 15089, 15090 | 48856002 | 52 | 1.00E-83 | Cytophaga hutchinsonii | hypothetical protein Chut02001232 [Cytophaga hutchinsonii] related to two-component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila LSv54] emb CAG36654.1 related to two- component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila LSv54] | | | 2.7.3.- |
| 15097, 15098 | 51245777 | 45 | 1.00E-37 | Desulfotalea psychrophila LSv54 | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|-----------------|-------------------------------------|---|--|--|---------|
| 15099, 15100 | 42526444 | 35 | 2.00E-47 | 35405 | Treponema denticola ATCC | adenylate/guanylate cyclase catalytic domain protein [Treponema denticola ATCC 35405] gb AA511423.1 adenylate/guanylate cyclase catalytic domain protein [Treponema denticola ATCC 35405] | | | 4.6.1.1 |
| 15101, 15102 | 15894375 | 31 | 8.00E-21 | ATCC 824 | Clostridium acetobutylicum | 5-formyltetrahydrofolate cyclo-ligase [Clostridium acetobutylicum ATCC 824] gb AAK79064.1 5-formyltetrahydrofolate cyclo-ligase [Clostridium acetobutylicum ATCC 824] pir E97034 5-formyltetrahydrofolate cyclo-ligase [imported] - Clostridium acetobutylicum | | | 6.3.3.2 |
| 15103, 15104 | 34556710 | 36 | 7.00E-08 | 1740 | Wolinella succinogenes DSM | LYTIC MUREIN TRANSGLYCOSYLASE [Wolinella succinogenes DSM 1740] emb CAE09425.1 LYTIC MUREIN TRANSGLYCOSYLASE [Wolinella succinogenes] | | | |
| 15105, 15106 | 34556820 | 39 | 9.00E-44 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS0389 [Wolinella succinogenes DSM 1740] emb CAE09535.1 hypothetical protein [Wolinella succinogenes] | | | |
| 15107, 15108 | 34556818 | 42 | 7.00E-39 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS0387 [Wolinella succinogenes DSM 1740] emb CAE09533.1 hypothetical protein [Wolinella succinogenes] | | | |
| 15113, 15114 | 57233930 | 56 | 6.00E-58 | | Dehalococcoides ethenogenes 195 | radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195] gb AAW39435.1 radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195] | | | |
| 15115, 15116 | 57233930 | 49 | 2.00E-35 | | Dehalococcoides ethenogenes 195 | radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195] gb AAW39435.1 radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195] | | | |
| 15117, 15118 | 23015157 | 41 | 2.00E-51 | MS-1 | Magnetospirillum magnetotacticum | hypothetical protein Magn03009598 [Magnetospirillum magnetotacticum MS-1] | | | |
| 15121, 15122 | 29349976 | 36 | 9.00E-27 | VPI-5482 | Bacteroides thetaiotaomicron | hypothetical protein BT4568 [Bacteroides thetaiotaomicron VPI-5482] gb AAC079673.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 15123, 15124 | 57167713 | 51 | 5.00E-29 | RM2228 | Campylobacter coli | probable proteinase Cj0701 [Campylobacter coli RM2228] gb EAL57499.1 probable proteinase Cj0701 [Campylobacter coli RM2228] | | | 3.4.--- |
| 15125, 15126 | 16329982 | 43 | 3.00E-34 | PCC 6803 | Synechocystis sp. | short-chain alcohol dehydrogenase family [Synechocystis sp. PCC 6803] dbj BAA17390.1 short-chain alcohol dehydrogenase family [Synechocystis sp. PCC 6803] pir S77543 short-chain alcohol dehydrogenase-related protein, 72K - Synechocystis sp. (strain PCC 6803) | | | 1.--- |
| 15129, 15130 | 20091293 | 31 | 9.00E-10 | acetivorans C2A | Methanosarcina acetivorans C2A | glucosaminyltransferase [Methanosarcina acetivorans C2A] gb AAM05848.1 glucosaminyltransferase [Methanosarcina acetivorans str. C2A] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|---|--|--|--|----------|
| 15131, | 34557246 | 29 | 1.00E-29 | Wollinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes] | | | | |
| 15132 | | | | Wollinella succinogenes DSM 1740 | TWO-COMPONENT HYBRID PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10077.1 TWO-COMPONENT HYBRID PROTEIN [Wollinella succinogenes] | | | | 2.7.3.- |
| 15137, | 34557382 | 45 | 8.00E-22 | Microbulifer degradans 2-40 | COG1033: Predicted exporters of the RND superfamily [Microbulifer degradans 2-40] | | | | |
| 15138, | 48863979 | 29 | 4.00E-11 | Campylobacter jejuni RM1221 | DNA repair protein RecN [Campylobacter jejuni RM1221] gb AAW34538.1 DNA repair protein RecN [Campylobacter jejuni RM1221] | | | | |
| 15141, | 57236955 | 44 | 5.00E-54 | Clostridium thermocellum ATCC 27405 | COG0500: SAM-dependent methyltransferases [Clostridium thermocellum ATCC 27405] | | | | 2.1.1.- |
| 15143, | 48859334 | 53 | 3.00E-61 | Clostridium thermocellum ATCC 27405 | COG1236: Predicted exonuclease of the beta-lactamase fold involved in RNA processing [Clostridium thermocellum ATCC 27405] | | | | |
| 15147, | 48859380 | 43 | 7.00E-60 | Francisella tularensis subsp. tularensis Schu 4 | DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45292.1 DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis] | | | | |
| 15151, | 56707780 | 58 | 1.00E-52 | Methanosarcina acetivorans C2A | Integrase [Methanosarcina acetivorans C2A] gb AAM07145.1 Integrase [Methanosarcina acetivorans str. C2A] | | | | |
| 15152, | 20092590 | 35 | 1.00E-41 | Pyrococcus furfiosus DSM 3638 | hypothetical protein PF1041 [Pyrococcus furiosus DSM 3638] gb AAL81165.1 hypothetical protein [Pyrococcus furiosus DSM 3638] | | | | |
| 15159, | 18977413 | 32 | 2.00E-14 | Xanthomonas campestris pv. campestris str. ATCC 33913 | anticonodon nuclease [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39782.1 anticonodon nuclease [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | | |
| 15163, | 21229941 | 57 | 7.00E-64 | Bacteroides thetaiotaomicron VPI-5482 | CDP-glucose 4,6-dehydratase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76457.1 CDP-glucose 4,6-dehydratase [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.2.1.45 |
| 15165, | 29346760 | 66 | 3.00E-99 | Wollinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE [Wollinella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wollinella succinogenes] | | | | 2.7.3.- |
| 15167, | 34557884 | 39 | 2.00E-49 | Polaribacter filamentus | nicotinate-nucleotide adenyllyltransferase [Polaribacter filamentus] possible acetolactate synthase large subunit [Rhodopseudomonas palustris CGA009] emb CAE29495.1 possible acetolactate synthase large subunit [Rhodopseudomonas palustris CGA009] | | | | 2.7.7.18 |
| 15169, | 36955846 | 46 | 2.00E-38 | Rhodopseudomona s palustris CGA009 | | | | | 4.1.3.18 |
| 15170 | | | | | | | | | |
| 1517, | 39937114 | 42 | 6.00E-40 | | | | | | |
| 1518 | | | | | | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|----------|---------|--|
| 15173, 15174 | 49481576 | 26 | 7.00E-08 | Bacillus thuringiensis serovar konkukian str. 97-27 | oligopeptide ABC transporter, oligopeptide-binding protein [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT63778.1 oligopeptide ABC transporter, oligopeptide-binding protein [Bacillus thuringiensis serovar konkukian str. 97-27] | | | | | |
| 15177, 15178 | 29349965 | 25 | 1.00E-13 | Bacteroides thetaitaomicron VPI-5482 | hypothetical protein BT4557 [Bacteroides thetaitaomicron VPI-5482] gb AAO79662.1 hypothetical protein [Bacteroides thetaitaomicron VPI- 5482] | | | | | |
| 15181, 15182 | 34556853 | 53 | 9.00E-57 | Wolinella succinogenes DSM 1740 | TRIOSEPHOSPHATE ISOMERASE TIM [Wolinella succinogenes DSM 1740] emb CAE09568.1 TRIOSEPHOSPHATE ISOMERASE TIM [Wolinella succinogenes] sp Q7MA77 TPIS_WOLSU Triosephosphate isomerase (TIM) (Triose-phosphate isomerase) | | | 5.3.1.1 | | |
| 15185, 15186 | 51246430 | 47 | 1.00E-66 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2578 [Desulfotalea psychrophila LSV54] emb CAG37307.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | | | |
| 15187, 15188 | 4234793 | 33 | 7.00E-35 | Leptospira borgpetersenii | unknown [Leptospira borgpetersenii] | | | | | |
| 1519, 1520 | 48894780 | 29 | 1.00E-29 | Trichodesmium erythraeum IMS101 | COG0006: Xaa-Pro aminopeptidase [Trichodesmium erythraeum IMS101] hypothetical protein PPRB0708 [Photobacterium profundum SS9] emb CAG22580.1 hypothetical protein [Photobacterium profundum] emb CAG22580.1 | | | 3.4.11.9 | | |
| 15191, 15192 | 54302387 | 38 | 7.00E-33 | Photobacterium profundum SS9 | transcriptional regulator [Methanosarcina mazel Go1] gb AAM32650.1 transcriptional regulator [Methanosarcina mazel Goe1] | | | | 2.7.3.- | |
| 15193, 15194 | 21229056 | 37 | 6.00E-20 | Methanosarcina mazel Go1 | COG0507: ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Clostridium thermocellum ATCC 27405] exodeoxyribonuclease V alpha chain [Clostridium tetani E88] gb AAO34963.1 exodeoxyribonuclease V alpha chain [Clostridium tetani E88] | | | 3.1.11.5 | | |
| 15195, 15196 | 48859134 | 29 | 1.00E-24 | Clostridium thermocellum ATCC 27405 | ATP-dependent DNA helicase recQ [Bacteroides thetaitaomicron VPI-5482] gb AAO78949.1 ATP-dependent DNA helicase recQ [Bacteroides thetaitaomicron VPI-5482] probable bax protein VC1430, putative [Campylobacter upsaliensis RM3195] gb EAL52888.1 probable bax protein VC1430, putative [Campylobacter upsaliensis RM3195] NADH oxidase, putative [Chlorobium tepidum TLS] gb AAM73295.1 NADH oxidase, putative [Chlorobium tepidum TLS] | | | 3.6.1.- | | |
| 15197, 15198 | 28210082 | 27 | 1.00E-13 | Clostridium tetani E88 | MinD superfamily P-loop ATPase [uncultured archaeon GZfos23H9] | | | | 1.6.4.- | |
| 15199, 15200 | 29349252 | 55 | 7.00E-73 | Bacteroides thetaitaomicron VPI-5482 | | | | | | |
| 15201, 15202 | 57505554 | 41 | 1.00E-44 | Campylobacter upsaliensis RM3195 | | | | | | |
| 15203, 15204 | 21674888 | 49 | 9.00E-26 | Chlorobium tepidum TLS | | | | | | |
| 15205, 15206 | 52549060 | 42 | 3.00E-52 | uncultured archaeon GZfos23H9 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|-------------|----------|
| 15207, 15208 | 57168617 | 52 | 3.00E-34 | Campylobacter coli RM2228 | HsdM [Campylobacter coli RM2228] gb EAL56578.1 HsdM [Campylobacter coli RM2228] | | | |
| 15217, 15218 | 34556560 | 31 | 3.00E-24 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] emb CAG36281.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 15219, 15220 | 51245404 | 37 | 1.00E-35 | Desulfotalea psychrophila LSV54 | ATP-dependent RNA helicase DbpA [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232192.1 ATP-dependent RNA helicase DbpA [Vibrio cholerae O1 biovar eltor str. N16961] pir B82060 ATP-dependent RNA helicase DbpA VC2564 [Imported] - Vibrio cholerae (strain N16961 group O1) | Desc.T. thermophila Hc1 cDNA. Org: Tetrahymena thermophila | 2.7.3.- | |
| 15225, 15226 | 9657150 | 58 | 2.00E-63 | Vibrio cholerae O1 biovar eltor str. N16961 | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | 97 8.00E-09 | 2.7.7.- |
| 15227, 15228 | 48855778 | 62 | 3.00E-32 | Cytophaga hutchinsonii | oxygen-independent coproporphyrinogen III oxidase, putative [Porphyromonas gingivalis W83] ref NP_904771.1 oxygen-independent coproporphyrinogen III oxidase, putative [Porphyromonas gingivalis W83] | | | 2.7.3.- |
| 15229, 15230 | 34396604 | 40 | 4.00E-32 | Porphyromonas gingivalis W83 | hypothetical protein RC0927 [Rickettsia conorii str. Malish 7] gb AAL03465.1 unknown [Rickettsia conorii str. Malish 7] pir G97815 hypothetical protein RC0927 [Imported] - Rickettsia conorii (strain Malish 7) | | | 1.-.-.- |
| 1523, 1524 | 15892850 | 62 | 5.00E-15 | Rickettsia conorii str. Malish 7 | tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76987.1 tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 15231, 15232 | 29347290 | 39 | 6.00E-23 | Bacteroides thetaiotaomicron VPI-5482 | COG0616: Periplasmic serine proteases (ClpP class) [Trichodesmium erythraeum IMS101] | | | 3.4.21.- |
| 15233, 15234 | 48894132 | 44 | 4.00E-38 | Trichodesmium erythraeum IMS101 | TonB-dependent receptor [uncultured bacterium 159] | | | |
| 15235, 15236 | 40062563 | 27 | 2.00E-10 | uncultured bacterium 159 | peptidyl-prolyl cis-trans isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79476.1 peptidyl-prolyl cis-trans isomerase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 15237, 15238 | 29349779 | 35 | 7.00E-17 | Bacteroides thetaiotaomicron VPI-5482 | COG0419: ATPase involved in DNA repair [Actinobacillus pleuropneumoniae serovar 1 str. 4074] COG0483: Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family [Cytophaga hutchinsonii] | | | 3.1.3.25 |
| 15239, 15240 | 53728999 | 27 | 8.00E-22 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | | | | |
| 15241, 15242 | 48855414 | 47 | 6.00E-36 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | |
|--------------------------|----------------------|----------|----------------------|--|--|--|--|----------|
| 15243, 15244 | 57241703 | 60 | 6.00E-85 | Campylobacter lari RM2100 | glutathionylspermidine synthase family protein [Campylobacter lari RM2100] gb EAL54373.1 glutathionylspermidine synthase family protein [Campylobacter lari RM2100] | | | 6.3.1.8 |
| 15245, 15246 | 53712009 | 32 | 9.00E-19 | Bacteroides fragilis YCH46 | hypothetical protein BF0720 [Bacteroides fragilis YCH46] dbj BAD47467.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 15247, 15248 | 29347624 | 26 | 5.00E-10 | Bacteroides thetataoamicon | hypothetical protein BT2214 [Bacteroides thetataoamicon VPI-5482] gb AAO77321.1 hypothetical protein [Bacteroides thetataoamicon VPI- 5482] | | | |
| 15249, 15250 | 53757541 | 33 | 9.00E-23 | Methylococcus capsulatus str. Bath | type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath] ref YP_114328.1 type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath] | | | |
| 1525, 15251, 15252 | 22126310 48834051 | 31 44 | 2.00E-12 4.00E-55 | Yersinia pestis KIM Magnetococcus sp. MC-1 | hypothetical protein y2426 [Yersinia pestis KIM] gb AAM85984.1 hypothetical [Yersinia pestis KIM] | | | 3.5.2.6 |
| 15253, 15254 | 34557847 | 34 | 8.00E-20 | Wolinella succinogenes DSM 1740 | COG2602: Beta-lactamase class D [Magnetococcus sp. MC-1] ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes DSM 1740] emb CAE10562.1 ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes] | | | 3.4.24.- |
| 15255, 15256 | 29345965 | 63 | 4.00E-86 | Bacteroides thetataoamicon VPI-5482 | amidophosphoribosyltransferase [Bacteroides thetataoamicon VPI-5482] gb AAO75662.1 amidophosphoribosyltransferase [Bacteroides thetataoamicon VPI-5482] | | | 2.4.2.14 |
| 15259, 15260 | 52144400 | 19 | 2.00E-15 | Bacillus cereus ZK | hypothetical protein BCZK0824 [Bacillus cereus ZK] gb AAU19419.1 conserved hypothetical protein [Bacillus cereus ZK] | | | |
| 15263, 15264 | 46581041 | 43 | 9.00E-34 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | HAMP domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97109.1 HAMP domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | 2.7.3.- |
| 15265, 15266 | 48845647 | 43 | 1.00E-46 | Geobacter metallireducens GS 15 | hypothetical protein Gmet02001892 [Geobacter metallireducens GS-15] | | | |
| 15267, 15268 | 53795087 | 35 | 8.00E-18 | Chloroflexus aurantiacus | COG0110: Acetyltransferase (isoleucine patch superfamily) [Chloroflexus aurantiacus] | | | 2.3.1.- |
| 1527, 1528 | 6967633 | 41 | 1.00E-22 | Campylobacter jejuni subsp. jejuni NCTC 11168 | putative endonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81431 probable endonuclease Cj0139 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281350.1 putative endonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] | | | |
| 15273, 15274 | 57237474 | 55 | 1.00E-33 | Campylobacter jejuni RM1221 | HIT family protein [Campylobacter jejuni RM1221] gb AAW35057.1 HIT family protein [Campylobacter jejuni RM1221] | | | |
| 15275, 15276 | 57241171 | 43 | 5.00E-18 | Campylobacter lari RM2100 | rhodanese family protein [Campylobacter lari RM2100] gb EAL54867.1 rhodanese family protein [Campylobacter lari RM2100] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|------------------|
| 15277, 15278 | 16330590 | 42 | 8.00E-59 | Synechocystis sp. PCC 6803 | hybrid sensory kinase [Synechocystis sp. PCC 6803] dbj BAA17998.1 hybrid sensory kinase [Synechocystis sp. PCC 6803] pir S75136 sensory transduction histidine kinase slr2104 - Synechocystis sp. (strain PCC 6803) | | | 2.7.3.- |
| 15281, 15282 | 34556518 | 74 | 3.00E-53 | Wolinella succinogenes DSM 1740 | CYCLASE HISF [Wolinella succinogenes DSM 1740] emb CAE09233.1 CYCLASE HISF [Wolinella succinogenes] sp Q7MAS1 HIS6_WOLSU Imidazole glycerol phosphate synthase subunit hisF (IGP synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase subunit hisF) (IGPS subunit hisF) | Desc.N. gonorrhoeae nucleotide sequence SEQ ID 2425. Org:Neisseria gonorrhoeae | 79 | 3.00E-07 4.1.3.- |
| 15283, 15284 | 48854967 | 53 | 2.00E-27 | Cytophaga hutchinsonii | COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 15285, 15286 | 23130537 | 44 | 3.00E-29 | Nostoc punctiforme PCC 73102 | COG0778: Nitroreductase [Nostoc punctiforme PCC 73102] | | | |
| 15287, 15288 | 24216675 | 34 | 2.00E-07 | Leptospira interrogans serovar Lai str. 56601 | putative globin-like protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51174.1 putative globin-like protein [Leptospira interrogans serovar lai str. 56601] | | | |
| 15289, 15290 | 34557884 | 28 | 5.00E-24 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE [Wolinella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolinella succinogenes] magnesium transporter, putative [Campylobacter lari RM2100] gb EAL55750.1 magnesium transporter, putative [Campylobacter lari RM2100] | | | |
| 15291, 15292 | 57240636 | 34 | 4.00E-23 | Campylobacter lari RM2100 | putative potassium channel protein, putative [Campylobacter lari RM2100] gb EAL55554.1 putative potassium channel protein, putative [Campylobacter lari RM2100] | | | |
| 15295, 15296 | 57240440 | 52 | 3.00E-63 | Campylobacter lari RM2100 | FERROCHELATASE LIKE PROTEIN, HemH [Wolinella succinogenes DSM 1740] emb CAE11151.1 FERROCHELATASE LIKE PROTEIN, HemH [Wolinella succinogenes] sp Q7M7P9 HEMZ_WOLSU Ferrochelatase (Protoheme ferro-lyase) (Heme synthetase) | | | 4.99.1.1 |
| 15297, 15298 | 34558436 | 48 | 3.00E-66 | Wolinella succinogenes DSM 1740 | hypothetical protein MTH376 [Methanothermobacter thermoautotrophicus str. Delta H] gb AAB84882.1 conserved protein [Methanothermobacter thermoautotrophicus str. Delta H] pir F69148 hypothetical protein MTH376 - Methanobacterium thermoautotrophicum (strain Delta H) | | | 2.4.1.- |
| 15301, 15302 | 48845271 | 47 | 6.00E-54 | Geobacter metallireducens GS-15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | 2.7.3.- |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|----------|
| 15303, 15304 | 48855575 | 49 | 5.00E-39 | Cytophaga hutchinsonii | COG0553: Superfamily II DNA/RNA helicases, SNF2 family [Cytophaga hutchinsonii] | | | 3.6.1.3 |
| 15307, 15308 | 57237008 | 43 | 2.00E-50 | Campylobacter jejuni RM1221 | hypothetical protein CJE0806 [Campylobacter jejuni RM1221] gb AAW34591.1 conserved hypothetical protein [Campylobacter jejuni RM1221] | | | |
| 15309, 15310 | 34557978 | 48 | 6.00E-35 | Wolinella succinogenes DSM 1740 | PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10693.1 PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes] | | | |
| 1531, 1532 | 34329419 | 37 | 1.00E-33 | Myxococcus xanthus | mutant NtrC-like activator [Myxococcus xanthus] | | | 2.7.-.- |
| 15311, 15312 | 48856940 | 31 | 2.00E-11 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | |
| 15313, 15314 | 32262492 | 41 | 2.00E-21 | Helicobacter hepaticus ATCC 51449 | transcriptional regulator [Helicobacter hepaticus ATCC 51449] ref NP_860473.1 transcriptional regulator [Helicobacter hepaticus ATCC 51449] | | | |
| 15315, 15316 | 57168674 | 53 | 4.00E-40 | Campylobacter coli RM2228 | RNA methyltransferase, TrmH family, group 3 [Campylobacter coli RM2228] gb EAL56635.1 RNA methyltransferase, TrmH family, group 3 [Campylobacter coli RM2228] | | | 2.1.1.- |
| 15317, 15318 | 34557846 | 44 | 1.00E-35 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1513 [Wolinella succinogenes DSM 1740] emb CAE10561.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 15319, 15320 | 32262437 | 68 | 4.00E-77 | Helicobacter hepaticus ATCC 51449 | carbamoylphosphate synthase small subunit [Helicobacter hepaticus ATCC 51449] ref NP_860419.1 carbamoylphosphate synthase small subunit [Helicobacter hepaticus ATCC 51449] | | | 6.3.5.5 |
| 15321, 15322 | 34558336 | 49 | 5.00E-45 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2051 [Wolinella succinogenes DSM 1740] emb CAE11051.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 15325, 15326 | 34558169 | 35 | 1.00E-38 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-DNA polymerase III delta subunit [Wolinella succinogenes DSM 1740] emb CAE10884.1 conserved hypothetical protein-DNA polymerase III delta subunit [Wolinella succinogenes] | | | |
| 15327, 15328 | 41725785 | 36 | 1.00E-29 | Dechloromonas aromatica RCB | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Dechloromonas aromatica RCB] | | | 2.7.3.- |
| 15333, 15334 | 28901068 | 29 | 3.00E-16 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA1213 [Vibrio parahaemolyticus RIMD 2210633] db BAC62556.1 hypothetical protein [Vibrio parahaemolyticus] | | | |
| 15335, 15336 | 34556480 | 62 | 6.00E-78 | Wolinella succinogenes DSM 1740 | GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes DSM 1740] emb CAE09195.1 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes] | | | 2.6.1.16 |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|--|-----------------------------------|----|----------|
| 15337, 15338 | 57241168 | 51 | 4.00E-28 | Campylobacter lari RM2100 | MiaB-like tRNA modifying enzyme [Campylobacter lari RM2100] gb EAL54864.1 MiaB-like tRNA modifying enzyme [Campylobacter lari RM2100] | | | 1.8.- |
| 15339, 15340 | 57242029 | 34 | 5.00E-08 | Campylobacter upsaliensis RM3195 | cell division protein (ftsH) [Campylobacter upsaliensis RM3195] gb EAL54002.1 cell division protein (ftsH) [Campylobacter upsaliensis RM3195] | | | 3.4.24.- |
| 15343, 15344 | 48833156 | 40 | 6.00E-29 | Magnetococcus sp. MC-1 | hypothetical protein Mmc102001351 [Magnetococcus sp. MC-1] | | | |
| 15345, 15346 | 34557782 | 43 | 2.00E-45 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | 2.7.3.- |
| 15347, 15348 | 34558185 | 83 | 1.00E-106 | Wolinella succinogenes DSM 1740 | RNA POLYMERASE SIGMA FACTOR [Wolinella succinogenes DSM 1740] emb CAE10900.1 RNA POLYMERASE SIGMA FACTOR [Wolinella succinogenes] | Campylobacter jejuni rpoD gene | 82 | 8.00E-43 |
| 15351, 15352 | 34558184 | 28 | 2.00E-08 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1889 [Wolinella succinogenes DSM 1740] emb CAE10899.1 hypothetical protein [Wolinella succinogenes] | | | |
| 15353, 15354 | 48854542 | 42 | 2.00E-58 | Cytophaga hutchinsonii | COG1748: Saccharopine dehydrogenase and related proteins [Cytophaga hutchinsonii] | | | 1.5.1.10 |
| 15355, 15356 | 34557593 | 39 | 4.00E-49 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1227 [Wolinella succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wolinella succinogenes] | | | |
| 15359, 15360 | 53691857 | 54 | 2.00E-28 | Desulfovibrio desulfuricans G20 | sp P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridylate synthase) (Uracil hydrolyase) COG1876: D-alanyl-D-alanine carboxypeptidase [Desulfovibrio desulfuricans G20] | | | |
| 15361, 15362 | 32262224 | 51 | 4.00E-65 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860206.1 hypothetical protein HH0675 [Helicobacter hepaticus ATCC 51449] | | | 2.7.7.22 |
| 15363, 15364 | 57238098 | 37 | 4.00E-22 | Campylobacter jejuni RM1221 | sensor histidine kinase [Campylobacter jejuni RM1221] gb AAW35681.1 sensor histidine kinase [Campylobacter jejuni RM1221] emb CAB73480.1 putative two-component sensor [Campylobacter jejuni subsp. jejuni NCTC 11168] pir D81329 probable two-component sensor Cj1226c [Imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282373.1 putative two- component sensor [Campylobacter jejuni subsp. jejuni NCTC 11168] | | | 2.7.3.- |
| 15367, 15368 | 48863248 | 24 | 2.00E-13 | Microbulifer degradans 2-40 | hypothetical protein Mdeg02001322 [Microbulifer degradans 2-40] | | | |
| 15369, 15370 | 21229061 | 40 | 5.00E-08 | Methanosarcina mazel Go1 | hypothetical protein MM2959 [Methanosarcina mazel Go1] gb AAM32655.1 hypothetical protein [Methanosarcina mazel Go1] | | | 2.7.3.- |
| 1537, 1538 | 48864231 | 29 | 8.00E-22 | Microbulifer degradans 2-40 | COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulifer degradans 2-40] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|-------------------|
| 15371, 15372 | 41724896 | 31 | 3.00E-20 | Dechloromonas aromatica RCB | COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB] | | | 2.7.3.- |
| 15373, 15374 | 48859895 | 37 | 2.00E-55 | Clostridium thermocellum ATCC 27405 | COG1168: Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities [Clostridium thermocellum ATCC 27405] | | | 2.6.1.- |
| 15375, 15376 | 23495599 | 39 | 3.00E-19 | Streptococcus oralis | L-cysteine desulfhydrase [Streptococcus oralis] | | | 2.6.1.- |
| 15377, 15378 | 48860720 | 59 | 4.00E-32 | Microbulifer degradans 2-40 | COG0019: Diaminopimelate decarboxylase [Microbulifer degradans 2-40] biotin--acetyl-CoA-carboxylase ligase [Porphyromonas gingivalis W83] ref NP_905731.1 biotin--acetyl-CoA-carboxylase ligase [Porphyromonas gingivalis W83] | | | 4.1.1.- |
| 15379, 15380 | 34397568 | 36 | 5.00E-32 | Porphyromonas gingivalis W83 | TRANSCRIPTION-REPAIR COUPLING FACTOR [Wolinella succinogenes DSM 1740] emb CAE10319.1 TRANSCRIPTION-REPAIR COUPLING FACTOR [Wolinella succinogenes] | | | 6.3.4.15 |
| 15381, 15382 | 34557604 | 61 | 1.00E-56 | Wolinella succinogenes DSM 1740 | COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii] | Oceanobacillus lheyensis HTE831 genomic DNA, section 5/13 | 95 | 4.00E-08 3.2.1.52 |
| 15387, 15388 | 48854182 | 53 | 4.00E-89 | Cytophaga hutchinsonii | 3-deoxy-manno-octulosonate cytidyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75852.1 3-deoxy-manno-octulosonate cytidyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.7.38 |
| 15391, 15392 | 29346155 | 57 | 3.00E-32 | Polaromonas sp. JS666 | COG3177: Uncharacterized conserved protein [Polaromonas sp. JS666] | | | |
| 15395, 15396 | 54032595 | 37 | 3.00E-28 | Wolinella succinogenes DSM 1740 | FDHD PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09949.1 FDHD PROTEIN [Wolinella succinogenes] | | | |
| 15397, 15398 | 34557234 | 66 | 8.00E-77 | Cytophaga hutchinsonii | hypothetical protein Chut02000849 [Cytophaga hutchinsonii] probable transcription regulator Cj0571 [Campylobacter lari RM2100] gb EAL55392.1 probable transcription regulator Cj0571 [Campylobacter lari RM2100] | | | |
| 15403, 15404 | 48855658 | 27 | 2.00E-18 | Campylobacter lari RM2100 | COG1366: Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor) [Cytophaga hutchinsonii] | | | |
| 15405, 15406 | 57240278 | 27 | 3.00E-20 | Cytophaga hutchinsonii | hypothetical protein ACIAD2753 [Acinetobacter sp. ADP1] emb CAG69498.1 hypothetical protein [Acinetobacter sp. ADP1] | | | |
| 15407, 15408 | 48856296 | 37 | 2.00E-14 | Acinetobacter sp. ADP1 | Beta-lactamase class C family protein [Idiomarina loihiensis L2TR] gb AAV80889.1 Beta-lactamase class C family protein [Idiomarina loihiensis L2TR] | | | 3.5.2.6 |
| 1541, 1542 | 50085810 | 27 | 7.00E-12 | Idiomarina loihiensis L2TR | | | | |
| | 56459157 | 40 | 9.00E-34 | | | | | |

| | | | | | | | | |
|--------|----------|----|-----------|--|---|---|---------------------|---------|
| 15413, | 34558461 | 40 | 1.00E-43 | Wolinella succinogenes DSM 1740 | WBFR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11176.1 WBFR PROTEIN [Wolinella succinogenes] | | | 6.3.5.4 |
| 15414 | | | | | | | | |
| 15417, | 48861826 | 27 | 2.00E-27 | Microbulifer degradans 2-40 | COG0842: Signal transduction histidine kinase [Microbulifer degradans 2-40] | | | |
| 15418 | | | | | | | | |
| 15421, | | | | | | | | |
| 15422 | 57240341 | 53 | 2.00E-37 | Campylobacter lari RM2100 | pyridoxal phosphate biosynthetic protein PdxJ [Campylobacter lari RM2100] gb EAL55455.1 pyridoxal phosphate biosynthetic protein PdxJ [Campylobacter lari RM2100] | | | |
| 15423, | | | | | | | | |
| 15424 | 32262410 | 37 | 6.00E-28 | Helicobacter hepaticus ATCC 51449 | pyridoxal phosphate biosynthetic protein A [Helicobacter hepaticus ATCC 51449] ref NP_860392.1 pyridoxal phosphate biosynthetic protein A [Helicobacter hepaticus ATCC 51449] | | 1.1.1.26 2 | |
| 15425, | AAB4706 | 2 | | | | | | |
| 15426 | | 40 | 3.00E-56 | | Desc: Cold-active beta galactosidase. Org: Pseudoalteromonas haloplanktis | | 3.2.1.23 | |
| 15427, | | | | | | | | |
| 15428 | 48854136 | 27 | 8.00E-12 | Cytophaga hutchinsonii | COG1566: Multidrug resistance efflux pump [Cytophaga hutchinsonii] hypothetical protein BT3282 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78388.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482] | | | |
| 1543, | | | | | | | | |
| 1544 | 29348691 | 42 | 3.00E-46 | Bacteroides thetaitaomicron VPI-5482 | COG0595: Predicted hydrolase of the metallo-beta-lactamase superfamily [Streptococcus suis 89/1591] | | 3.--- | |
| 15431, | 50591193 | 36 | 5.00E-43 | Streptococcus suis 89/1591 | hypothetical protein sl0241 [Synecocystis sp. PCC 6803] dbj BAA17961.1 sl0241 [Synecocystis sp. PCC 6803] pir S75099 hypothetical protein sl0241 - Synecocystis sp. (strain PCC 6803) | | | |
| 15432 | | | | | | | | |
| 15433, | 16330553 | 26 | 4.00E-09 | Synechocystis sp. PCC 6803 | hypothetical protein WS0441 [Wolinella succinogenes DSM 1740] emb CAE09583.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 15434 | | | | Wolinella succinogenes DSM 1740 | | | | |
| 15435, | 34556868 | 33 | 8.00E-43 | | | | | |
| 15436 | | | | | | | | |
| 15439, | | | | | | | | |
| 15440 | 34556793 | 32 | 3.00E-19 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0360 [Wolinella succinogenes DSM 1740] emb CAE09508.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 15441, | | | | | | | | |
| 15442 | 48853518 | 47 | 2.00E-60 | Cytophaga hutchinsonii | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | | | |
| 15443, | | | | | | | | |
| 15444 | 48854173 | 25 | 9.00E-12 | Cytophaga hutchinsonii | hypothetical protein Chut02002840 [Cytophaga hutchinsonii] putative abc transporter, ATP-binding protein [Helicobacter pylori J99] gb AAD06381.1 putative abc transporter, ATP-binding protein [Helicobacter pylori J99] pir H71886 probable ABC transporter, ATP-binding protein - Helicobacter pylori (strain J99) | Oceanobacillus ihayensis HTE831 genomic DNA, section 11/13 | 93 1.00E-08 1.8.--- | |
| 15445, | | | | | | | | |
| 15446 | 15611856 | 68 | 1.00E-113 | Helicobacter pylori J99 | | | | |
| 15447, | | | | | | | | |
| 15448 | 53712013 | 51 | 3.00E-35 | Bacteroides fragilis YCH46 | putative ATP/GTP hydrolase [Bacteroides fragilis YCH46] dbj BAD47471.1 putative ATP/GTP hydrolase [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 15449, 15450 | 34557246 | 39 | 4.00E-35 | Wollinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09861.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes] | | | 2.7.3.- |
| 1545, 1546 | 29348024 | 52 | 3.00E-52 | Bacteroides thetaiotaomicron VPI-5482 | putative mobilization protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO77721.1 putative mobilization protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 15453, 15454 | 15896153 | 52 | 7.00E-37 | Clostridium acetobutylicum ATCC 824 | Spore photoproduct lyase, SPL related protein [Clostridium acetobutylicum ATCC 824] gb AAK80842.1 Spore photoproduct lyase, SPL related protein [Clostridium acetobutylicum ATCC 824] pir G97256 spore photoproduct lyase, SPL related protein [Imported] - Clostridium acetobutylicum | | | 4.1.99.- |
| 15455, 15456 | 34557288 | 43 | 4.00E-43 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0898 [Wollinella succinogenes DSM 1740] emb CAE10003.1 conserved hypothetical protein [Wollinella succinogenes] | | | |
| 15457, 15458 | 53713589 | 51 | 1.00E-65 | Bacteroides fragilis YCH46 | putative phosphoserine phosphatase [Bacteroides fragilis YCH46] dbj BAD49047.1 putative phosphoserine phosphatase [Bacteroides fragilis YCH46] | | | 3.1.3.3 |
| 15459, 15460 | 57241729 | 56 | 2.00E-52 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54399.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 15461, 15462 | 48846045 | 48 | 1.00E-17 | Geobacter metallireducens GS 15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] general glycosylation pathway protein [Campylobacter lari RM2100] gb EAL54661.1 general glycosylation pathway protein [Campylobacter lari RM2100] | | | |
| 15463, 15464 | 57241549 | 49 | 4.00E-50 | Campylobacter lari RM2100 | hypothetical protein bli7765 [Bradyrhizobium japonicum USDA 110] dbj BAC53030.1 bli7765 [Bradyrhizobium japonicum USDA 110] | | | |
| 15465, 15466 | 27382876 | 47 | 2.00E-25 | Bradyrhizobium japonicum USDA 110 | HsdM protein [Staphylococcus aureus] | | | 2.1.1.72 |
| 15469, 15470 | 49257053 | 33 | 3.00E-27 | Staphylococcus aureus | Methionyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78039.1 Methionyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | 6.1.1.10 |
| 1547, 1548 | 29348342 | 70 | 2.00E-77 | Bacteroides thetaiotaomicron VPI-5482 | thymidylate kinase [Clostridium tetani E88] gb AAO35554.1 thymidylate kinase [Clostridium tetani E88] | | | 2.7.4.9 |
| 15471, 15472 | 28210673 | 41 | 2.00E-52 | Clostridium tetani E88 | hypothetical protein Chut02003004 [Cytophaga hutchinsonii] | | | |
| 15473, 15474 | 48854333 | 34 | 1.00E-33 | Cytophaga hutchinsonii | LysM domain protein [Shewanella oneidensis MR-1] gb AAN53120.1 LysM domain protein [Shewanella oneidensis MR-1] | | | |
| 15475, 15476 | 24371633 | 35 | 9.00E-45 | Shewanella oneidensis MR-1 | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|---|----|----------|----------|
| 15479, 15480 | 29350128 | 35 | 9.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79825.1 putative RNA polymerase ECF- type sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 15481, 15482 | 34557246 | 58 | 1.00E-86 | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | Leptospira interrogans serovar lai str. 56601 chromosome I, section 363 of 397 of the complete sequence | 97 | 7.00E-07 | 2.7.3.- |
| 15483, 15484 | 34557246 | 39 | 2.00E-51 | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | | | | 2.7.3.- |
| 15485, 15486 | 34558230 | 42 | 4.00E-50 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR-CheY like receiver domain [Wolinella succinogenes DSM 1740] emb CAE10945.1 PUTATIVE TWO- COMPONENT REGULATOR-CheY like receiver domain [Wolinella succinogenes] | | | | |
| 15487, 15488 | 32261568 | 41 | 1.00E-10 | Helicobacter hepaticus ATCC 51449 | two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] | | | | 2.7.3.- |
| 15489, 15490 | 27363715 | 37 | 1.00E-15 | Vibrio vulnificus CMCP6 | Predicted integral membrane protein [Vibrio vulnificus CMCP6] ref NP_933746.1 hypothetical protein VV0953 [Vibrio vulnificus YJ016] gb AAO08770.1 Predicted integral membrane protein [Vibrio vulnificus CMCP6] db BAC93717.1 conserved hypothetical protein [Vibrio vulnificus YJ016] | | | | |
| 15493, 15494 | 34556564 | 48 | 3.00E-74 | Wolinella succinogenes DSM 1740 | PUTATIVE OXIDOREDUCTASE [Wolinella succinogenes DSM 1740] emb CAE09279.1 PUTATIVE OXIDOREDUCTASE [Wolinella succinogenes] | | | | 1.-.-.- |
| 15495, 15496 | 57241076 | 34 | 1.00E-25 | Campylobacter lari RM2100 | peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL54772.1 peptidase, M23/M37 family [Campylobacter lari RM2100] | | | | |
| 15499, 15500 | 29345941 | 56 | 5.00E-53 | Bacteroides thetaiotaomicron VPI-5482 | anthranilate synthase component II [Bacteroides thetaiotaomicron VPI-5482] gb AAO75638.1 anthranilate synthase component II [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.1.3.27 |
| 155, 156 | 15678404 | 46 | 7.00E-45 | Methanothermobac ter thermautotrophicus str. Delta H | hypothetical protein MTH376 [Methanothermobacter thermautotrophicus str. Delta H] gb AAB84882.1 conserved protein [Methanothermobacter thermautotrophicus str. Delta H] p F69148 hypothetical protein MTH376 - Methanobacterium thermoautotrophicum (strain Delta H) | | | | 2.4.1.- |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|----------|
| 15505, 15506 | 42524949 | 30 | 5.00E-16 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bc3605 [Bdellovibrio bacteriovorus HD100] embjCAE80983.1] hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100] | | | |
| 15507, 15508 | 45360231 | 33 | 1.00E-25 | Pseudomonas aeruginosa | putative transposase [Pseudomonas aeruginosa] | | | |
| 15511, 15512 | 48853348 | 29 | 1.00E-11 | Cytophaga hutchinsonii | hypothetical protein Chut0200390.1 [Cytophaga hutchinsonii] serine/threonine protein kinase [Picrophilus torridus DSM 9790] gb AAAT42720.1 serine/threonine protein kinase [Picrophilus torridus DSM 9790] | | | |
| 15515, 15516 | 48477207 | 37 | 4.00E-22 | Picrophilus torridus DSM 9790 | probable periplasmic protein Cj0114 [Campylobacter coli RM2228] gb EAL56678.1 probable periplasmic protein Cj0114 [Campylobacter coli RM2228] | | | 2.7.1.37 |
| 15521, 15522 | 57168717 | 33 | 2.00E-15 | Campylobacter coli RM2228 | TagD protein [Mannheimia succiniciproducens MBEL55E] gb AAU37265.1 TagD protein [Mannheimia succiniciproducens MBEL55E] | | | 2.7.7.39 |
| 15523, 15524 | 52424713 | 74 | 4.00E-51 | Mannheimia succiniciproducens MBEL55E | Histidinol-phosphate aminotransferase/Tyrosine aminotransferase [Thermoanaerobacter tengcongensis MB4] gb AAM25302.1 Histidinol- phosphate aminotransferase/Tyrosine aminotransferase [Thermoanaerobacter tengcongensis MB4] sp Q8R5Q4 HIS8_THETN Histidinol-phosphate aminotransferase (Imidazole acetol-phosphate transaminase) | | | |
| 15525, 15526 | 20808527 | 34 | 5.00E-36 | Thermoanaerobact er tengcongensis MB4 | hydrolase, HD family [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT63786.1 hydrolase, HD family [Bacillus thuringiensis serovar konkukian str. 97-27] | | Zea mays clone EL01N0430C11.c mRNA sequence 88 | 2.6.1.9 |
| 15529, 15530 | 49481584 | 50 | 7.00E-53 | Bacillus thuringiensis serovar konkukian str. 97-27 | hypothetical protein WS0003 [Wolnella succinogenes DSM 1740] embjCAE09177.1] conserved hypothetical protein [Wolnella succinogenes] hypothetical protein BF2483 [Bacteroides fragilis YCH46] dbj BAD49232.1 hypothetical protein [Bacteroides fragilis YCH46] COG0229: Conserved domain frequently associated with peptide methionine sulfoxide reductase [Cytophaga hutchinsonii] | | | |
| 15531, 15532 | 34556462 | 71 | 6.00E-49 | Wolnella succinogenes DSM 1740 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] | | | |
| 15533, 15534 | 53713774 | 29 | 3.00E-07 | Bacteroides fragilis YCH46 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] | | | |
| 15535, 15536 | 48856175 | 67 | 7.00E-46 | Cytophaga hutchinsonii | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] | | | 1.8.4.6 |
| 15537, 15538 | 48832299 | 43 | 2.00E-50 | Magnetococcus sp. MC-1 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] | | | |
| 15539, 15540 | 48832299 | 47 | 2.00E-35 | Magnetococcus sp. MC-1 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] | | | 3.1.4.17 |

| | | | | | | | | | |
|-------------------------------------|----------------------|----------|----------------------|---|--|----|----------|----------|--|
| 15541, 15542, 15543, 15544 | 15679233 38016731 | 29 43 | 1.00E-08 1.00E-30 | Methanothermobacter thermautotrophicus str. Delta H Klebsiella pneumoniae | inosine-5'-monophosphate dehydrogenase related protein I [Methanothermobacter thermotrophicus str. Delta H] gb AAB85711.1 inosine-5'-monophosphate dehydrogenase related protein I [Methanothermobacter thermotrophicus str. Delta H] pir C69030 MJ1225 protein homolog MTH1222 - Methanobacterium thermoautotrophicum (strain Delta H) unknown [Klebsiella pneumoniae] ref NP_943402.1 hypothetical protein LV233 [Klebsiella pneumoniae] DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes] sp Q7MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [Includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)] | | | | |
| 15547, 15548 | 34556892 | 82 | 1.00E-139 | Wollinella succinogenes DSM 1740 | Ehrlichia ruminantium RNA polymerase beta subunit (rpoB) gene, partial cds | 88 | 4.00E-45 | 2.7.7.6 | |
| 15549, 15550 | 34557851 | 31 | 2.00E-29 | Wollinella succinogenes DSM 1740 | hypothetical protein WS1518 [Wollinella succinogenes DSM 1740] emb CAE10566.1 conserved hypothetical protein [Wollinella succinogenes] conserved hypothetical integral membrane protein [Campylobacter upsaliensis RM3195] gb EAL54000.1 conserved hypothetical integral membrane protein [Campylobacter upsaliensis RM3195] | | | | |
| 15551, 15552 | 57242027 | 49 | 7.00E-39 | Campylobacter upsaliensis RM3195 | anticonodon nuclease [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39782.1 anticonodon nuclease [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | | |
| 15553, 15554 | 21229941 | 62 | 4.00E-77 | Wollinella succinogenes DSM 1740 | PUTATIVE AMINOTRANSFERASE PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09898.1 PUTATIVE AMINOTRANSFERASE PROTEIN [Wollinella succinogenes] | | | 2.6.1.1 | |
| 15555, 15556 | 34557183 | 40 | 3.00E-50 | Campylobacter lari RM2100 | signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54233.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100] | | | 2.7.3.- | |
| 15559, 15560 | 52006638 | 39 | 8.00E-14 | Thiobacillus denitrificans ATCC 25259 | COG2833: Uncharacterized protein conserved in bacteria [Thiobacillus denitrificans ATCC 25259] | | | | |
| 15561, 15562 | 29653699 | 29 | 6.00E-10 | Coxiella burnetii RSA 493 | 3-demethylubiquinone-9 3-methyltransferase [Coxiella burnetii RSA 493] gb AAO89905.1 3-demethylubiquinone-9 3-methyltransferase [Coxiella burnetii RSA 493] sp Q820B5 UBIG_COXBU 3-demethylubiquinone-9 3- methyltransferase (3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHMB methyltransferase) | | | 2.1.1.64 | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|---|--|--|--|---------------------|
| 15563, 15564 | 34558827 | 44 | 6.00E-23 | Alvinella pompejana epibiont 7G3 | riboflavin biosynthesis protein [Alvinella pompejana epibiont 7G3] | | | | 3.5.4.26 |
| 15565, 15566 | 53715600 | 46 | 2.00E-36 | Bacteroides fragilis YCH46 | hypothetical protein BF4320 [Bacteroides fragilis YCH46] dbj BAD51058.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 15567, 15568 | 47222369 | 47 | 8.00E-27 | Tetraodon nigroviridis | unnamed protein product [Tetraodon nigroviridis] | | | | |
| 15569, 15570 | 32262380 | 48 | 5.00E-44 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860362.1 hypothetical protein HH0831 [Helicobacter hepaticus ATCC 51449] | | | | 3.1.7.2 |
| 1557, 1558 | 45681187 | 35 | 5.00E-21 | Mesorhizobium sp. BNC1 | COG3734: 2-keto-3-deoxy-galactonokinase [Mesorhizobium sp. BNC1] TRIOSEPHOSPHATE ISOMERASE TIM [Wolnella succinogenes DSM 1740] emb CAE09568.1 TRIOSEPHOSPHATE ISOMERASE TIM [Wolnella succinogenes] sp Q7MA77 TPIS_WOLSU Triosephosphate isomerase (TIM) (Triose-phosphate isomerase) | | | | 2.7.1.58 |
| 15575, 15576 | 34556853 | 51 | 3.00E-63 | Wolnella succinogenes DSM 1740 | sensory box histidine kinase/response regulator [Shewanella oneidensis MR- 1] gbl AAN53935.1 sensory box histidine kinase/response regulator [Shewanella oneidensis MR-1] | | | | 5.3.1.1 |
| 15577, 15578 | 24372448 | 46 | 5.00E-47 | Shewanella oneidensis MR-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | | 2.7.3.- |
| 15579, 15580 | 48833325 | 27 | 9.00E-26 | Magnetococcus sp. MC-1 | hypothetical protein VVA1343 [Vibrio vulnificus YJ016] dbj BAC87369.1 conserved hypothetical protein [Vibrio vulnificus YJ016] | | | | 2.7.3.- |
| 15581, 15582 | 37677003 | 22 | 5.00E-15 | Vibrio vulnificus YJ016 | Desc:H. pylori GHPO 881 protein. Org:Helicobacter pylori ABC-type multidrug transport system, ATPase component [Thermoanaerobacter tengcongensis MB4] gbl AAM25341.1 ABC-type multidrug transport system, ATPase component [Thermoanaerobacter tengcongensis MB4] | | | | |
| 15585, 15586 | AAW9831 1 | 33 | 2.00E-34 | Thermoanaerobact er tengcongensis MB4 | putative lipoprotein [Streptococcus equi] | | | | 3.4.21.- |
| 15587, 15588 | 20808566 | 35 | 2.00E-29 | Streptococcus equi MB4 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 74 of 197 of the complete genome | | | | 1.8.4.6 |
| 15589, 15590 | 23380366 | 41 | 1.00E-22 | Desulfotobacterium hafniense DCB-2 | COG0225: Peptide methionine sulfoxide reductase [Desulfotobacterium hafniense DCB-2] | | | | |
| 15591, 15592 | 53686114 | 59 | 6.00E-75 | Bacillus pseudofirmus | hypothetical 23.6 kDa protein [Bacillus pseudofirmus] | | | | |
| 15593, 15594 | 15426420 | 28 | 1.00E-12 | pseudofirmus | | | | | 91 2.00E-16 1.8.4.6 |

| | | | | | | | | |
|---|---------------------------------|----------------|----------------------------------|---|--|---|----|----------------------|
| 15595, 15596 | 34558334 | 51 | 2.00E-34 | Wollinella succinogenes DSM 1740 | PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wollinella succinogenes DSM 1740] emb CAE11049.1 PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wollinella succinogenes] | | | 2.4.2.- |
| 15597, 15598 | 47526988 | 38 | 3.00E-15 | Bacillus anthracis str. 'Ames Ancestor' | tpg/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] | | | |
| 15599, 15600 15603, 15604 15607, 15608 | 56413961 48314770 4839711 | 34 32 46 | 5.00E-17 6.00E-34 9.00E-25 | Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150 Burkholderia cepacia R18194 Methanosarcina barkeri str. fusaro | putative membrane protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV77724.1 putative membrane protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Burkholderia cepacia R18194] COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro] | | | 3.1.1.24 3.1.21.3 |
| 15609, 15610 | 48868930 | 36 | 9.00E-17 | Haemophilus Influenzae 86- 028NP | COG1943: Transposase and inactivated derivatives [Haemophilus Influenzae 86-028NP] | | | |
| 1561, 1562 | 15896308 | 27 | 2.00E-16 | Clostridium acetobutylicum ATCC 824 | Glycosyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK80997.1 Glycosyltransferase [Clostridium acetobutylicum ATCC 824] pir B97276 glycosyltransferase [imported] - Clostridium acetobutylicum | | | |
| 15611, 15612 | 34558283 | 72 | 9.00E-70 | Wollinella succinogenes DSM 1740 | 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE [Wollinella succinogenes DSM 1740] emb CAE10998.1 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE [Wollinella succinogenes] sp Q7M7Z0 DXS_WOLSU 1-deoxy-D-xylulose-5-phosphate synthase (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS) | Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome | 92 | 3.00E-11 4.1.3.37 |
| 15615, 15616 15617, 15618 | 34558493 48856844 | 58 31 | 1.00E-88 5.00E-31 | Wollinella succinogenes DSM 1740 Cytophaga hutchinsonii | PUTATIVE ZINC PROTEASE [Wollinella succinogenes DSM 1740] emb CAE11208.1 PUTATIVE ZINC PROTEASE [Wollinella succinogenes] COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | 3.4.- |
| 15619, 15620 | 42527469 | 28 | 1.00E-15 | Treponema denticola ATCC 35405 | Na/Pi cotransporter family protein [Treponema denticola ATCC 35405] gb AAS12478.1 Na/Pi cotransporter family protein [Treponema denticola ATCC 35405] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|-----------------------------------|---|--|--|----------|
| 15621, 15622 | 50745174 | 32 | 2.00E-24 | Gallus gallus | PREDICTED: similar to L-gulono-gamma-lactone oxidase precursor [Gallus gallus] | | | 1.1.3.8 |
| 15623, 15624 | 48833463 | 47 | 5.00E-26 | Magnetococcus sp. MC-1 | COG2202: FOG: PAS/PAC domain [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 15625, 15626 | 34558828 | 32 | 4.00E-19 | Alvinella pompejana epibiont 7G3 | KIAA1005 protein [Alvinella pompejana epibiont 7G3] | | | |
| 15627, 15628 | 27366393 | 30 | 4.00E-22 | Vibrio vulnificus CMCP6 | Response regulator [Vibrio vulnificus CMCP6] gb AAO11448.1 Response regulator [Vibrio vulnificus CMCP6] | | | 2.7.3.- |
| 15629, 15630 | 34556560 | 33 | 2.00E-25 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | |
| 1563, 1564 | 28974569 | 49 | 5.00E-60 | Pseudomonas sp. Y2 | putative ring-oxydation complex protein 5 [Pseudomonas sp. Y2] | | | 1.-.-.- |
| 15631, 15632 | 34557905 | 54 | 6.00E-29 | Wolinella succinogenes DSM 1740 | PROLYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10620.1 PROLYL-TRNA SYNTHETASE [Wolinella succinogenes] | | | 6.1.1.15 |
| 15633, 15634 | 32261568 | 29 | 2.00E-25 | Helicobacter hepaticus ATCC 51449 | two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] | | | 2.7.3.- |
| 15635, 15636 | 53712269 | 37 | 1.00E-34 | Bacteroides fragilis YCH46 | dipeptidyl peptidase IV [Bacteroides fragilis YCH46] dbj BAD47727.1 dipeptidyl peptidase IV [Bacteroides fragilis YCH46] | | | 3.4.14.- |
| 15637, 15638 | 34557444 | 47 | 6.00E-50 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1061 [Wolinella succinogenes DSM 1740] emb CAE10159.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 15639, 15640 | 15643810 | 32 | 1.00E-08 | Thermotoga maritima MSB8 | comEA protein-related protein [Thermotoga maritima MSB8] gb AAD36129.1 comEA protein-related protein [Thermotoga maritima MSB8] pir F72301 comEA protein-related protein - Thermotoga maritima (strain MSB8) | | | |
| 15641, 15642 | 34557665 | 50 | 7.00E-35 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | 2.7.3.- |
| 15643, 15644 | 27379227 | 29 | 5.00E-28 | Bradyrhizobium japonicum USDA 110 | hypothetical protein bir4116 [Bradyrhizobium japonicum USDA 110] dbj BAC49381.1 bir4116 [Bradyrhizobium japonicum USDA 110] | | | |
| 15645, 15646 | 34557014 | 45 | 3.00E-42 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0597 [Wolinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 15647, 15648 | 39997537 | 37 | 6.00E-38 | Geobacter sulfurreducens PCA | ReA/Spot domain protein [Geobacter sulfurreducens PCA] gb AAR35815.1 ReA/Spot domain protein [Geobacter sulfurreducens PCA] | | | |

| | | | | | | | | |
|--------|----------|----|----------|-------------------------------|---|------------|--|-------------|
| 1565, | 18266398 | 33 | 6.00E-22 | Escherichia coli | putative galactosyltransferase WbgM [Escherichia coli] | | | 2.4.1.52 |
| 15655, | | | | Burkholderia | | | | |
| 15656 | 48788830 | 35 | 8.00E-44 | fungorum LB400 | COG0845: Membrane-fusion protein [Burkholderia fungorum LB400] | | | |
| 15657, | | | | Wollinella | GLUTAMATE SYNTHASE SMALL CHAIN [Wollinella succinogenes DSM | | | |
| 15658 | 34557570 | 60 | 1.00E-97 | succinogenes DSM 1740 | [1740] emb CAE10285.1 GLUTAMATE SYNTHASE SMALL CHAIN [Wollinella succinogenes] | | | 1.4.1.13 |
| 15661, | | | | Helicobacter | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] | | | |
| 15662 | 32262440 | 23 | 1.00E-11 | hepaticus ATCC 51449 | ref NP_860422.1 hypothetical protein HH0891 [Helicobacter hepaticus ATCC 51449] | | | |
| 15663, | | | | Enterococcus | | | | |
| 15664 | 29377041 | 36 | 3.00E-07 | faecalis V583 | hemK protein [Enterococcus faecalis V583] gb AAO82265.1 hemK protein [Enterococcus faecalis V583] | | | |
| 15665, | | | | Streptococcus | | | | |
| 15666 | 21552727 | 23 | 1.00E-06 | pneumoniae | putative alpha-1,3-galactosyltransferase Cps9vG [Streptococcus pneumoniae] | | | |
| 15667, | | | | Dechloromonas | | | | |
| 15668 | 41726155 | 26 | 5.00E-08 | aromatica RCB | COG0438: Glycosyltransferase [Dechloromonas aromatica RCB] | | | |
| 15669, | | | | Magnetococcus sp. | | | | |
| 15670 | 48831520 | 29 | 5.00E-08 | MC-1 | hypothetical protein Mmc102002973 [Magnetococcus sp. MC-1] | | | |
| 1567, | | | | Escherichia coli | | | | |
| 1568 | 24527254 | 28 | 1.00E-08 | Geobacter | putative glycosyl transferase [Escherichia coli] | | | |
| 15671, | | | | metallireducens GS- | | | | 2.7.3.- |
| 15672 | 48846045 | 37 | 3.00E-42 | 15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | |
| 15675, | | | | Rhodopirellula | hypothetical protein RB3944 [Rhodopirellula baltica SH 1] emb CAD73501.1 | | | |
| 15676 | 32472822 | 48 | 1.00E-21 | baltica SH 1 | conserved hypothetical protein [Pirellula sp.] | | | |
| 15679, | | | | Thermococcus | methylmalonyl-CoA decarboxylase, gamma subunit [Thermococcus kodakaraensis] ref YP_184037.1 methylmalonyl-CoA decarboxylase, | | | |
| 15680 | 57159883 | 38 | 7.00E-19 | kodakaraensis | gamma subunit [Thermococcus kodakaraensis] | | | 4.1.1.41 |
| 15681, | | | | Nostoc punctiforme | | | | |
| 15682 | 23130207 | 35 | 9.00E-19 | PCC 73102 | COG0732: Restriction endonuclease S subunits [Nostoc punctiforme PCC 73102] | | | 3.1.21.3 |
| 15683, | | | | Vibrio | | | | |
| 15684 | 28901068 | 27 | 2.00E-15 | parahaemolyticus RIMD 2210633 | hypothetical protein VPA1213 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62556.1 hypothetical protein [Vibrio parahaemolyticus] | | | |
| 15685, | AAB5259 | | | | | Wollinella | succinogenes, complete genome; segment 6/7 | 86 4.00E-20 |
| 15686 | 6 | 39 | 1.00E-39 | | Desc:Helicobacter pylori bait polypeptide #114, Org:Helicobacter pylori transcriptional regulator, merR family [Clostridium tetani E88] | | | |
| 15687, | | | | Clostridium tetani E88 | | | | |
| 15688 | 28210659 | 24 | 8.00E-09 | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|---------------|
| 15691, 15692 | 52006879 | 30 | 3.00E-32 | Thiobacillus denitrificans ATCC 25259 | COG2199: FOG: GGDEF domain [Thiobacillus denitrificans ATCC 25259] | | | 1.1.1.20 5 |
| 15695, 15696 | 53713382 | 39 | 4.00E-63 | Bacteroides fragilis YCH46 | outer membrane efflux protein [Bacteroides fragilis YCH46] dbj BAD48840.1 outer membrane efflux protein [Bacteroides fragilis YCH46] | | | |
| 15697, 15698 | 48850440 | 61 | 3.00E-48 | Novosphingobium aromaticivorans DSM 12444 | COG2029: Conserved domain frequently associated with peptide methionine sulfoxide reductase [Novosphingobium aromaticivorans DSM 12444] | | | 1.8.4.6 |
| 15699, 15700 | 34557204 | 28 | 5.00E-12 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0806 [Wolinella succinogenes DSM 1740] emb CAE09919.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 15703, 15704 | 46202599 | 34 | 3.00E-22 | Magnetospirillum magnetotacticum MS-1 | hypothetical protein Magn03007449 [Magnetospirillum magnetotacticum MS- 1] | | | |
| 15705, 15706 | 34558477 | 47 | 1.00E-14 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2202 [Wolinella succinogenes DSM 1740] emb CAE11192.1 hypothetical protein [Wolinella succinogenes] | | | |
| 15709, 15710 | 38637724 | 39 | 7.00E-41 | Cupriavidus necator | putative integrase/recombinase [Cupriavidus necator] gb AAP85812.1 putative integrase/recombinase [Ralstonia eutropha] | | | |
| 1571, 1572 | 21674598 | 44 | 4.00E-60 | Chlorobium tepidum TLS | GTP-binding protein [Chlorobium tepidum TLS] gb AAM73005.1 GTP- binding protein [Chlorobium tepidum TLS] sp Q8KBK3 ENGA_CHLTE GTP- binding protein engA | | | |
| 15711, 15712 | 38637719 | 23 | 5.00E-11 | Cupriavidus necator | hypothetical protein PHG054 [Cupriavidus necator] gb AAP85807.1 hypothetical protein PHG054 [Ralstonia eutropha] | | | |
| 15713, 15714 | 34558361 | 30 | 8.00E-38 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-PREDICTED PEMEASE [Wolinella succinogenes DSM 1740] emb CAE11076.1 conserved hypothetical protein- PREDICTED PEMEASE [Wolinella succinogenes] | | | |
| 15715, 15716 | 57241443 | 49 | 3.00E-34 | Campylobacter lari RM2100 | HAD-superfamily hydrolase, subfamily IIA subfamily [Campylobacter lari RM2100] gb EAL54555.1 HAD-superfamily hydrolase, subfamily IIA subfamily [Campylobacter lari RM2100] | | | 3.1.3.41 |
| 15717, 15718 | 47575513 | 49 | 5.00E-59 | Rubrivivax gelatinosus PM1 | COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Rubrivivax gelatinosus PM1] | | | 3.4.21.- |
| 15719, 15720 | 48862943 | 48 | 2.00E-70 | Microbulbifer degradans 2-40 | COG0845: Membrane-fusion protein [Microbulbifer degradans 2-40] | | | |
| 15721, 15722 | 56315986 | 23 | 9.00E-14 | Azoarcus sp. Ebn1 Wolinella succinogenes DSM 1740 | hypothetical protein [Azoarcus sp. Ebn1] | | | |
| 15723, 15724 | 34557291 | 28 | 3.00E-27 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 15725, 15726 | 51573391 | 21 | 1.00E-08 | Borrelia garinii PBI | hypothetical protein BG0579 [Borrelia garinii PBI] ref YP_073008.1 | | | |
| 15727, 15728 | 48853937 | 53 | 2.00E-63 | Cytophaga hutchinsonii | COG0482: Predicted tRNA(5-methylaminomethyl-2-thiouridylylate) methyltransferase, contains the PP-loop ATPase domain [Cytophaga hutchinsonii] | | | 2.1.1.61 |
| 15729, 15730 | 51209444 | 29 | 6.00E-07 | Campylobacter coli | csp12 [Campylobacter coli] gb AAR29496.1 csp12 [Campylobacter coli] ref YP_063457.1 csp12 [Campylobacter jejuni] gb AAR29546.1 csp12 [Campylobacter jejuni] | | | |
| 15731, 15732 | 23015878 | 47 | 2.00E-60 | Magnetospirillum magnetotacticum MS-1 | COG2703: Hemerythrin [Magnetospirillum magnetotacticum MS-1] | | | |
| 15733, 15734 | 28901068 | 30 | 2.00E-10 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA1213 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62556.1 hypothetical protein [Vibrio parahaemolyticus] | | | |
| 15737, 15738 | 52842767 | 39 | 6.00E-38 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | ATP-dependent DNA helicase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28619.1 ATP-dependent DNA helicase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] probable outer membrane component of efflux system Cj1031 [Campylobacter upsaliensis RM3195] | | | 3.6.1.- |
| 15739, 15740 | 57241976 | 33 | 2.00E-19 | Campylobacter upsaliensis RM3195 | alcohol dehydrogenase, zinc-containing [Bacillus cereus ATCC 10987] gb AAS39808.1 alcohol dehydrogenase, zinc-containing [Bacillus cereus ATCC 10987] | | | 1.1.1.1 |
| 15741, 15742 | 42779953 | 55 | 7.00E-49 | Bacillus cereus ATCC 10987 | hypothetical protein SO4465 [Shewanella oneidensis MR-1] gb AAN57430.1 conserved domain protein [Shewanella oneidensis MR-1] sensory transduction histidine kinase [Methanothermobacter thermotrophicus str. Delta H] gb AAB85323.1 sensory transduction histidine kinase [Methanothermobacter thermotrophicus str. Delta H] pirl A69210 sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Delta H) | | | 2.7.3.- |
| 15747, 15748 | 15678845 | 32 | 3.00E-19 | Str. Delta H | ferric uptake regulation protein, putative [Campylobacter coli RM2228] gb EAL57643.1 ferric uptake regulation protein, putative [Campylobacter coli RM2228] | | | |
| 15749, 15750 | 57167857 | 36 | 2.00E-13 | Campylobacter coli RM2228 | COG4564: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 15751, 15752 | 48853443 | 26 | 3.00E-09 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | 2.7.3.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|--|---------|
| 15757, 15758 | 54031229 | 39 | 7.00E-33 | Polaromonas sp. JS666 | COG1032: Fe-S oxidoreductase [Polaromonas sp. JS666] hypothetical protein sil0624 [Synechocystis sp. PCC 6803] dbj BAA18682.1 sil0624 [Synechocystis sp. PCC 6803] pir S76770 hypothetical protein - Synechocystis sp. (strain PCC 6803) | | | | |
| 15759, 15760 | 16332142 | 36 | 6.00E-14 | Synechocystis sp. PCC 6803 | oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96557.1 oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinnella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinnella succinogenes] | | | | 2.7.3.- |
| 15761, 15762 | 46580489 | 38 | 4.00E-50 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | long-chain-fatty-acid-CoA ligase (fadD-7) [Archaeoglobus fulgidus DSM 4304] gb AAB89478.1 long-chain-fatty-acid-CoA ligase (fadD-7) [Archaeoglobus fulgidus DSM 4304] pir C6947.1 probable fatty-acid-CoA ligase (EC 6.2.1.-) fadD7 - Archaeoglobus fulgidus | | | | 6.2.1.3 |
| 15763, 15764 | 34557573 | 34 | 1.00E-28 | Archaeoglobus fulgidus DSM 4304 | hypothetical protein MTH528 [Methanothermobacter thermotrophicus str. Delta H] gb AAB85034.1 unknown [Methanothermobacter thermotrophicus str. Delta H] pir F69169 conserved hypothetical protein MTH528 - Methanothermobacter thermotrophicus (strain Delta H) COG2360: LeuPhe-tRNA-protein transferase [Dechloromonas aromatica RCB] | | | | 2.3.2.6 |
| 1577, 1578 | 15678556 | 44 | 1.00E-18 | Methanothermobac ter thermotrophicus str. Delta H | hypothetical protein BT1422 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76529.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482] NAD dependent epimerase/dehydratase [Prochlorococcus marinus subsp. marinus str. CCMP1375] gb AAQ00326.1 NAD dependent epimerase/dehydratase [Prochlorococcus marinus subsp. marinus str. CCMP1375] | | | | 5.1.3.- |
| 15771, 15772 | 46140415 | 55 | 1.00E-55 | Dechloromonas aromatica RCB | NAD dependent epimerase/dehydratase [Prochlorococcus marinus subsp. marinus str. CCMP1375] NAD dependent epimerase/dehydratase [Prochlorococcus marinus subsp. marinus str. CCMP1375] | | | | |
| 15773, 15774 | 29346832 | 32 | 3.00E-12 | Bacteroides thetaitaomicron VPI-5482 | POLYPHOSPHATE KINASE [Wolinnella succinogenes DSM 1740] emb CAE10955.1 POLYPHOSPHATE KINASE [Wolinnella succinogenes] | | | | 2.7.4.1 |
| 15777, 15778 | 33240731 | 21 | 4.00E-10 | Prochlorococcus marinus subsp. marinus str. CCMP1375 | amine oxidase, flavin-containing [Pseudomonas syringae pv. tomato str. DC3000] ref NP_790952.1 amine oxidase, flavin-containing [Pseudomonas syringae pv. tomato str. DC3000] | | | | |
| 15779, 15780 | 33240731 | 26 | 9.00E-08 | Prochlorococcus marinus subsp. marinus str. CCMP1375 | | | | | |
| 15781, 15782 | 34558240 | 57 | 2.00E-64 | Wolinnella succinogenes DSM 1740 | | | | | |
| 15783, 15784 | 28851570 | 43 | 5.00E-47 | Pseudomonas syringae pv. tomato str. DC3000 | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|---|--|----|-------------------|
| 15785, 15786 | 34558264 | 50 | 8.00E-69 | Wollinella succinogenes DSM 1740 | TRNA DELTA-2-ISOPENTENYL PYROPHOSPHATE [Wollinella succinogenes DSM 1740] emb CAE10979.1 TRNA DELTA-2- ISOPENTENYL PYROPHOSPHATE [Wollinella succinogenes] | | | 2.5.1.8 |
| 15787, 15788 | 39936981 | 49 | 9.00E-54 | Rhodopseudomonas palustris CGA009 | possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] emb CAE29361.1 possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] | | | 2.7.-.- |
| 15789, 15790 | 34762625 | 37 | 7.00E-17 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | hypothetical protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24781.1 hypothetical protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | |
| 1579, 1580 | 29347556 | 44 | 6.00E-87 | Bacteroides thetaiotaomicron VPI-5482 | 4-alpha-glucanotransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77253.1 4-alpha-glucanotransferase [Bacteroides thetaiotaomicron VPI-5482] | Desc: Genomic sequence of Lactococcus lactis IL1403. Org: Lactococcus lactis IL1403 | 90 | 2.00E-07 2.4.1.25 |
| 15793, 15794 | 2314704 | 35 | 8.00E-30 | Helicobacter pylori 26695 | H. pylori predicted coding region HP1519 [Helicobacter pylori 26695] pir G64709 hypothetical protein HP1519 - Helicobacter pylori (strain 26695) ref NP_208310.1 hypothetical protein HP1519 [Helicobacter pylori 26695] | | | |
| 15803, 15804 | 34557709 | 39 | 3.00E-40 | Wollinella succinogenes DSM 1740 | AMINOPEPTIDASE [Wollinella succinogenes DSM 1740] emb CAE10424.1 AMINOPEPTIDASE [Wollinella succinogenes] sp Q7M8W6 AMPA_WOLSU Probable cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) | | | 3.4.11.1 |
| 15805, 15806 | 34557341 | 49 | 6.00E-62 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0953 [Wollinella succinogenes DSM 1740] emb CAE10056.1 conserved hypothetical protein [Wollinella succinogenes] | | | |
| 1581, 1582 | 48892457 | 26 | 1.00E-09 | Trichodesmium erythraeum IMS101 | COG0438: Glycosyltransferase [Trichodesmium erythraeum IMS101] hypothetical protein DET0620 [Dehalococcoides ethenogenes 195] | | | |
| 15811, 15812 | 57234561 | 26 | 8.00E-15 | Dehalococcoides ethenogenes 195 | gb AAW40066.1 conserved domain protein [Dehalococcoides ethenogenes 195] | | | |
| 15819, 15820 | 34556768 | 70 | 1.00E-101 | Wollinella succinogenes DSM 1740 | DIAMINOPELMATE DECARBOXYLASE DAP DECARBOXYLASE [Wollinella succinogenes DSM 1740] emb CAE09483.1 DIAMINOPELMATE DECARBOXYLASE DAP DECARBOXYLASE [Wollinella succinogenes] | | | 4.1.1.20 |
| 15821, 15822 | 53711856 | 41 | 2.00E-29 | Bacteroides fragilis YCH46 | 5'-nucleotidase precursor [Bacteroides fragilis YCH46] db BAD47314.1 5'- nucleotidase precursor [Bacteroides fragilis YCH46] | | | 3.1.3.5 |

| | | | | | | | | |
|-----------------|--------------|----|----------|---|--|--|--|----------|
| 15823, 15824 | 53757968 | 35 | 9.00E-14 | Methylococcus capsulatus str. Bath | response regulator [Methylococcus capsulatus str. Bath] ref YP_113897.1 response regulator [Methylococcus capsulatus str. Bath] | | | 2.7.3.- |
| 15825, 15826 | 29346674 | 41 | 1.00E-40 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76371.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.3.- |
| 15827, 15828 | AA0666 8 | 28 | 2.00E-08 | | Desc:Nisin T of Lactobacillus lactis. Org:Lactobacillus lactis | | | |
| 1583, 1584 | 33862380 | 30 | 1.00E-09 | Prochlorococcus marinus str. MIT 9313 | hypothetical protein PMT0107 [Prochlorococcus marinus str. MIT 9313] emb CAE20282.1 conserved hypothetical protein [Prochlorococcus marinus str. MIT 9313] | | | |
| 15833, 15834 | 48855091 | 38 | 4.00E-32 | Cytophaga hutchinsonii | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii] | | | |
| 15835, 15836 | 34557844 | 27 | 6.00E-26 | Wolinella succinogenes DSM 1740 | MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10559.1 MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes] | | | |
| 15837, 15838 | 48860427 | 50 | 1.00E-58 | Clostridium thermocellum ATCC 27405 | COG1052: Lactate dehydrogenase and related dehydrogenases [Clostridium thermocellum ATCC 27405] | | | 1.1.1.95 |
| 15839, 15840 | AAW7151 3 | 52 | 8.00E-55 | Wolinella succinogenes DSM 1740 | Desc:Helicobacter polypeptide GHPO 1378. Org:Helicobacter pylori TRANSCRIPTION ELONGATION FACTOR [Wolinella succinogenes DSM 1740] emb CAE10800.1 TRANSCRIPTION ELONGATION FACTOR [Wolinella succinogenes] | | | 1.3.99.1 |
| 15843, 15844 | 34558085 | 49 | 2.00E-78 | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | |
| 15847, 15848 | 48854902 | 35 | 3.00E-52 | Methanosarcina acetivorans C2A | hypothetical protein MA4278 [Methanosarcina acetivorans C2A] gb AAM07622.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | 3.2.1.8 |
| 1585, 1586 | 20093067 | 44 | 1.00E-21 | Cytophaga hutchinsonii | COG0812: UDP-N-acetylmuramate dehydrogenase [Cytophaga hutchinsonii] | | | 1.1.1.15 |
| 15851, 15852 | 48855478 | 45 | 2.00E-67 | | hypothetical protein PA1368 [Pseudomonas aeruginosa PAO1] pir E83474 hypothetical protein PA1368 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_250059.1 hypothetical protein PA1368 [Pseudomonas aeruginosa PAO1] | | | 8 |
| 15853, 15854 | 9947311 | 34 | 8.00E-18 | Pseudomonas aeruginosa PAO1 | putative cystathionine beta-synthase [Streptomyces coelicolor A3(2)] ref NP_627297.1 putative cystathionine beta-synthase [Streptomyces coelicolor A3(2)] | | | 4.2.1.22 |
| 15861, 15862 | 7672260 | 35 | 2.00E-42 | Streptomyces coelicolor A3(2) | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|---|----|----------|--|
| 15863, 15864 | 34557509 | 55 | 8.00E-79 | Wollinella succinogenes DSM 1740 | hypothetical protein WS1135 [Wollinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wollinella succinogenes] 19718] emb CAD85036.1 AMP-dependent synthetase and ligase [Nitrosomonas europaea ATCC 19718] | Wollinella succinogenes, complete genome; segment 4/7 | 85 | 6.00E-10 | |
| 15865, 15866 | 30249114 | 31 | 2.00E-23 | Nitrosomonas europaea ATCC 19718 | hypothetical protein RB8789 [Rhodopirellula baltica SH 1] emb CAD75922.1 conserved hypothetical protein [Pirellula sp.] | | | 6.2.1.3 | |
| 15867, 15868 | 32475551 | 41 | 4.00E-35 | Rhodopirellula baltica SH 1 | hypothetical protein RB8789 [Rhodopirellula baltica SH 1] emb CAD75922.1 conserved hypothetical protein [Pirellula sp.] | | | | |
| 15869, 15870 | 32475551 | 44 | 4.00E-15 | Rhodopirellula baltica SH 1 | DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221] | | | 2.7.- | |
| 15871, 15872 | 57238514 | 32 | 3.00E-27 | Campylobacter jejuni RM1221 | two-component sensor histidine kinase [Nostoc sp. PCC 7120] pir AE1966 two-component sensor histidine kinase all1280 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73237.1 two-component sensor histidine kinase (Nostoc sp. PCC 7120) | | | 2.7.3.- | |
| 15873, 15874 | 17228775 | 36 | 2.00E-21 | Nostoc sp. PCC 7120 | SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wollinella succinogenes DSM 1740] emb CAE10959.1 SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wollinella succinogenes] | | | 2.7.3.- | |
| 15875, 15876 | 34558244 | 30 | 2.00E-23 | Wollinella succinogenes DSM 1740 | | | | | |
| 15877, 15878 | 2314136 | 57 | 6.00E-45 | Helicobacter pylori 26695 | H. pylori predicted coding region HP0994 [Helicobacter pylori 26695] pir B64644 hypothetical protein HP0994 - Helicobacter pylori (strain 26695) ref NP_207785.1 hypothetical protein HP0994 [Helicobacter pylori 26695] | Helicobacter pylori strain PeCan188 plasticity zone, containing type IV secretion system number three (tfs3) gene cluster, complete sequence | 91 | 3.00E-07 | |
| 15879, 15880 | 53714586 | 26 | 1.00E-14 | Bacteroides fragilis YCH46 | hypothetical protein BF3300 [Bacteroides fragilis YCH46] dbj BAD50044.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 15881, 15882 | 15611103 | 40 | 2.00E-09 | Helicobacter pylori J99 | hypothetical protein jhp0032 [Helicobacter pylori J99] gb AAD05603.1 putative [Helicobacter pylori J99] pir F71983 hypothetical protein jhp0032 - Helicobacter pylori (strain J99) | | | | |
| 15883, 15884 | 23128114 | 34 | 1.00E-21 | Nostoc punctiforme PCC 73102 | hypothetical protein Npun02002480 [Nostoc punctiforme PCC 73102] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---------------------------------------|--|--|--|----------|----------|
| 15885, 15886 | 46142567 | 34 | 2.00E-37 | Methanococcoides burtonii DSM 6242 | COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242] | | | | 2.1.1.73 |
| 15887, 15888 | 48853824 | 55 | 6.00E-80 | Cytophaga hutchinsonii | COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii] | | | | |
| 15889, 15890 | 48853824 | 56 | 9.00E-36 | Cytophaga hutchinsonii | COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii] ribonucleotide reductase (nrd) [Archaeoglobus fulgidus DSM 4304] gb AAB89584.1 ribonucleotide reductase (nrd) [Archaeoglobus fulgidus DSM 4304] pir G69457 ribonucleoside-diphosphate reductase (EC 1.17.4.1) large chain nrd - Archaeoglobus fulgidus | | | 1.17.4.1 | |
| 1589, 1590 | 11499254 | 35 | 1.00E-30 | Archaeoglobus fulgidus DSM 4304 | ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09403.1 ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wolinella succinogenes] | | | 1.8.-:- | |
| 15891, 15892 | 34556688 | 50 | 9.00E-26 | Wolinella succinogenes DSM 1740 | COG1011: Predicted hydrolase (HAD superfamily) [Cytophaga hutchinsonii] COG0542: ATPases with chaperone activity, ATP-binding subunit [Cytophaga hutchinsonii] | | | 3.8.1.2 | |
| 15893, 15894 | 48856129 | 39 | 5.00E-45 | Cytophaga hutchinsonii | hypothetical protein [Streptomyces avermitilis MA-4680] ref NP_823856.1 hypothetical protein SAV2480 [Streptomyces avermitilis MA-4680] | | | | |
| 15895, 15896 | 48854713 | 53 | 2.00E-45 | Streptomyces avermitilis MA-4680 | DNA polymerase I (polA) [Campylobacter coli RM2228] gb EAL56958.1 DNA polymerase I (polA) [Campylobacter coli RM2228] two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] dbj BAB81218.1 two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] PUTATIVE AMINOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10273.1 PUTATIVE AMINOTRANSFERASE [Wolinella succinogenes] | | | 2.7.7.7 | |
| 15897, 15898 | 29606128 | 40 | 1.00E-15 | Campylobacter coli RM2228 | COG0642: Signal transduction histidine kinase [Crocosphaera watsonii] WH 8501] | | | | |
| 15899, 15900 | 57168476 | 42 | 1.00E-56 | Clostridium perfringens str. 13 | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] hypothetical protein DP1552 [Desulfotalea psychrophila LSV54] emb CAG36281.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | | |
| 159, 160 | 18310494 | 31 | 1.00E-23 | Wolinella succinogenes DSM 1740 | GGDEF DOMAIN PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09494.1 GGDEF DOMAIN PROTEIN [Wolinella succinogenes] | | | | |
| 15901, 15902 | 34557558 | 53 | 1.00E-54 | Crocosphaera watsonii WH 8501 | | | | | |
| 15903, 15904 | 53734795 | 39 | 6.00E-43 | Cytophaga hutchinsonii | | | | | |
| 15907, 15908 | 48853652 | 28 | 3.00E-18 | Desulfotalea psychrophila LSV54 | | | | | |
| 15911, 15912 | 51245404 | 36 | 4.00E-20 | Wolinella succinogenes DSM 1740 | | | | | |
| 15913, 15914 | 34556779 | 35 | 4.00E-10 | | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|--|---|--|----|----------|----------|
| 15915, 15916 | AAW7148 1 | 46 | 3.00E-39 | | Desc:Helicobacter polypeptide GHPO 240. Org:Helicobacter pylori | | | | |
| | | | | | putative acetyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV79310.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] ref NP_807484.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi Ty2] ref NP_462554.1 putative acetyltransferase [Salmonella typhimurium LT2] ref NP_458272.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. CT18] gb AAL22513.1 putative acetyltransferase [Salmonella typhimurium LT2] gb AAO71344.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD07975.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi] pir JAC0981 probable acetyltransferase STY4148 [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) | | | 2.3.1.- | |
| 15917, 15918 | 56415547 | 48 | 3.00E-37 | Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150 | | | | | |
| 15921, 15922 | 53727492 | 51 | 3.00E-16 | Pseudomonas aeruginosa UC8PP-PA14 | COG2199: FOG: GGDEF domain [Pseudomonas aeruginosa UC8PP-PA14] | | | | 2.7.3.- |
| 15923, 15924 | 56470397 | 27 | 3.00E-07 | Entamoeba histolytica HM-1:IMSS | Viral A-type inclusion protein repeat, putative [Entamoeba histolytica HM-1:IMSS] | | | | |
| 15927, 15928 | 34557828 | 68 | 6.00E-46 | Wolinella succinogenes DSM 1740 | PUTATIVE CYTOCHROME C551 PEROXIDASE [Wolinella succinogenes DSM 1740] emb CAE10543.1 PUTATIVE CYTOCHROME C551 PEROXIDASE [Wolinella succinogenes] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 90 | 5.00E-12 | 1.11.1.5 |
| 15929, 15930 | 19704976 | 37 | 5.00E-09 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Hypothetical cytosolic protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93770.1 Hypothetical cytosolic protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | |
| 1593, 1594 | 42525090 | 44 | 4.00E-49 | Bdellovibrio bacteriovorus HD100 | Adventurous gliding motility protein R [Bdellovibrio bacteriovorus HD100] emb CAE81124.1 Adventurous gliding motility protein R [Bdellovibrio bacteriovorus HD100] | | | | 3.6.3.16 |
| 15933, 15934 | 57236934 | 42 | 8.00E-28 | Campylobacter jejuni RM1221 | RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221] gb AAW34517.1 RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221] | | | | 4.2.1.70 |
| 15935, 15936 | 57505678 | 32 | 1.00E-07 | Campylobacter upsaliensis RM3195 | conserved hypothetical protein [Campylobacter upsaliensis RM3195] gb EAL52739.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195] | | | | |

| | | | | | | | | |
|--|--|--|---|---|---|--|---------------------|---------------|
| 15937, 15938 15939, 15940 | 20805519 42453422 | 42 33 | 1.00E-42 2.00E-22 | Thermoanaerobacter tengcongensis MB4 Rickettsia rickettsii | Zn-dependent dipeptidase, microsomal dipeptidase homolog [Thermoanaerobacter tengcongensis MB4] COG223: Methionyl-tRNA formyltransferase [Rickettsia rickettsii] | | | 3.4.13.1 9 |
| 15941, 15942 15943, 15944 | 15614411 32262087 | 32 22 | 3.00E-09 7.00E-10 | Bacillus halodurans C-125 Helicobacter hepaticus ATCC 51449 | hypothetical protein BH1848 [Bacillus halodurans C-125] dbj BAB05567.1 BH1848 [Bacillus halodurans C-125] pir H83880 hypothetical protein hypothetical protein HH0539 [Helicobacter hepaticus ATCC 51449] ref NP_860070.1 hypothetical protein HH0539 [Helicobacter hepaticus ATCC 51449] | | | 2.1.2.9 |
| 15947, 15948 15949, 15950 1595, 1596 15951, 15952 15955, 15956 15957, 15958 15959, 15960 15961, 15962 | 57240977 57240598 29348750 57168666 53756870 48859576 48859576 13472651 | 63 27 33 55 35 29 24 32 | 1.00E-120 2.00E-09 3.00E-16 1.00E-53 6.00E-24 3.00E-22 2.00E-14 1.00E-11 | Campylobacter lari RM2100 Campylobacter lari RM2100 Bacteroides thetaiotaomicron VPI-5482 Campylobacter coli RM2228 Methylococcus capsulatus str. Bath Clostridium thermocellum ATCC 27405 Clostridium thermocellum ATCC 27405 Mesorhizobium loti MAFF303099 | DNA-directed RNA polymerase, beta subunit [Campylobacter lari RM2100] gb EAL55370.1 DNA-directed RNA polymerase, beta subunit [Campylobacter lari RM2100] probable periplasmic protein Cj0683 [Campylobacter lari RM2100] gb EAL55712.1 probable periplasmic protein Cj0683 [Campylobacter lari RM2100] hypothetical protein BT3341 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78447.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] molybdopterin cofactor biosynthesis protein A [Campylobacter coli RM2228] gb EAL56627.1 molybdopterin cofactor biosynthesis protein A [Campylobacter coli RM2228] hypothetical protein MCA2752 [Methylococcus capsulatus str. Bath] ref YP_115150.1 hypothetical protein MCA2752 [Methylococcus capsulatus str. Bath] COG1078: HD superfamily phosphohydrolases [Clostridium thermocellum ATCC 27405] COG1078: HD superfamily phosphohydrolases [Clostridium thermocellum ATCC 27405] 5'-nucleotidase [Mesorhizobium loti MAFF303099] dbj BAB50004.1 5'-nucleotidase [Mesorhizobium loti MAFF303099] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 84 6.00E-32 2.7.7.6 | 3.1.3.5 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--------------|----------|
| 15963, 15964 | 6968164 | 49 | 1.00E-67 | Campylobacter jejuni subsp. jejuni NCTC 11168 | 3-deoxy-D-manno-octulosonic-acid transferase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281879.1 3-deoxy-D-manno-octulosonic-acid transferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir F81341.3- deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38) Cj0707 [similarity] - Campylobacter jejuni (strain NCTC 11168) HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] emb CAE80147.1 HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] phosphoenolpyruvate synthase [Bacteroides fragilis YCH46] db BAD50376.1 phosphoenolpyruvate synthase [Bacteroides fragilis YCH46] | | | 2.4.99.- |
| 15965, 15966 | 42523774 | 34 | 9.00E-23 | Bdellovibrio bacteriovorus HD100 | | | | |
| 15967, 15968 | 53714918 | 49 | 3.00E-48 | Bacteroides fragilis YCH46 | | | | |
| 15969, 15970 | 20808872 | 29 | 9.00E-33 | Thermoanaerobact er tengcongensis MB4 | transposase [Thermoanaerobacter tengcongensis MB4] ref NP_623662.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM25647.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM25266.1 transposase [Thermoanaerobacter tengcongensis MB4] | | | |
| 15971, 15972 | 48859784 | 41 | 1.00E-59 | Clostridium thermocellum ATCC 27405 | COG0771: UDP-N-acetylmuramoylalanine-D-glutamate ligase [Clostridium thermocellum ATCC 27405] | | | 6.3.2.9 |
| 15973, 15974 | 42632042 | 39 | 5.00E-12 | Haemophilus influenzae R2866 | COG1708: Predicted nucleotidyltransferases [Haemophilus influenzae R2866] | | | |
| 15975, 15976 | 27466960 | 40 | 2.00E-17 | Staphylococcus epidermidis ATCC 12228 | abortive phage resistance protein [Staphylococcus epidermidis ATCC 12228] gb AAO03639.1 abortive phage resistance protein [Staphylococcus epidermidis ATCC 12228] db BAC67555.1 hypothetical protein [Staphylococcus aureus] gb AAQ18167.1 abortive phage resistance protein [Staphylococcus aureus] | | | |
| 15977, 15978 | 48858932 | 48 | 1.00E-38 | Clostridium thermocellum ATCC 27405 | COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | 2.7.3.- |
| 15979, 15980 | 34556843 | 39 | 1.00E-41 | Wolfinella succinogenes DSM 1740 | hypothetical protein WS0414 [Wolfinella succinogenes DSM 1740] emb CAE09558.1 conserved hypothetical protein [Wolfinella succinogenes] related to glycine cleavage system, T protein [Desulfotalea psychrophila LSv54] emb CAG35030.1 related to glycine cleavage system, T protein [Desulfotalea psychrophila LSv54] | | | 2.7.3.- |
| 15981, 15982 | 51244153 | 48 | 1.00E-42 | Desulfotalea psychrophila LSv54 | | | | 2.1.2.10 |
| 15983, 15984 | 51244152 | 65 | 5.00E-44 | Desulfotalea psychrophila LSv54 | probable glycine cleavage system, H protein [Desulfotalea psychrophila LSv54] emb CAG35029.1 probable glycine cleavage system, H protein [Desulfotalea psychrophila LSv54] | Desulfotalea psychrophila LSv54 chromosome | 84 9.00E-08 | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 15985, 15986 | 51244716 | 26 | 1.00E-20 | Desulfotalea psychrophila LSV54 | hypothetical protein DP0864 [Desulfotalea psychrophila LSV54] emb CAG35593.1 unknown protein [Desulfotalea psychrophila LSV54] | | | |
| 15989, 15990 | 29655303 | 40 | 2.00E-34 | Coxiella burnetii RSA 493 | hypothetical protein CBU2021 [Coxiella burnetii RSA 493] gb AAO91509.1 conserved hypothetical protein [Coxiella burnetii RSA 493] hypothetical protein RPA1515 [Rhodopseudomonas palustris CGA009] emb CAE26957.1 conserved unknown protein [Rhodopseudomonas palustris CGA009] | | | |
| 15991, 1600 | 39934587 | 21 | 7.00E-09 | Rhodopseudomonas palustris CGA009 | hypothetical protein aq_563 [Aquifex aeolicus VF5] gb AAC06808.1 hypothetical protein [Aquifex aeolicus VF5] pir G70350 conserved hypothetical protein aq_563 - Aquifex aeolicus | | | |
| 15993, 15994 | 15606018 | 32 | 3.00E-29 | Aquifex aeolicus VF5 | hypothetical protein all3839 [Nostoc sp. PCC 7120] pir AH2285 hypothetical protein all3839 [imported] - Nostoc sp. (strain PCC 7120) db BAB75538.1 all3839 [Nostoc sp. PCC 7120] | | | |
| 15995, 15996 | 17231331 | 25 | 2.00E-09 | Nostoc sp. PCC 7120 | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] guanylate kinase (GMP kinase) [Bacteroides thetaiotaomicron VPI-5482] gb AAO77116.1 guanylate kinase (GMP kinase) [Bacteroides thetaiotaomicron VPI-5482] sp Q8A677 KGUA_BACTN Guanylate kinase (GMP kinase) | | | 2.7.4.8 |
| 15997, 15998 | 29347419 | 53 | 2.00E-46 | Cytophaga hutchinsonii | COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Cytophaga hutchinsonii] | | | 1.7.99.4 |
| 15999, 16000 | 48855088 | 39 | 2.00E-13 | Bacteroides thetaiotaomicron VPI-5482 | sensor histidine kinase/response regulator [Bdellovibrio bacteriovorus HD100] emb CAE80630.1 sensor histidine kinase/response regulator [Bdellovibrio bacteriovorus HD100] | | | |
| 16001, 16002 | 42524257 | 33 | 2.00E-07 | Bdellovibrio bacteriovorus HD100 | hypothetical protein BF0014 [Bacteroides fragilis YCH46] db BAD46763.1 conserved hypothetical protein [Bacteroides fragilis YCH46] CTP synthase [Chlorobium tepidum TLS] gb AAM71390.1 CTP synthase [Chlorobium tepidum TLS] sp P59040 PYRG_CHLTE CTP synthase (UTP- ammonia ligase) (CTP synthetase) | | | 6.3.4.2 |
| 16005, 16006 | 53711305 | 31 | 1.00E-20 | Bacteroides fragilis YCH46 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861188.1 hypothetical protein HH1657 [Helicobacter hepaticus ATCC 51449] | | | 2.7.3.- |
| 16007, 16008 | 21672983 | 58 | 3.00E-48 | Chlorobium tepidum TLS | COG0657: Esterase/lipase [Microbulifer degradans 2-40] dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46097.1 dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis] gb AAS60264.1 sugar dehydratase [Francisella tularensis subsp. tularensis] | | | 4.2.1.- |
| 16009, 16010 | 32263209 | 33 | 3.00E-28 | Helicobacter hepaticus ATCC 51449 | | | | |
| 1601, 1602 | 48863777 | 44 | 2.00E-14 | Microbulifer degradans 2-40 | | | | |
| 16011, 16012 | 56708505 | 43 | 1.00E-59 | Francisella tularensis subsp. tularensis Schu 4 | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|----------|
| 16013, 16014 | 56708505 | 66 | 2.00E-94 | Francisella tularensis subsp. tularensis Schu 4 | dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46097.1 dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis] gb AAS60264.1 sugar dehydratase [Francisella tularensis subsp. tularensis] | Francisella tularensis subsp. tularensis insertion sequence ISFtu2 and O-antigen gene cluster, complete sequence | 83 | 2.00E-09 | 4.2.1.- |
| 16023, 16024 | 52550245 | 23 | 2.00E-07 | uncultured archaeon GZfos37B2 | hypothetical protein GZ37B2_1 [uncultured archaeon GZfos37B2] | | | | |
| 16025, 16026 | 1722856 | 24 | 1.00E-06 | | Structural maintenance of chromosome 2 (Chromosome-associated protein E) (Chromosome assembly protein XCAP-E) pir B55094 chromosomal protein XCAP-E - African clawed frog gb AA64680.1 XCAP-E | | | | |
| 16027, 16028 | 34556560 | 37 | 2.00E-36 | Wollinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes] | | | | 2.7.3.- |
| 16029, 16030 | 34556560 | 45 | 3.00E-68 | Wollinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes] | | | | |
| 1603, 1604 | 48855850 | 30 | 2.00E-15 | Cytophaga hutchinsonii | hypothetical protein Chut02001063 [Cytophaga hutchinsonii] | | | | |
| 16031, 16032 | 34557923 | 38 | 3.00E-25 | Wollinella succinogenes DSM 1740 | UROPOPHYRINOGEN III COSYNTHASE (HEMD) [Wollinella succinogenes DSM 1740] emb CAE10638.1 UROPOPHYRINOGEN III COSYNTHASE (HEMD) [Wollinella succinogenes] | | | | 4.2.1.75 |
| 16033, 16034 | 34557752 | 56 | 4.00E-14 | Wollinella succinogenes DSM 1740 | hypothetical protein WS1402 [Wollinella succinogenes DSM 1740] emb CAE10467.1 hypothetical protein [Wollinella succinogenes] | | | | |
| 16035, 16036 | 41722689 | 38 | 8.00E-36 | Dechloromonas aromatica RCB | COG0426: Uncharacterized flavoproteins [Dechloromonas aromatica RCB] | | | | |
| 16037, 16038 | 28974233 | 53 | 2.00E-50 | Campylobacter fetus | hypothetical protein C00333 [Campylobacter fetus] | | | | |
| 16039, 16040 | 28974233 | 43 | 4.00E-41 | Campylobacter fetus | hypothetical protein C00333 [Campylobacter fetus] | | | | |
| 16041, 16042 | 34557958 | 44 | 2.00E-51 | Wollinella succinogenes DSM 1740 | FLAGELLAR BIOSYNTHESIS PROTEIN FLHF FLAGELLA ASSOCIATED GTP-BINDINGPROTEIN [Wollinella succinogenes DSM 1740] emb CAE10673.1 FLAGELLAR BIOSYNTHESIS PROTEIN FLHF FLAGELLA ASSOCIATED GTP-BINDINGPROTEIN [Wollinella succinogenes] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|---|----|----------|----------|
| 16045, 16046 | 48860009 | 50 | 3.00E-81 | Clostridium thermocellum ATCC 27405 | COG0696: Phosphoglyceromutase [Clostridium thermocellum ATCC 27405] | Desc: Mycoplasma genitalium genome. Org: Mycoplasma genitalium | 93 | 8.00E-07 | 5.4.2.1 |
| 16047, 16048 | 2128139 | 33 | 7.00E-10 | | hypothetical protein MJ0126 - Methanococcus jannaschii | | | | 2.7.7.- |
| 16049, 16050 | 20090160 | 30 | 1.00E-11 | Methanosarcina acetivorans C2A | hypothetical protein MA1296 [Methanosarcina acetivorans C2A] gb AA04715.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] sp Q8TR85 YC96_METAC Hypothetical UPF0331 protein MA1296 | | | | 2.7.7.- |
| 1605, 1606 | 48855574 | 37 | 2.00E-16 | Cytophaga hutchinsonii | COG0782: Transcription elongation factor [Cytophaga hutchinsonii] | | | | |
| 16051, 16052 | 34557570 | 54 | 2.00E-87 | Wolinella succinogenes DSM 1740 | GLUTAMATE SYNTHASE SMALL CHAIN [Wolinella succinogenes DSM 1740] emb CAE10285.1 GLUTAMATE SYNTHASE SMALL CHAIN [Wolinella succinogenes] | | | | 1.4.1.13 |
| 16053, 16054 | 29346178 | 37 | 4.00E-15 | Bacteroides thetaiotaomicron VPI-5482 | putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482] gb AAO75875.1 putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.--- |
| 16055, 16056 | 34557268 | 65 | 5.00E-49 | Wolinella succinogenes DSM 1740 | TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09983.1 TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wolinella succinogenes] | | | | |
| 16057, 16058 | 26991094 | 42 | 3.00E-56 | Pseudomonas putida KT2440 | sensory box protein [Pseudomonas putida KT2440] gb AAN69983.1 sensory box protein [Pseudomonas putida KT2440] | | | | 2.7.3.- |
| 16059, 16060 | 23129412 | 26 | 2.00E-18 | Nostoc punctiforme PCC 73102 | COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 16061, 16062 | 48860427 | 49 | 2.00E-38 | Clostridium thermocellum ATCC 27405 | COG1052: Lactate dehydrogenase and related dehydrogenases [Clostridium thermocellum ATCC 27405] | | | | 1.1.1.95 |
| 16067, 16068 | 50084270 | 75 | 1.00E-56 | Acinetobacter sp. ADP1 | cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyrinic acid synthase | | | | 3.--- |
| 16069, 16070 | 57241466 | 67 | 7.00E-40 | Campylobacter lari RM2100 | beta-ketoacyl-acc synthase III [Campylobacter lari RM2100] gb EAL54578.1 beta-ketoacyl-acc synthase III [Campylobacter lari RM2100] | | | | 2.3.1.41 |
| 16071, 16072 | 29349736 | 50 | 1.00E-38 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT4328 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79433.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|-------------|----------|
| 16073, 16074 | 48861626 | 28 | 1.00E-32 | Microbulbifer degradans 2-40 | COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40] | | | 2.7.3.- |
| 16075, 16076 | 13516917 | 26 | 1.00E-19 | Myxococcus xanthus | hybrid sensor [Myxococcus xanthus] | | | |
| 16077, 16078 | 34398055 | 73 | 8.00E-50 | Porphyromonas gingivalis W83 | glycyl-tRNA synthetase [Porphyromonas gingivalis W83] ref[NP_906216.1] | | | |
| 16079, 16080 | 29349019 | 71 | 1.00E-87 | Bacteroides thetaiotaomicron VPI-5482 | glycyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78716.1 glycyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] | Myroides odoratimimus metallo-beta- lactamase (MUS-1) gene, complete cds | 88 2.00E-30 | 6.1.1.14 |
| 16081, 16082 | 32262994 | 42 | 3.00E-41 | Helicobacter hepaticus ATCC 51449 | putative endonuclease [Helicobacter hepaticus ATCC 51449] ref[NP_860974.1] putative endonuclease [Helicobacter hepaticus ATCC 51449] | | | 6.1.1.14 |
| 16083, 16084 | 34557543 | 36 | 8.00E-50 | Wolinella succinogenes DSM 1740 | PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10258.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] emb CAD5552.1 NapL protein [Wolinella succinogenes] | | | |
| 16085, 16086 | 34556868 | 28 | 3.00E-17 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0441 [Wolinella succinogenes DSM 1740] emb CAE09583.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 16089, 16090 | 53728999 | 29 | 1.00E-15 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | COG0419: ATPase involved in DNA repair [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | |
| 16093, 16094 | 54308776 | 33 | 4.00E-07 | Photobacterium profundum SS9 | hypothetical protein PBPRA1583 [Photobacterium profundum SS9] emb CAG19994.1 hypothetical protein [Photobacterium profundum] | | | |
| 16095, 16096 | 29346283 | 41 | 2.00E-58 | Bacteroides thetaiotaomicron VPI-5482 | putative sulfatase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75980.1 putative sulfatase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 16101, 16102 | 27365538 | 27 | 1.00E-22 | Vibrio vulnificus CMCP6 | hypothetical protein VV12211 [Vibrio vulnificus CMCP6] gb AAO10593.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] | | | 2.7.3.- |
| 16103, 16104 | 39996209 | 44 | 1.00E-33 | Geobacter sulfurreducens PCA | conserved hypothetical protein TIGR00296 [Geobacter sulfurreducens PCA] gb AAR34433.1 conserved hypothetical protein TIGR00296 [Geobacter sulfurreducens PCA] | | | |
| 16109, 16110 | 34558474 | 42 | 5.00E-63 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2199 [Wolinella succinogenes DSM 1740] emb CAE11189.1 conserved hypothetical protein [Wolinella succinogenes] | | | |

| | | | | | | | | | |
|-----------------|--------------|----|-----------|---|--|---|----|----------|----------|
| 1611, 1612 | 48854837 | 37 | 2.00E-31 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | | |
| 16115, 16116 | 34556483 | 63 | 1.00E-112 | Wolinella succinogenes DSM 1740 | PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolinella succinogenes DSM 1740] embjCAE09198.1 PUTATIVE UDP- GLUCURONIC ACID EPIMERASE [Wolinella succinogenes] hypothetical protein sir1575 [Synecocystis sp. PCC 6803] dbj BAA18716.1 sir1575 [Synecocystis sp. PCC 6803] pir S76804 hypothetical protein - Synecocystis sp. (strain PCC 6803) | B.thuringiensis PK1 & cap genes, putative | 85 | 3.00E-18 | 5.1.3.- |
| 16117, 16118 | 16332176 | 26 | 4.00E-08 | Synechocystis sp. PCC 6803 | probable oxidoreductase [Sinorhizobium meliloti 1021] gb AAK65774.1 probable oxidoreductase [Sinorhizobium meliloti 1021] pir D95401 probable oxidoreductase Sma2041 [Imported] - Sinorhizobium meliloti (strain 1021) | | | | |
| 16121, 16122 | 16263569 | 36 | 5.00E-24 | Sinorhizobium meliloti 1021 | magaplasmid pSymA | | | | 1.2.99.2 |
| 16125, 16126 | 39997114 | 52 | 8.00E-55 | Geobacter sulfurreducens PCA | sensory box/GGDEF family protein [Geobacter sulfurreducens PCA] gb AAR35392.1 sensory box/GGDEF family protein [Geobacter sulfurreducens PCA] | | | | 2.7.3.- |
| 16127, 16128 | 37677003 | 24 | 8.00E-15 | Vibrio vulnificus YJ016 | hypothetical protein VVA1343 [Vibrio vulnificus YJ016] dbj BAC97369.1 conserved hypothetical protein [Vibrio vulnificus YJ016] | | | | |
| 16129, 16130 | AAB5259 6 | 28 | 5.00E-18 | Thermotoga maritima MSB8 | Desc:Helicobacter pylori bait polypeptide #114. Org:Helicobacter pylori | | | | |
| 1613, 1614 | 15644379 | 38 | 1.00E-09 | Thermoanaerobact er tengcongensis MB4 | hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD36698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | | 3.1.11.5 |
| 16133, 16134 | 20806994 | 33 | 2.00E-26 | Leptospira interrogans serovar Lai str. 56601 | ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Thermoanaerobacter tengcongensis MB4] gb AAM23769.1 ATP-dependent exoDNase (exonuclease V), alpha subunit helicase superfamily I member [Thermoanaerobacter tengcongensis MB4] | | | | |
| 16135, 16136 | 24214122 | 37 | 4.00E-30 | Leptospira interrogans serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] | | | | |
| 16137, 16138 | 57240902 | 50 | 1.00E-26 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55295.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---------------------------------------|---|--|----|-------------------|
| 16139, 16140 | 21228703 | 28 | 4.00E-18 | [Methanosarcina mazel Go1] | Zinc metalloprotease [Methanosarcina mazel Go1] gb AAM32297.1 Zinc metalloprotease [Methanosarcina mazel Go1] | | | 3.4.24.- |
| 16141, 16142 | 23098814 | 55 | 2.00E-26 | Oceanobacillus theysensis HTE831 | truncated nitrogen fixation positive activator [Oceanobacillus theysensis HTE831] dbj BAC13315.1 nitrogen fixation positive activator (partial) | | | |
| 16145, 16146 | 21885306 | 44 | 6.00E-18 | Vibrio cholerae | unknown [Vibrio cholerae] | | | 3.1.21.- |
| 16149, 16150 | 34556927 | 59 | 1.00E-69 | Wolinella succinogenes DSM 1740 | PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09642.1 PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes] | | | |
| 1615, 1616 | 48854579 | 38 | 2.00E-12 | Cytophaga hutchinsonii | hypothetical protein Chut0202781 [Cytophaga hutchinsonii] | | | |
| 16151, 16152 | 30249180 | 51 | 1.00E-22 | Nitrosomonas europaea ATCC 19718 | ATPase component ABC-type nitrate transport system [Nitrosomonas europaea ATCC 19718] emb CAD85106.1 ATPase component ABC-type nitrate transport system [Nitrosomonas europaea ATCC 19718] | | | |
| 16153, 16154 | 29347576 | 45 | 4.00E-61 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77273.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.3.- |
| 16155, 16156 | 34558820 | 57 | 3.00E-53 | Alvinella pompejana epibiont 7G3 | NAD(P)H-flavin oxidoreductase [Alvinella pompejana epibiont 7G3] | | | 1.-.-.- |
| 16157, 16158 | 46142136 | 37 | 2.00E-23 | Methanococcoides burtonii DSM 6242 | COG5002: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242] | | | 2.7.3.- |
| 16163, 16164 | 24373111 | 92 | 1.00E-46 | Shewanella oneidensis MR-1 | isocitrate dehydrogenase, NAD-dependent [Shewanella oneidensis MR-1] gb AAN54598.1 isocitrate dehydrogenase, NAD-dependent [Shewanella oneidensis MR-1] | Shewanella oneidensis MR-1 section 148 of 457 of the complete genome | 80 | 1.00E-27 1.1.1.41 |
| 16165, 16166 | 48854568 | 31 | 9.00E-19 | Cytophaga hutchinsonii | COG0849: Actin-like ATPase involved in cell division [Cytophaga hutchinsonii] | | | |
| 16167, 16168 | 53715653 | 37 | 2.00E-21 | Bacteroides fragilis YCH46 | hypothetical protein BF4373 [Bacteroides fragilis YCH46] dbj BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 1617, 1618 | 48853807 | 43 | 3.00E-60 | Cytophaga hutchinsonii | COG0793: Periplasmic protease [Cytophaga hutchinsonii] | | | 3.4.21.- |
| 16171, 16172 | 51244492 | 27 | 4.00E-08 | Desulfotalea psychrophila LSv54 | hypothetical membrane protein (BatD) [Desulfotalea psychrophila LSv54] emb CAG35369.1 hypothetical membrane protein (BatD) [Desulfotalea psychrophila LSv54] | | | |
| 16175, 16176 | 48861337 | 33 | 3.00E-07 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02003513 [Microbulbifer degradans 2-40] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|----|----------|----------|
| 16177, 16178 | 38482512 | 44 | 1.00E-27 | Photobacterium luminescens | putative toxin transporter [Photobacterium luminescens] hypothetical protein aq_563 [Aquifex aeolicus VF5] gb AAC06808.1 | | | | |
| 16179, 16180 | 15606018 | 34 | 1.00E-47 | Aquifex aeolicus VF5 | hypothetical protein [Aquifex aeolicus VF5] pir G70350 conserved hypothetical protein aq_563 - Aquifex aeolicus | | | | 2.7.3.- |
| 16187, 16188 | 48845132 | 44 | 2.00E-39 | Geobacter metallireducens GS-15 | COG0643: Chemotaxis protein histidine kinase and related kinases [Geobacter metallireducens GS-15] | | | | 2.7.3.- |
| 16189, 16190 | 34557884 | 52 | 1.00E-16 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE [Wolinella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolinella succinogenes] | | | | 2.7.3.- |
| 16191, 16192 | 6968929 | 41 | 1.00E-52 | Campylobacter jejuni subsp. jejuni NCTC 11168 | putative selenide,water dikinase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir D81297 probable selenide, water dikinase (EC 2.7.9.3) Cj1504c [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282641.1 putative selenide,water dikinase [Campylobacter jejuni subsp. jejuni NCTC 11168] | | | | 2.7.9.3 |
| 16197, 16198 | 48730848 | 48 | 1.00E-24 | Pseudomonas fluorescens PfO-1 | hypothetical protein Pflu02002728 [Pseudomonas fluorescens PfO-1] | | | | |
| 16199, 16200 | 47527379 | 25 | 1.00E-09 | Bacillus anthracis str. 'Ames Ancestor' | acetyltransferase, gnat family [Bacillus anthracis str. 'Ames Ancestor'] ref YP_028202.1 acetyltransferase, GNAT family [Bacillus anthracis str. Sterne] ref NP_844486.1 acetyltransferase, GNAT family [Bacillus anthracis str. Ames] ref NP_655942.1 Acetyltransf. Acetyltransferase (GNAT) family [Bacillus anthracis str. A2012] gb AAP25972.1 acetyltransferase, GNAT family [Bacillus anthracis str. Ames] gb AAT31203.1 acetyltransferase, GNAT family [Bacillus anthracis str. 'Ames Ancestor'] gb AAT54253.1 acetyltransferase, GNAT family [Bacillus anthracis str. Sterne] | | | | 2.7.3.- |
| 16201, 16202 | 53730018 | 44 | 2.00E-52 | Dechloromonas aromatica RCB | COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB] | | | | |
| 16203, 16204 | 29347584 | 45 | 8.00E-49 | Bacteroides thetaitaomicron VPI-5482 | ABC transporter ATP-binding protein [Bacteroides thetaitaomicron VPI- 5482] gb AAO77281.1 ABC transporter ATP-binding protein [Bacteroides thetaitaomicron VPI-5482] | | | | 1.8.- |
| 16205, 16206 | 51246820 | 65 | 9.00E-92 | Desulfotalea psychrophila Lsv54 | probable 2-isopropylmalate synthase [Desulfotalea psychrophila Lsv54] emb CAG37497.1 probable 2-isopropylmalate synthase [Desulfotalea psychrophila Lsv54] | Desulfotalea psychrophila Lsv54 chromosome | 94 | 2.00E-19 | 4.1.3.12 |
| 16207, 16208 | 46201501 | 33 | 8.00E-19 | Magnetospirillum magnetotacticum MS-1 | COG2208: Serine phosphatase RsbU, regulator of sigma subunit [Magnetospirillum magnetotacticum MS-1] | | | | |
| 1621, 1622 | 48854610 | 39 | 1.00E-18 | Cytophaga hutchinsonii | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|---------|
| 16211, 16212 | 39997484 | 31 | 1.00E-19 | Geobacter sulfurreducens PCA | ABC transporter, periplasmic substrate-binding protein, putative [Geobacter sulfurreducens PCA] gbJAAR35762.1 ABC transporter, periplasmic substrate-binding protein, putative [Geobacter sulfurreducens PCA] | | | | |
| 16215, 16216 | 48846045 | 39 | 3.00E-15 | Geobacter metallireducens GS-15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] DNA repair protein RecN [Treponema denticola ATCC 35405] gbJAAS11818.1 DNA repair protein RecN [Treponema denticola ATCC 35405] | | | | 2.7.3.- |
| 16219, 16220 | 42526809 | 32 | 4.00E-34 | Treponema denticola ATCC 35405 | | | | | |
| 16223, 16224 | 34558828 | 23 | 8.00E-18 | Alvinella pompejana epibiont 7G3 | KIAA1005 protein [Alvinella pompejana epibiont 7G3] | | | | |
| 16225, 16226 | 34558828 | 28 | 3.00E-17 | Alvinella pompejana epibiont 7G3 | KIAA1005 protein [Alvinella pompejana epibiont 7G3] | | | | |
| 16227, 16228 | 15643985 | 44 | 3.00E-69 | Thermotoga maritima MSB8 | hypothetical protein TM1229 [Thermotoga maritima MSB8] gbJAAD36304.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir F72278 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | | |
| 16229, 16230 | 56460387 | 49 | 5.00E-67 | Idiomarina loihlensis L2TR | NAD-specific glutamate dehydrogenase [Idiomarina loihlensis L2TR] gb AAV82119.1 NAD-specific glutamate dehydrogenase [Idiomarina loihlensis L2TR] | | | | 1.4.1.2 |
| 1623, 1624 | 40556689 | 27 | 1.00E-09 | Bacillus cereus Wolfinella succinogenes DSM 1740 | putative peptide synthetase/polyketide synthase [Bacillus cereus] PUTATIVE TWO-COMPONENT SENSOR [Wolfinella succinogenes DSM 1740] emb CAE09456.1 PUTATIVE TWO-COMPONENT SENSOR [Wolfinella succinogenes] | | | | |
| 16231, 16232 | 34556741 | 45 | 2.00E-67 | Mimivirus | DNA mismatch repair ATPase MutS [Mimivirus] gb AAV50628.1 DNA mismatch repair ATPase MutS [Mimivirus] | | | | 2.7.3.- |
| 16235, 16236 | 55819234 | 26 | 9.00E-28 | Bacteroides thetaiotaomicron VPI-5482 | putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO78738.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 16237, 16238 | 29349041 | 30 | 3.00E-10 | Bacteroides thetaiotaomicron VPI-5482 | primosomal protein N' (replication factor Y) [Bacteroides thetaiotaomicron VPI-5482] gb AAO77858.1 primosomal protein N' (replication factor Y) [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 16239, 16240 | 29348161 | 47 | 9.00E-21 | Photobacterium luminescens subsp. laumondii TTO1 | Transposase, IS30 family [Photobacterium luminescens subsp. laumondii TTO1] emb CAE15390.1 Transposase, IS30 family [Photobacterium luminescens subsp. laumondii TTO1] | | | | |
| 16241, 16242 | 37526904 | 51 | 6.00E-27 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--------------|----------|
| 16243, 16244 | 57241555 | 35 | 2.00E-38 | Campylobacter lari RM2100 | lipopolysaccharide heptosyltransferase-1 (rfc) [Campylobacter lari RM2100] gb EAL54667.1 lipopolysaccharide heptosyltransferase-1 (rfc) [Campylobacter lari RM2100] | | | 2.4.1.- |
| 16247, 16248 | 57237448 | 56 | 2.00E-95 | Campylobacter jejuni RM1221 | malate:quinone oxidoreductase, putative [Campylobacter jejuni RM1221] gb AAW35031.1 malate:quinone oxidoreductase, putative [Campylobacter jejuni RM1221] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 86 1.00E-146 | 1.1.99.1 |
| 16249, 16250 | 53713571 | 29 | 3.00E-22 | Bacteroides fragilis YCH46 | putative outer membrane protein [Bacteroides fragilis YCH46] db BAD49029.1 putative outer membrane protein [Bacteroides fragilis YCH46] | | | 2.7.7.7 |
| 1625, 1626 | 48853082 | 31 | 2.00E-14 | Ferroplasma acidarmanus | COG0417: DNA polymerase elongation subunit (family B) [Ferroplasma acidarmanus] | | | 2.4.1.83 |
| 16251, 16252 | 53714415 | 69 | 3.00E-93 | Bacteroides fragilis YCH46 | dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] db BAD49873.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] | | | |
| 16253, 16254 | 53756578 | 38 | 4.00E-39 | Methylococcus capsulatus str. Bath | conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_115444.1 hypothetical protein MCA3057 [Methylococcus capsulatus str. Bath] | | | |
| 16257, 16258 | 34557072 | 34 | 5.00E-10 | Wolinella succinogenes DSM 1740 | TWO COMPONENT RESPONSE REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09787.1 TWO COMPONENT RESPONSE REGULATOR [Wolinella succinogenes] | | | |
| 16263, 16264 | 53713669 | 33 | 2.00E-10 | Bacteroides fragilis YCH46 | hypothetical protein BF2378 [Bacteroides fragilis YCH46] db BAD49127.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 16265, 16266 | 29348287 | 61 | 1.00E-30 | Bacteroides thetaiotaomicron VPI-5482 | putative translation initiation factor SU1 [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78984.1 putative translation initiation factor SU1 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 16267, 16268 | 53713299 | 58 | 5.00E-61 | Bacteroides fragilis YCH46 | putative aminopeptidase C [Bacteroides fragilis YCH46] db BAD48757.1 putative aminopeptidase C [Bacteroides fragilis YCH46] | | | 3.4.22.- |
| 16269, 16270 | 48856607 | 57 | 1.00E-49 | Cytophaga hutchinsonii | COG1321: Mn-dependent transcriptional regulator [Cytophaga hutchinsonii] bacterial signal domain protein [Geobacter sulfurreducens PCA] | | | |
| 1627, 1628 | 39996651 | 26 | 3.00E-22 | Geobacter sulfurreducens PCA | gb AAR34925.1 bacterial signal domain protein [Geobacter sulfurreducens PCA] | | | 3.1.3.16 |
| 16271, 16272 | 28974235 | 41 | 3.00E-46 | Campylobacter fetus | putative putative two-component sensor Cf0035 [Campylobacter fetus] | | | 2.7.3.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 16275, 16276 | 45657982 | 46 | 9.00E-21 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | sugar transferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_711831.1 hemolysin hemolytic protein hlpA [Leptospira interrogans serovar Lai str. 56601] gb AA048849.1 hemolysin hemolytic protein hlpA [Leptospira interrogans serovar lai str. 56601] gb AAK19900.1 unknown [Leptospira interrogans] gb AAD52178.1 unknown [Leptospira interrogans] gb AAS70705.1 sugar transferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | |
| 16277, 16278 | 46580432 | 28 | 2.00E-24 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | hypothetical protein DVU2025 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96500.1 conserved hypothetical protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 16279, 16280 | 41720084 | 50 | 4.00E-54 | Methanococcoides burtonii DSM 6242 | COG2865: Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen [Methanococcoides burtonii DSM 6242] | | | |
| 16281, 16282 | 15826957 | 32 | 2.00E-17 | Mycobacterium leprae TN | hypothetical protein ML0126 [Mycobacterium leprae TN] emb CAC29634.1 hypothetical protein [Mycobacterium leprae] pir F86924 hypothetical protein [imported] - Mycobacterium leprae | | | |
| 16283, 16284 | 22298538 | 36 | 1.00E-09 | Thermosynechococcus elongatus BP-1 | putative glycosyl transferase [Thermosynechococcus elongatus BP-1] db BAC08547.1 gi0995 [Thermosynechococcus elongatus BP-1] | | | |
| 1629, 1630 | 48861626 | 46 | 2.00E-38 | Microbulbifer degradans 2-40 | COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40] | | | 3.1.21.3 |
| 16295, 16296 | 24461248 | 54 | 4.00E-22 | Lactobacillus sakei | HsdS [Lactobacillus sakei] ref NP_862273.1 HsdS [Lactobacillus sakei] | | | |
| 16299, 16300 | 34557975 | 49 | 9.00E-61 | Wolinella succinogenes DSM 1740 | AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes] | | | |
| 16301, 16302 | 40063094 | 48 | 6.00E-77 | uncultured bacterium 561 | Polysphosphate kinase [uncultured bacterium 561] | | | 2.7.4.1 |
| 16303, 16304 | 29346970 | 57 | 5.00E-71 | Bacteroides thetaiotaomicron VPI-5482 | nicotinate-nucleotide pyrophosphorylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76667.1 nicotinate-nucleotide pyrophosphorylase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.4.2.19 |
| 16305, 16306 | 34556546 | 53 | 2.00E-80 | Wolinella succinogenes DSM 1740 | LIN1802 PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09261.1 LIN1802 PROTEIN [Wolinella succinogenes] | | | |
| 16307, 16308 | 41725785 | 40 | 1.00E-29 | Dechloromonas aromatica RCB | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Dechloromonas aromatica RCB] | | | 2.7.3.- |

| | | | | | | | | | |
|-----------------|---------------|----|----------|---|---|--|--|--|----------|
| 16308, 16310 | 29349346 | 35 | 1.00E-28 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 1631, 1632 | 48733660 | 51 | 9.00E-57 | Pseudomonas fluorescens PFO-1 | COG1638: TRAP-type C4-dicarboxylate transport system, periplasmic component [Pseudomonas fluorescens PFO-1] | | | | |
| 16311, 16312 | 15602874 | 64 | 4.00E-53 | Pasteurella multocida subsp. multocida str. Pm70 | WbjD [Pasteurella multocida subsp. multocida str. Pm70] gb AAK03093.1 WbjD [Pasteurella multocida subsp. multocida str. Pm70] | | | | 5.1.3.14 |
| 16313, 16314 | AAAY4377 4 | 56 | 2.00E-22 | | Desc:Amino acid sequence of eps8 of Streptococcus thermophilus Sfi39. Org:Streptococcus thermophilus | | | | 2.--- |
| 16315, 16316 | 34557838 | 65 | 3.00E-84 | Wolinella succinogenes DSM 1740 | QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes] | | | | |
| 16317, 16318 | 42526943 | 35 | 1.00E-41 | Treponema denticola ATCC 35405 | hypothetical protein TDE1435 [Treponema denticola ATCC 35405] gb AAS11952.1 hypothetical protein TDE1435 [Treponema denticola ATCC 35405] | | | | |
| 16319, 16320 | 53712204 | 71 | 6.00E-81 | Bacteroides fragilis YCH46 | putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides fragilis YCH46] dbj BAD47662.1 putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides fragilis YCH46] | | | | 6.3.3.1 |
| 16321, 16322 | 48733100 | 27 | 1.00E-30 | Pseudomonas fluorescens PFO-1 | COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Pseudomonas fluorescens PFO-1] | | | | |
| 16323, 16324 | 53711799 | 40 | 1.00E-37 | Bacteroides fragilis YCH46 | putative protoporphyrinogen oxidase [Bacteroides fragilis YCH46] dbj BAD47257.1 putative protoporphyrinogen oxidase [Bacteroides fragilis YCH46] | | | | 2.1.1.- |
| 16327, 16328 | 57168512 | 52 | 3.00E-54 | Campylobacter coli RM2228 | phosphoglycerate dehydrogenase [Campylobacter coli RM2228] gb EAL56694.1 phosphoglycerate dehydrogenase [Campylobacter coli RM2228] | | | | 1.1.1.95 |
| 16331, 16332 | 51246430 | 58 | 3.00E-73 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2578 [Desulfotalea psychrophila LSV54] emb CAG37307.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | | 1.6.5.3 |
| 16335, 16336 | 57241512 | 31 | 3.00E-22 | Campylobacter lari RM2100 | probable periplasmic protein Cj1289 [Campylobacter lari RM2100] gb EAL54624.1 probable periplasmic protein Cj1289 [Campylobacter lari RM2100] | | | | |
| 16337, 16338 | 33862569 | 36 | 7.00E-10 | Prochlorococcus marinus str. MIT 9313 | TPR repeat [Prochlorococcus marinus str. MIT 9313] emb CAE20471.1 TPR repeat [Prochlorococcus marinus str. MIT 9313] | | | | |
| 16341, 16342 | 57241555 | 38 | 8.00E-55 | Campylobacter lari RM2100 | lipopolysaccharide heptosyltransferase-1 (rfuC) [Campylobacter lari RM2100] gb EAL54667.1 lipopolysaccharide heptosyltransferase-1 (rfuC) [Campylobacter lari RM2100] | | | | 2.4.1.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|--|
| 16343, 16344 | 24216023 | 42 | 1.00E-13 | Leptospira interrogans serovar Lai str. 56601 | Leucine-rich repeat containing protein [Leptospira interrogans serovar Lai str. 56601] [Leptospira interrogans serovar lai str. 56601] | | | | |
| 16347, 16348 | 34556857 | 65 | 3.00E-68 | Wolinella succinogenes DSM 1740 | DNA POLYMERASE I [Wolinella succinogenes DSM 1740] emb CAE09572.1 DNA POLYMERASE I [Wolinella succinogenes] | | | 2.7.7.7 | |
| 1635, 1636 | 53711474 | 43 | 2.00E-32 | Bacteroides fragilis YCH46 | hypothetical protein BF0183 [Bacteroides fragilis YCH46] dbj BAD46932.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 16351, 16352 | 54293057 | 47 | 1.00E-49 | Legionella pneumophila str. Lens | hypothetical protein lpi0094 [Legionella pneumophila str. Lens] emb CAH14324.1 hypothetical protein [Legionella pneumophila str. Lens] | | | 3.1.3.5 | |
| 16353, 16354 | 34557014 | 43 | 6.00E-57 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0597 [Wolinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wolinella succinogenes] conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_902615.1 hypothetical protein CV2945 [Chromobacterium violaceum ATCC 12472] | | | | |
| 16355, 16356 | 34104254 | 37 | 2.00E-56 | Rhodopirellula baltica SH 1 | putative Na(+)-linked D-alanine glycine permease [Rhodopirellula baltica SH 1] emb CAD76934.1 putative Na(+)-linked D-alanine glycine permease [Pirellula sp.] | | | | |
| 16357, 16358 | 32476567 | 61 | 6.00E-53 | Bacteroides fragilis YCH46 | hypothetical protein BF0448 [Bacteroides fragilis YCH46] dbj BAD47197.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 16359, 16360 | 53711739 | 24 | 1.00E-06 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | COG1123: ATPase components of various ABC-type transport systems, contain duplicated ATPase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | 1.8.-.- | |
| 16363, 16364 | 32033790 | 33 | 5.00E-26 | Thiocapsa roseopersicina | HoxY [Thiocapsa roseopersicina] | | | 1.12.-.- | |
| 16365, 16366 | 37787354 | 48 | 2.00E-42 | Clostridium acetobutylicum ATCC 824 | FerriC uptake regulator (FUR family), YGAG B. subtilis ortholog [Clostridium acetobutylicum ATCC 824] gb AAK80581.1 FerriC uptake regulator (FUR family), YGAG B. subtilis ortholog [Clostridium acetobutylicum ATCC 824] pir B97224 ferriC uptake regulator (FUR family), YGAG B. subtilis ortholog [Imported] - Clostridium acetobutylicum | | | | |
| 16367, 16368 | 15895892 | 39 | 3.00E-17 | Pseudomonas putida KT2440 | hypothetical protein PP1921 [Pseudomonas putida KT2440] gb AAAN67538.1 hypothetical protein [Pseudomonas putida KT2440] | | | | |
| 16371, 16372 | 26988649 | 31 | 1.00E-13 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|---|-------------|----------|
| 16375, 16376 | 34558196 | 36 | 1.00E-32 | Wollinella succinogenes DSM 1740 | DNA PRIMASE PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wollinella succinogenes] | | | 2.7.7.- |
| 16377, 16378 | 45358661 | 69 | 1.00E-35 | Methanococcus maripaludis S2 | phosphate ABC transporter, ATP-binding protein [Methanococcus maripaludis S2] emb CAF30654.1 phosphate ABC transporter, ATP-binding protein [Methanococcus maripaludis S2] | Staphylococcus aureus subsp. aureus strain MRSA252, complete genome | 85 4.00E-12 | 1.8.- |
| 16379, 16380 | 57286071 | 25 | 1.00E-07 | Staphylococcus aureus subsp. aureus COL | phosphate transport system protein PhoU, putative [Staphylococcus aureus subsp. aureus COL] ref YP_043448.1 putative phosphate transport system protein [Staphylococcus aureus subsp. aureus MSSA476] ref NP_646090.1 hypothetical protein MW1273 [Staphylococcus aureus subsp. aureus MW2] ref NP_374498.1 hypothetical protein SA1217 [Staphylococcus aureus subsp. aureus N315] emb CAG43102.1 putative phosphate transport system protein [Staphylococcus aureus subsp. aureus MSSA476] dbj BAB57547.1 similar to negative regulator PhoU [Staphylococcus aureus subsp. aureus Mu50] dbj BAB95138.1 MW1273 [Staphylococcus aureus subsp. aureus MW2] dbj BAB42477.1 SA1217 [Staphylococcus aureus subsp. aureus N315] pir JAB9915 hypothetical protein SA1217 [imported] - Staphylococcus aureus (strain N315) ref NP_371909.1 similar to negative regulator PhoU [Staphylococcus aureus subsp. aureus Mu50] ref YP_186272.1 phosphate transport system protein PhoU, putative [Staphylococcus aureus subsp. aureus COL] | | | |
| 16381, 16382 | 34557665 | 50 | 1.00E-38 | Wollinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes] | | | 2.7.3.- |
| 16383, 16384 | 51244082 | 42 | 1.00E-36 | Desulfotalea psychrophila L Sv54 | hypothetical protein DP0230 [Desulfotalea psychrophila L Sv54] emb CAG34959.1 hypothetical protein [Desulfotalea psychrophila L Sv54] | | | 2.7.3.- |
| 16387, 16388 | 57241681 | 58 | 3.00E-81 | Campylobacter lari RM2100 | DNA gyrase, B subunit [Campylobacter lari RM2100] gb EAL54351.1 DNA gyrase, B subunit [Campylobacter lari RM2100] | Desc:Staphylococ- us epidermidis ORF nucleic acid sequence SEQ ID NO:2390. Org:Staphylococcus epidermidis | 92 6.00E-16 | 5.99.1.3 |
| 16389, 16390 | 27366980 | 22 | 5.00E-12 | Vibrio vulnificus CMCP6 | Predicted signal transduction protein [Vibrio vulnificus CMCP6] gb AAO07497.1 Predicted signal transduction protein [Vibrio vulnificus CMCP6] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|--|---------------|
| 16395, 16396 | 21232019 | 30 | 8.00E-15 | Xanthomonas campestris pv. campestris str. ATCC 33913 | lipoprotein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AA041860.1 lipoprotein [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | | |
| 16397, 16398 | 46581041 | 26 | 3.00E-28 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | HAMP domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97109.1 HAMP domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | 2.7.3.- |
| 16399, 16400 | 34556884 | 56 | 3.00E-80 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0457 [Wolinella succinogenes DSM 1740] emb CAE09599.1 conserved hypothetical protein [Wolinella succinogenes] | | | | 1.-.-.- |
| 16401, 16402 | 20808732 | 39 | 2.00E-18 | Thermoanaerobact er tengcongensis MB4 | 6-pyruvoyl-tetrahydropterin synthase [Thermoanaerobacter tengcongensis MB4] gb AAM25507.1 6-pyruvoyl-tetrahydropterin synthase [Thermoanaerobacter tengcongensis MB4] | | | | 4.6.1.10 |
| 16403, 16404 | 48833156 | 46 | 2.00E-44 | Magnetococcus sp. MC-1 | hypothetical protein Mmc102001351 [Magnetococcus sp. MC-1] putative periplasmic protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir B81399 probable periplasmic protein Cj0530 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281714.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni NCTC 11168] | | | | |
| 16405, 16406 | 6967998 | 24 | 1.00E-08 | Campylobacter jejuni subsp. jejuni NCTC 11168 | alanine racemase, putative [Campylobacter upsaliensis RM3195] gb EAL53686.1 alanine racemase, putative [Campylobacter upsaliensis RM3195] | | | | 5.1.1.1 |
| 16407, 16408 | 57242224 | 42 | 8.00E-22 | Bacteriophage Aeh1 | NudE nudix hydrolase [Bacteriophage Aeh1] ref NP_942229.1 NudE nudix hydrolase [Bacteriophage Aeh1] | | | | |
| 16409, 16410 | 33414958 | 36 | 2.00E-12 | Photobacterium luminescens subsp. laumondii TTO1 | adenosylmethionine-8-amino-7-oxononanoate transaminase (DAPA aminotransferase) [Photobacterium luminescens subsp. laumondii TTO1] emb CAE13777.1 adenosylmethionine-8-amino-7-oxononanoate transaminase (DAPA aminotransferase) [Photobacterium luminescens subsp. laumondii TTO1] | | | | 2.6.1.62 |
| 16413, 16414 | 37525435 | 51 | 7.00E-58 | Cytophaga hutchinsonii | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | | |
| 16419, 16420 | 48853840 | 27 | 2.00E-18 | Cytophaga hutchinsonii | COG0206: Cell division GTPase [Cytophaga hutchinsonii] | | | | 3.4.24.- |
| 16421, 16422 | 48854567 | 36 | 8.00E-42 | Clostridium acetobutylicum ATCC 824 | O-acetylhomoserine sulphydrylase [Clostridium acetobutylicum ATCC 824] gb AAK78087.1 O-acetylhomoserine sulphydrylase [Clostridium acetobutylicum ATCC 824] pir D96912 O-acetylhomoserine sulphydrylase [imported] - Clostridium acetobutylicum | | | | 4.2.99.1 0 |
| 16423, 16424 | 15893398 | 34 | 9.00E-36 | Vibrio parahaemolyticus RIMD 2210633 | DPS family protein [Vibrio parahaemolyticus RIMD 2210633] db BAC61906.1 DPS family protein [Vibrio parahaemolyticus] | | | | |
| 16425, 16426 | 28900418 | 56 | 1.00E-32 | | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|---------|----------|--|
| 1643, 1644 | 32262346 | 35 | 3.00E-30 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860328.1 hypothetical protein HH0797 [Helicobacter hepaticus ATCC 51449] | | | 2.7.7.- | |
| 16431, 16432 | 48855803 | 62 | 6.00E-73 | Cytophaga hutchinsonii | COG0042: tRNA-dihydrouridine synthase [Cytophaga hutchinsonii] | | | | |
| 16435, 16436 | 57505258 | 44 | 1.00E-34 | Campylobacter upsallensis RM3195 | conserved hypothetical protein [Campylobacter upsallensis gb EAL53179.1 conserved hypothetical protein [Campylobacter upsallensis RM3195] | | | | |
| 16437, 16438 | 29346214 | 56 | 1.00E-97 | Bacteroides thetaiotaomicron VPI-5482 | putative carbon-nitrogen hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75911.1 putative carbon-nitrogen hydrolase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 16439, 16440 | 34557033 | 59 | 5.00E-64 | Wolinella succinogenes DSM 1740 | GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09748.1 GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes] sp Q7M9X0 HIS5_WOLSU Imidazole glycerol phosphate synthase subunit hisH (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH) | | 2.4.2.- | | |
| 16441, 16442 | 17231520 | 39 | 3.00E-12 | Nostoc sp. PCC 7120 | hypothetical protein air4028 [Nostoc sp. PCC 7120] pir AE2309 hypothetical protein air4028 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75727.1 air4028 [Nostoc sp. PCC 7120] | | | | |
| 16443, 16444 | 34557685 | 34 | 3.00E-43 | Wolinella succinogenes DSM 1740 | HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10400.1 HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes] | | | | |
| 16445, 16446 | 29346628 | 38 | 2.00E-34 | Bacteroides thetaiotaomicron VPI-5482 | conserved hypothetical protein, with conserved domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76325.1 conserved hypothetical protein, with conserved domain [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 16447, 16448 | 56478721 | 30 | 3.00E-12 | Azoarcus sp. EbN1 | transposase, is4 family [Azoarcus sp. EbN1] ref YP_160303.1 transposase (IS4) [Azoarcus sp. EbN1] ref YP_159286.1 transposase (IS4) [Azoarcus sp. EbN1] ref YP_157078.1 transposase (IS4) [Azoarcus sp. EbN1] ref YP_157069.1 transposase (IS4) [Azoarcus sp. EbN1] emb CAI09409.1 transposase, is4 family [Azoarcus sp. EbN1] emb CAI09402.1 Transposase (IS4) [Azoarcus sp. EbN1] emb CAI08385.1 Transposase (IS4) [Azoarcus sp. EbN1] emb CAI06177.1 Transposase (IS4) [Azoarcus sp. EbN1] emb CAI06168.1 Transposase (IS4) [Azoarcus sp. EbN1] | | | | |
| 16449, 16450 | 53690822 | 47 | 5.00E-67 | Desulfovibrio desulfuricans G20 | COG0380: Trehalose-6-phosphate synthase [Desulfovibrio desulfuricans G20] | | | 2.4.1.15 | |
| 1645, 1646 | 55978212 | 29 | 6.00E-10 | Thermus thermophilus HB8 | hypothetical protein TTHB029 [Thermus thermophilus HB8] dbj BAD71825.1 conserved hypothetical protein [Thermus thermophilus HB8] | | | | |

| | | | | | | | | |
|---|----------------------------------|----------------|----------------------------------|--|--|--|----|----------|
| 16451, 16452, 16453, 16454, 16455, 16456 | 48864235 48863907 51893967 | 29 26 32 | 7.00E-31 5.00E-07 7.00E-20 | Microbulbifer degradans 2-40 Microbulbifer degradans 2-40 Symbiobacterium thermophilum IAM 14863 | COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40] COG5651: PPE-repeat proteins [Microbulbifer degradans 2-40] hypothetical protein STH2829 [Symbiobacterium thermophilum IAM 14863] dbj BAD41814.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863] | | | |
| 16457, 16458 | 45658050 | 50 | 9.00E-23 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | mannose-1-phosphate guanylttransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] guanylttransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.7.7.13 |
| 16461, 16462 | 28896971 | 80 | 7.00E-49 | Vibrio parahaemolyticus RIMD 2210633 | putative capsular polysaccharide biosynthesis protein D [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58460.1 putative capsular polysaccharide biosynthesis protein D [Vibrio parahaemolyticus] | Vibrio parahaemolyticus DNA, chromosome 1, complete sequence | 84 | 1.00E-15 |
| 16463, 16464 | 45658032 | 28 | 4.00E-07 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC12183 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711780.1 hypothetical protein LA1599 [Leptospira interrogans serovar Lai str. 56601] gb AA48798.1 hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AA50755.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 16467, 16468, 16469, 16470 | 46143757 48834423 | 31 38 | 5.00E-13 9.00E-40 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 Magnetococcus sp. MC-1 | COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Actinobacillus pleuropneumoniae serovar 1 str. 4074] COG0535: Predicted Fe-S oxidoreductases [Magnetococcus sp. MC-1] | | | 1.97.1.4 |
| 16477, 16478 | 48856329 | 62 | 2.00E-92 | Cytophaga hutchinsonii | COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | 1.8.-.- |
| 16481, 16482 | 32262336 | 24 | 5.00E-22 | Helicobacter hepaticus ATCC 51449 | cell division protein FtsX [Helicobacter hepaticus ATCC 51449] ref NP_860318.1 cell division protein FtsX [Helicobacter hepaticus ATCC 51449] | | | |
| 16483, 16484 | 34556592 | 35 | 3.00E-44 | Wolinella succinogenes DSM 1740 | PUTATIVE FIBRONECTIN DOMAIN-CONTAINING LIPOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE09307.1 PUTATIVE FIBRONECTIN DOMAIN-CONTAINING LIPOPROTEIN [Wolinella succinogenes] | | | |

| | | | | | | | | | |
|--------------|----------|----|----------|-----------------------------------|--|---|----|----------|----------|
| 16485, 16486 | 34558443 | 36 | 2.00E-13 | Wollinella succinogenes DSM 1740 | hypothetical protein WS2166 [Wollinella succinogenes DSM 1740] emb CAE11158.1 hypothetical protein [Wollinella succinogenes] | | | | |
| 16487, 16488 | ABB9146 | 44 | 7.00E-32 | | Desc:Herbicide active polypeptide SEQ ID NO 672. Org:Arabidopsis thaliana | | | | 3.4.21.- |
| 16489, 16490 | 48831039 | 56 | 3.00E-33 | Magnetococcus sp. MC-1 | COG0686: Alanine dehydrogenase [Magnetococcus sp. MC-1] | | | | 1.4.1.1 |
| 1649, 1650 | 23508398 | 26 | 2.00E-08 | Plasmodium falciparum 3D7 | hypothetical protein PF11_0207 [Plasmodium falciparum 3D7] gb AAN35791.1 hypothetical protein [Plasmodium falciparum 3D7] | | | | |
| 16491, 16492 | 53721220 | 24 | 6.00E-10 | Burkholderia pseudomallei K96243 | hypothetical protein BPSS0184 [Burkholderia pseudomallei K96243] emb CAH37629.1 hypothetical protein [Burkholderia pseudomallei K96243] | | | | |
| 16493, 16494 | 48862581 | 31 | 1.00E-18 | Microbulbifer degradans 2-40 | COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40] | | | | |
| 16495, 16496 | 55981423 | 47 | 7.00E-75 | Thermus thermophilus HB8 | succinate dehydrogenase, flavoprotein subunit [Thermus thermophilus HB8] dbj BAD71277.1 succinate dehydrogenase, flavoprotein subunit [Thermus thermophilus HB8] | | | | 1.3.99.1 |
| 16499, 16500 | 56478683 | 38 | 1.00E-15 | Azoarcus sp. Ebn1 | two-component system response regulator [Azoarcus sp. Ebn1] emb CAI09371.1 Two-component system response regulator [Azoarcus sp. Ebn1] | | | | 2.7.-.- |
| 165, 166 | 48854579 | 38 | 2.00E-12 | Cytophaga hutchinsonii | hypothetical protein Chut0202781 [Cytophaga hutchinsonii] | | | | |
| 16501, 16502 | 48856514 | 45 | 7.00E-52 | Cytophaga hutchinsonii | COG2148: Sugar transferases involved in lipopolysaccharide synthesis [Cytophaga hutchinsonii] | | | | 2.-.-.- |
| 16503, 16504 | 940147 | 42 | 3.00E-19 | | CheA | | | | 2.7.3.- |
| 16505, 16506 | 34557407 | 36 | 3.00E-49 | Wollinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes] | | | | 2.7.3.- |
| 16507, 16508 | 32263159 | 42 | 2.00E-26 | Helicobacter hepaticus ATCC 51449 | two-component system histidine kinase [Helicobacter hepaticus ATCC 51449] ref NP_861138.1 two-component system histidine kinase [Helicobacter hepaticus ATCC 51449] | | | | 2.7.3.- |
| 16509, 16510 | 558571 | 58 | 1.00E-95 | Escherichia coli | site-specific DNA-methyltransferase (cytosine-specific) [Escherichia coli] sp P50196 MTE8_ECOLI Modification methylase Eco47II (Cytosine-specific methyltransferase Eco47II) (M.Eco47II) prf 2115269B methyltransferase Eco47IIM | Myoplasma mycoides subsp. mycoides SC genomic DNA, complete sequence; segment 1/4 | 94 | 2.00E-10 | 2.1.1.73 |
| 1651, 1652 | 48854286 | 45 | 1.00E-56 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | | |

| | | | | | | |
|---|--|--|--|---|---|--|
| 16511, 16512, 16513, 16514, 16515, 16516, 16517, 16518, 16521, 16522, 16523, 16524, 16525, 16526, 16527, 16528, 16529, 16530, 16535, 16536, 16537, 16538, 16539, 16540, 16541, 16542 | 42527140 28212137 48859709 57238687 32262724 21672936 46140339 34558149 46096329 50083834 50955568 21243215 46142672 | 37 53 29 41 40 33 37 24 52 32 39 37 41 | 3.00E-32 3.00E-54 2.00E-15 2.00E-22 5.00E-20 6.00E-33 4.00E-15 1.00E-07 4.00E-57 6.00E-32 3.00E-17 3.00E-47 5.00E-21 | Treponema denticola ATCC 35405 Clostridium tetani E88 Clostridium thermocellum ATCC 27405 Campylobacter jejuni RM1221 Helicobacter hepaticus ATCC 51449 Chlorobium tepidum TLS Dechloromonas aromatica RCB Wolinella sucinogenes DSM 1740 Ustilago maydis 521 Acinetobacter sp. ADP1 Leifsonia xyl subsp. xyl str. CTCB07 Xanthomonas axonopodis pv. citri str. 306 Methanococcoides burtonii DSM 6242 | citrate lyase, beta subunit [Treponema denticola ATCC 35405] gb AAAS12149.1 citrate lyase, beta subunit [Treponema denticola ATCC 35405] citrate lyase alpha chain [Clostridium tetani E88] gb AAO37018.1 citrate lyase alpha chain [Clostridium tetani E88] COG4191: Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Clostridium thermocellum ATCC 27405] UDP-N-acetylpyruvoylglucosamine reductase [Campylobacter jejuni RM1221] reductase [Campylobacter jejuni RM1221] dimethyladenosine transferase (rRNA methylation) [Helicobacter hepaticus ATCC 51449] ref NP_860705.1 dimethyladenosine transferase (rRNA methylation) [Helicobacter hepaticus ATCC 51449] aspartokinase [Chlorobium tepidum TLS] gb AAM71343.1 aspartokinase [Chlorobium tepidum TLS] COG2863: Cytochrome c553 [Dechloromonas aromatica RCB] SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes DSM 1740] emb CAE10864.1 SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes] hypothetical protein UM00177.1 [Ustilago maydis 521] ref XP_397792.1 hypothetical protein UM00177.1 [Ustilago maydis 521] hypothetical protein ACIAD0599 [Acinetobacter sp. ADP1] emb CAG67522.1 conserved hypothetical protein [Acinetobacter sp. ADP1] glycosyltransferase [Leifsonia xyl subsp. xyl str. CTCB07] gb AAT89751.1 glycosyltransferase [Leifsonia xyl subsp. xyl str. CTCB07] transcriptional regulator [Xanthomonas axonopodis pv. citri str. 306] gb AAM37333.1 transcriptional regulator [Xanthomonas axonopodis pv. citri str. 306] COG3769: Predicted hydrolase (HAD superfamily) [Methanococcoides burtonii DSM 6242] | 4.1.3.6 2.8.3.10 2.7.3.- 1.1.1.15 8 2.1.1.- 2.7.2.4 2.7.3.- |
|---|--|--|--|---|---|--|

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------|--|----|----------|--|----------|
| 16543, | 52550565 | 32 | 7.00E-19 | uncultured archaeon | mannosyl-3-phosphoglycerate phosphatase [uncultured archaeon GZfos9E5] | | | | |
| 16544 | | | | GZfos9E5 | | | | | |
| 16545, | | | | Wolinella | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) | | | | 2.7.3.- |
| 16546 | 34557665 | 44 | 3.00E-30 | succinogenes DSM 1740 | [Wolinella succinogenes] | | | | |
| 16547, | | | | Wolinella | PUTATIVE TONB-INDEPENDENT PROTEIN-UTAKE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09658.1 PUTATIVE TONB-INDEPENDENT PROTEIN-UTAKE PROTEIN [Wolinella succinogenes] | | | | |
| 16548 | 34556943 | 43 | 1.00E-57 | succinogenes DSM 1740 | GGDEF domain/HD domain protein [Dehalococcoides ethenogenes 195] gb AAW39390.1 GGDEF domain/HD domain protein [Dehalococcoides ethenogenes 195] | | | | 2.7.3.- |
| 1655, | 57233885 | 25 | 6.00E-20 | Dehalococcoides ethenogenes 195 | conserved hypothetical protein [Carnylobacter upsaliensis RM3195] | | | | |
| 1656 | | | | Carnylobacter upsaliensis | gb EAL52510.1 conserved hypothetical protein [Carnylobacter upsaliensis RM3195] | | | | |
| 16551, | 57505920 | 32 | 2.00E-08 | RM3195 | | | | | |
| 16552 | | | | | | | | | |
| 16553, | | | | Cytophaga | COG0445: NAD/FAD-utilizing enzyme apparently involved in cell division [Cytophaga hutchinsonii] | | | | |
| 16554 | 48854031 | 55 | 8.00E-94 | hutchinsonii | Desc:Streptococcus pyogenes | 86 | 1.00E-11 | | |
| 16557, | ABP2948 | | | | pyogenes | | | | |
| 16558 | 1 | 39 | 2.00E-15 | Clostridium tetani | hypothetical protein CTC00439 [Clostridium tetani E88] gb AAO35073.1 conserved protein [Clostridium tetani E88] | | | | |
| 16559, | 28210192 | 29 | 3.00E-07 | E88 | | | | | |
| 16560 | | | | | | | | | |
| 16561, | | | | Methanococcoides | COG0726: Predicted xylanase/chitin deacetylase [Methanococcoides burtonii DSM 6242] | | | | |
| 16562 | 46142687 | 37 | 2.00E-21 | burtonii DSM 6242 | | | | | |
| 16563, | | | | Wolinella | AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] | | | | |
| 16564 | 34557975 | 46 | 9.00E-83 | succinogenes DSM 1740 | emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes] | | | | |
| 16565, | | | | Wolinella | AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] | | | | 3.4.24.- |
| 16566 | 34557975 | 70 | 3.00E-79 | succinogenes DSM 1740 | emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes] | | | | |
| 16567, | | | | Wolinella | conserved hypothetical protein CJO172C [Wolinella succinogenes DSM 1740] emb CAE09330.1 conserved hypothetical protein CJO172C [Wolinella succinogenes] | | | | 1.1.1.- |
| 16568 | 34556615 | 67 | 9.00E-42 | succinogenes DSM 1740 | | | | | |
| 16569, | | | | Rubrivivax | COG0270: Site-specific DNA methylase [Rubrivivax gelatinosus PM1] | | | | 2.1.1.73 |
| 16570 | 47572668 | 23 | 5.00E-12 | gelatinosus PM1 | Desc:C glutamicum protein fragment SEQ ID NO: 6894. | | | | |
| 16571, | AAG9314 | | | | Org:Corynebacterium glutamicum | | | | |
| 16572 | 0 | 28 | 2.00E-15 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|---------|--|--|
| 16573, 16574 | 53715006 | 52 | 1.00E-54 | Bacteroides fragilis YCH46 | cation efflux system protein [Bacteroides fragilis YCH46] dbj BAD50464.1 cation efflux system protein [Bacteroides fragilis YCH46] | | | |
| 16575, 16576 | 48860160 | 37 | 1.00E-21 | Clostridium thermocellum ATCC 27405 | COG111: Phosphoglycerate dehydrogenase and related dehydrogenases [Clostridium thermocellum ATCC 27405] | | | |
| 16577, 16578 | 57240770 | 37 | 9.00E-46 | Campylobacter lari RM2100 | flagellar motor switch protein FlmM [Campylobacter lari RM2100] gb EAL55163.1 flagellar motor switch protein FlmM [Campylobacter lari RM2100] | | | |
| 16579, 16580 | 29347938 | 30 | 2.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | putative Na+-dependent phosphate transporter [Bacteroides thetaiotaomicron VPI-5482] gb AAO77635.1 putative Na+-dependent phosphate transporter [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 16581, 16582 | 46446644 | 47 | 3.00E-70 | Parachlamydia sp. UWE25 | hypothetical protein pc1010 [Parachlamydia sp. UWE25] emb CAF23734.1 conserved hypothetical protein [Parachlamydia sp. UWE25] | | | |
| 16585, 16586 | 57236909 | 63 | 3.00E-40 | Campylobacter jejuni RM1221 | GTP cyclohydrolase I family protein [Campylobacter jejuni RM1221] gb AAW34492.1 GTP cyclohydrolase I family protein [Campylobacter jejuni RM1221] | | | |
| 16587, 16588 | 48862944 | 43 | 7.00E-31 | Microbulifer degradans 2-40 | COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Microbulifer degradans 2-40] | | | |
| 16589, 16590 | 4838141 | 29 | 6.00E-24 | Bacteroides fragilis | BatD [Bacteroides fragilis] | | | |
| 16591, 16592 | 48853811 | 51 | 9.00E-80 | Cytophaga hutchinsonii | COG0587: DNA polymerase III, alpha subunit [Cytophaga hutchinsonii] hypothetical protein aq_429 [Aquifex aeolicus VF5] gb AAC06701.1 putative protein [Aquifex aeolicus VF5] pir C70339 hypothetical protein aq_429 - Aquifex aeolicus | 2.7.7.7 | | |
| 16593, 16594 | 15605926 | 24 | 6.00E-07 | Aquifex aeolicus VF5 | | | | |
| 16595, 16596 | 34556462 | 70 | 4.00E-47 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0003 [Wolinella succinogenes DSM 1740] emb CAE09177.1 conserved hypothetical protein [Wolinella succinogenes] hypothetical protein LIC12325 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711602.1 hypothetical protein LA1421 [Leptospira interrogans serovar Lai str. 56601] gb AAN48620.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS70896.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 16597, 16598 | 45658173 | 32 | 9.00E-14 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|----------|
| 16599, 16600 | 45658174 | 38 | 2.00E-18 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | hypothetical protein LIC12326 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70897.1] conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | |
| 16601, 16602 | 48730848 | 47 | 1.00E-23 | Pseudomonas fluorescens PfO-1 | hypothetical protein PflU02002728 [Pseudomonas fluorescens PfO-1] | | | |
| 16603, 16604 | 56419029 | 35 | 2.00E-11 | Geobacillus kaustophilus HTA426 | transcriptional repressor of PBSX genes [Geobacillus kaustophilus HTA426] dbj BAD74779.1] transcriptional repressor of PBSX genes [Geobacillus kaustophilus HTA426] | | | |
| 16605, 16606 | 16127072 | 32 | 2.00E-15 | Caulobacter crescentus CB15 | hypothetical protein CC2840 [Caulobacter crescentus CB15] | | | |
| 16607, 16608 | 48854772 | 42 | 3.00E-47 | Cytophaga hutchinsonii | gb AAK24804.1] hypothetical protein [Caulobacter crescentus CB15] pir H87600 hypothetical protein CC2840 [imported] - Caulobacter crescentus | | | |
| 16609, 16610 | 48832299 | 48 | 1.00E-43 | Magnetococcus sp. MC-1 | COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii] | | | 3.4.11.- |
| 16611, 16612 | 50841972 | 43 | 4.00E-16 | Propionibacterium acnes KPA171202 | COG2206: HD-GYP domain [Magnetococcus sp. MC-1] | | | 3.1.4.17 |
| 16613, 16614 | 23475955 | 44 | 2.00E-24 | Desulfovibrio desulfuricans G20 | UTP-glucose-1-phosphate uridylyltransferase [Propionibacterium acnes KPA171202] KPA171202] gb AAT82241.1] UTP-glucose-1-phosphate uridylyltransferase [Propionibacterium acnes KPA171202] | | | 2.7.7.9 |
| 16617, 16618 | 48846045 | 38 | 2.00E-24 | Geobacter metallireducens GS | COG4284: UDP-glucose pyrophosphorylase [Desulfovibrio desulfuricans G20] | | | 2.7.7.9 |
| | | | | | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 16621, 16622 | 17935724 | 34 | 7.00E-20 | Agrobacterium tumefaciens str. C58 | mutT like protein [Agrobacterium tumefaciens str. C58] gb AAL42830.1] mutT like protein [Agrobacterium tumefaciens str. C58] gb AAK87603.1] AGR_C_3368p [Agrobacterium tumefaciens str. C58] pir AH2801 mutT like protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir B97581 hypothetical protein AGR_C_3368 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) ref NP_354818.1] hypothetical protein AGR_C_3368 [Agrobacterium tumefaciens str. C58] | | | 3.6.1.- |
| 16623, 16624 | 34558202 | 40 | 9.00E-22 | Wolfinella succinogenes DSM 1740 | LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wolfinella succinogenes DSM 1740] emb CAE10917.1] LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wolfinella succinogenes] | | | 2.3.1.- |
| 16625, 16626 | 48832666 | 45 | 1.00E-56 | Magnetococcus sp. MC-1 | COG3959: Transketolase, N-terminal subunit [Magnetococcus sp. MC-1] | | | 2.2.1.1 |
| 16629, 16630 | 48854899 | 56 | 2.00E-26 | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | 2.1.1.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 1663, 1664 | 18976925 | 46 | 1.00E-27 | Pyrococcus furiosus DSM 3638 | arsenate reductase [Pyrococcus furiosus DSM 3638] gb AAL80677.1 arsenate reductase: (arsC) [Pyrococcus furiosus DSM 3638] | | | | 1.97.1.5 |
| 16631, 16632 | 48853718 | 35 | 6.00E-44 | Cytophaga hutchinsonii | COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii] | | | | |
| 16633, 16634 | 34558265 | 53 | 3.00E-34 | Wolinella succinogenes DSM 1740 | PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes] | | | | |
| 16635, 16636 | 32262573 | 44 | 2.00E-38 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860554.1 hypothetical protein HH1023 [Helicobacter hepaticus ATCC 51449] | | | | |
| 16637, 16638 | 57241759 | 35 | 3.00E-07 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54429.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 16639, 16640 | 21673017 | 36 | 8.00E-32 | Chlorobium tepidum TLS | penicillin-binding protein 1 [Chlorobium tepidum TLS] gb AAM71424.1 penicillin-binding protein 1 [Chlorobium tepidum TLS] | | | | 2.4.2.- |
| 16641, 16642 | 32263042 | 23 | 4.00E-10 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861022.1 hypothetical protein HH1491 [Helicobacter hepaticus ATCC 51449] | | | | |
| 16643, 16644 | 48856580 | 47 | 2.00E-20 | Cytophaga hutchinsonii | hypothetical protein Chut02000314 [Cytophaga hutchinsonii] | | | | |
| 16645, 16646 | 29346299 | 46 | 2.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0889 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75996.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 16647, 16648 | 53687530 | 65 | 2.00E-37 | Nostoc punctiforme PCC 73102 | hypothetical protein Npun02005570 [Nostoc punctiforme PCC 73102] | | | | |
| 16649, 16650 | 53713319 | 49 | 6.00E-76 | Bacteroides fragilis YCH46 | putative TonB-dependent outer membrane receptor protein [Bacteroides fragilis YCH46] db BAD48777.1 putative TonB-dependent outer membrane receptor protein [Bacteroides fragilis YCH46] | | | | |
| 16651, 16652 | 37811998 | 29 | 4.00E-07 | Aeromonas hydrophila | putative cII protein [Aeromonas hydrophila] | | | | |
| 16655, 16656 | 34558493 | 58 | 3.00E-82 | Wolinella succinogenes DSM 1740 | PUTATIVE ZINC PROTEASE [Wolinella succinogenes DSM 1740] emb CAE11208.1 PUTATIVE ZINC PROTEASE [Wolinella succinogenes] | | | | 3.4.- |
| 16657, 16658 | 34556560 | 46 | 4.00E-66 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | |
| 16659, 16660 | 34558171 | 28 | 4.00E-26 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1876 [Wolinella succinogenes DSM 1740] emb CAE10886.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|----------|----------------|
| 16661, 16662 | 34557356 | 37 | 3.00E-55 | Wolinnella succinogenes DSM 1740 | NRFI PROTEIN [Wolinnella succinogenes DSM 1740] emb CAE10071.1 NRFI PROTEIN [Wolinnella succinogenes] emb CAB53161.1 NrfI protein [Wolinnella succinogenes] sp Q9S1E4 NRFI_WOLSU NrfI protein | | | | | |
| 16663, 16664 | 57207873 | 23 | 1.00E-14 | Staphylococcus aureus | hypothetical protein [Staphylococcus aureus] | | | | | |
| 16665, 16666 | 34557782 | 35 | 4.00E-33 | Wolinnella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinnella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinnella succinogenes] | | | | 2.7.3.- | |
| 16667, 16668 | 31195231 | 60 | 2.00E-71 | Anopheles gambiae | ENSANGP00000001058 [Anopheles gambiae] gb EAA02216.1 ENSANGP00000001058 [Anopheles gambiae str. PEST] ref XP_561308.1 ENSANGP00000001058 [Anopheles gambiae str. PEST] | | | | 1.1.1.34 | |
| 16669, 16670 | 48855423 | 26 | 2.00E-20 | Cytophaga hutchinsonii | COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] | | | | 5.2.1.8 | |
| 1667, 1668 | 53713909 | 33 | 3.00E-16 | Bacteroides fragilis YCH46 | hypothetical protein BF2617 [Bacteroides fragilis YCH46] dbj BAD49367.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | | |
| 16671, 16672 | 34558447 | 54 | 4.00E-78 | Wolinnella succinogenes DSM 1740 | PUTATIVE CATION-TRANSPORTING ATPASE [Wolinnella succinogenes DSM 1740] emb CAE11162.1 PUTATIVE CATION-TRANSPORTING ATPASE [Wolinnella succinogenes] | | | | 3.6.1.- | |
| 16673, 16674 | 53684563 | 38 | 2.00E-37 | Desulfitobacterium hafniense DCB-2 | COG1373: Predicted ATPase (AAA+ superfamily) [Desulfitobacterium hafniense DCB-2] | | | | | |
| 16677, 16678 | 20806705 | 37 | 8.00E-29 | Thermoanaerobact er tengcongensis MB4 | hypothetical protein TTE0179 [Thermoanaerobacter tengcongensis MB4] gb AAM23480.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4] | | | | | |
| 16679, 16680 | 34397903 | 53 | 1.00E-40 | Porphyromonas gingivalis W83 | excinuclease ABC, C subunit [Porphyromonas gingivalis W83] ref NP_906065.1 excinuclease ABC, C subunit [Porphyromonas gingivalis W83] | | | | | |
| 16681, 16682 | 34396304 | 38 | 6.00E-46 | Porphyromonas gingivalis W83 | mannosyltransferase [Porphyromonas gingivalis W83] ref NP_904472.1 mannosyltransferase [Porphyromonas gingivalis W83] | | | | 2.4.1.- | |
| 16689, 16690 | 57168872 | 56 | 2.00E-54 | Campylobacter coli RM2228 | MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228] gb EAL56394.1 MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228] | | | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 89 | 4.00E-07 1.8.- |
| 1669, 1670 | 48854786 | 40 | 1.00E-41 | Cytophaga hutchinsonii | COG0584: Glycerophosphoryl diester phosphodiesterase [Cytophaga hutchinsonii] | | | | | 3.1.4.46 |

| | | | | | | | | | |
|-----------------|----------|----|----------|------------------------------------|---|--|----|----------|---------|
| 16691, 16692 | 57168872 | 56 | 1.00E-41 | Campylobacter coli RM2228 | MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228] gb EAL56394.1 MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 89 | 3.00E-07 | 1.8.-.- |
| 16693, 16694 | 28211918 | 24 | 2.00E-09 | Clostridium tetani E88 | sensory transduction protein kinase [Clostridium tetani E88] gb AAO36799.1 sensory transduction protein kinase [Clostridium tetani E88] | | | | |
| 16695, 16696 | 45915115 | 42 | 5.00E-18 | Mesorhizobium sp. BNC1 | COG0489: ATPases involved in chromosome partitioning [Mesorhizobium sp. BNC1] | | | | |
| 16697, 16698 | 5739402 | 51 | 3.00E-60 | Flavobacterium johnsoniae | TruB [Flavobacterium johnsoniae] sp Q9RB36 TRUB_CYTJO tRNA pseudouridine synthase B (tRNA pseudouridine 55 synthase) (Psi55 synthase) (Pseudouridyate synthase) (Uracil hydrolyase) | | | 4.2.1.70 | |
| 16699, 16700 | 52548848 | 27 | 6.00E-18 | archaeon GZfos19A5 | transposase [uncultured archaeon GZfos19A5] | | | | |
| 167, 168 | 48853766 | 33 | 6.00E-26 | Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii] | | | 2.7.3.- | |
| 16703, 16704 | 48767890 | 52 | 1.00E-30 | Ralstonia metallidurans CH34 | COG0796: Glutamate racemase [Ralstonia metallidurans CH34] | | | 5.1.1.3 | |
| 16705, 16706 | 53715260 | 54 | 8.00E-30 | Bacteroides fragilis YCH46 | putative transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD50718.1 putative transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 16707, 16708 | AAO2094 | 8 | 3.00E-25 | | Desc:Protein of the Bpm1 M1 methylase gene (Bpm1M1). Org:Baillus pumilus | | | 2.1.1.72 | |
| 16709, 16710 | 48833968 | 41 | 4.00E-63 | Magnetococcus sp. MC-1 | COG0673: Predicted dehydrogenases and related proteins [Magnetococcus sp. MC-1] | | | 1.-.-.- | |
| 1671, 1672 | 48853961 | 37 | 4.00E-19 | Cytophaga hutchinsonii | COG1995: Pyridoxal phosphate biosynthesis protein [Cytophaga hutchinsonii] | | | 1.1.1.26 | 2 |
| 16711, 16712 | 48863156 | 34 | 1.00E-14 | Microbulifer degradans 2-40 | COG4067: Uncharacterized protein conserved in archaea [Microbulifer degradans 2-40] | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|------|--|--|--|--|--|----------|
| 16723, 16724 | 48847450 | 39 | 3.00E-15 | 15 | Geobacter metallireducens GS-15 | COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301665.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301374.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300257.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300170.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298468.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298384.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] | | | | |
| 16725, 16726 | 34397615 | 33 | 7.00E-22 | | Porphyromonas gingivalis W83 | ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ66097.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65881.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65455.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65413.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_905778.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_905198.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904782.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904556.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904514.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAD38020.1 transposase [Porphyromonas gingivalis] | | | | |
| 16729, 16730 | 34556563 | 46 | 6.00E-66 | 1740 | Wolinella succinogenes DSM 1740 | PANTOATE-BETA-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09278.1 PANTOATE-BETA-ALANINE LIGASE [Wolinella succinogenes] | | | | 6.3.2.1 |
| 16731, 16732 | 34556563 | 53 | 2.00E-38 | 1740 | Wolinella succinogenes DSM 1740 | PANTOATE-BETA-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09278.1 PANTOATE-BETA-ALANINE LIGASE [Wolinella succinogenes] | | | | 6.3.2.1 |
| 16733, 16734 | 57242486 | 32 | 8.00E-19 | | Campylobacter upsaliensis RM3195 | methyl-accepting chemotaxis protein (tpa) [Campylobacter upsaliensis RM3195] gb EAL53554.1 methyl-accepting chemotaxis protein (tpa) [Campylobacter upsaliensis RM3195] | | | | |
| 16735, 16736 | 48855820 | 44 | 3.00E-35 | | Cytophaga hutchinsonii | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | | |
| 16737, 16738 | 23478426 | 21 | 1.00E-09 | | Plasmodium yoelii yoelii | hypothetical protein [Plasmodium yoelii yoelii] | | | | 3.1.11.- |
| 16741, 16742 | AA3437 | 3 | 3.00E-25 | | | Desc: Porphyromonas gingivalis protein PG4. Org: Porphyromonas gingivalis COG0726: Predicted xylanase/chitin deacetylase [Microbulifer degradans 2- 40] | | | | |
| 16743, 16744 | 48861641 | 36 | 1.00E-26 | | Microbulifer degradans 2-40 | | | | | |

| | | | | | | | | |
|-----------------|--------------|----|----------|---|---|--|--|---------------|
| 16745, 16746 | 15606040 | 40 | 6.00E-21 | Aquifex aeolicus VF5 | hypothetical protein aq_598 [Aquifex aeolicus VF5] gb AAC06817.1 putative protein [Aquifex aeolicus VF5] pir E70353 hypothetical protein aq_598 - Aquifex aeolicus | | | |
| 16747, 16748 | 28898380 | 38 | 2.00E-13 | Vibrio parahaemolyticus RIMD 2210633 | tail-specific protease [Vibrio parahaemolyticus RIMD 2210633] dbj BAC59869.1 tail-specific protease [Vibrio parahaemolyticus] tail-specific protease [Xanthomonas axonopodis pv. citri str. 306] gb AAM35558.1 tail-specific protease [Xanthomonas axonopodis pv. citri str. 306] | | | 3.4.21.- |
| 16749, 16750 | 21241440 | 48 | 5.00E-76 | Xanthomonas axonopodis pv. citri str. 306 | | | | 3.4.21.- |
| 1675, 1676 | 48856102 | 51 | 5.00E-42 | Cytophaga hutchinsonii | COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii] putative integrase/recombinase [Cupriavidus necator] gb AAP65797.1 putative integrase/recombinase [Ralstonia eutropha] | | | |
| 16753, 16754 | 38637709 | 30 | 2.00E-12 | Cupriavidus necator | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | |
| 16757, 16758 | 34557419 | 35 | 9.00E-11 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10495.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes] | | | 2.7.3.- |
| 16759, 16760 | 34557780 | 38 | 2.00E-40 | Wolinella succinogenes DSM 1740 | Desc:Chondroitinase AC. Org:Flavobacterium heparinum | | | |
| 16761, 16762 | AAR8914 5 | 30 | 7.00E-09 | | putative glycosyl transferase [Thermosynechococcus elongatus BP-1] dbj BAC08547.1 t 0995 [Thermosynechococcus elongatus BP-1] DNA repair protein Rada [Campylobacter lari RM2100] gb EAL55738.1 DNA repair protein Rada [Campylobacter lari RM2100] | | | 2.4.1.- |
| 16763, 16764 | 22298538 | 41 | 5.00E-25 | Thermosynechococcus elongatus BP-1 | COG0006: Xaa-Pro aminopeptidase [Trichodesmium erythraeum IMS101] putative ABC transporter ATP-binding protein yhiH [Azoarcus sp. Ebn1] emb CAI09981.1 putative ABC transporter ATP-binding protein yhiH [Azoarcus sp. Ebn1] | | | |
| 16769, 16770 | 57240624 | 64 | 2.00E-61 | Campylobacter lari RM2100 | hypothetical protein PBPRB0710 [Photobacterium profundum SS9] emb CAG22582.1 hypothetical protein [Photobacterium profundum] | | | 1.8.- |
| 1677, 1678 | 48894780 | 31 | 2.00E-29 | Trichodesmium erythraeum IMS101 | SIROHEME SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE10105.1 SIROHEME SYNTHASE [Wolinella succinogenes] Desc:High growth methanotrophic bacterial strain polypeptide #26. Org:Methylobacter 16a | | | 2.1.1.10 7 |
| 16771, 16772 | 58479293 | 50 | 5.00E-19 | Azoarcus sp. Ebn1 | | | | |
| 16773, 16774 | 54302389 | 54 | 1.00E-23 | Photobacterium profundum SS9 | | | | |
| 16775, 16776 | 34557390 | 40 | 7.00E-49 | Wolinella succinogenes DSM 1740 | | | | |
| 16777, 16778 | ABG6157 6 | 35 | 5.00E-41 | | | | | 1.7.99.4 |

| | | | | | | | | | |
|-----------------|----------|----|----------|-------------------------------|-------------------------------------|--|--|--|----------|
| 16779, 16780 | 28209890 | 31 | 5.00E-19 | E88 | Clostridium tetani | acyl-acyl carrier protein thioesterase [Clostridium tetani E88] gb AAO34771.1 acyl-acyl carrier protein thioesterase [Clostridium tetani E88] | | | |
| 16781, 16782 | 17233315 | 39 | 4.00E-08 | 7120 | Nostoc sp. PCC | hypothetical protein alr7299 [Nostoc sp. PCC 7120] dbj BAB78383.1 alr7299 [Nostoc sp. PCC 7120] pir JAC2515 hypothetical protein alr7299 [Imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha | | | |
| 16785, 16786 | 27127146 | 46 | 1.00E-60 | NRCPB-10 | Agrobacterium sp. | phosphoenol pyruvate carboxylase [Agrobacterium sp. NRCPB-10] | | | 4.1.1.49 |
| 16787, 16788 | 17940320 | 23 | 6.00E-13 | PBC5 | Sinorhizobium melloti phage | putative DNA methylase [Sinorhizobium melloti phage PBC5] ref NP_542283.1 putative DNA methylase [Sinorhizobium melloti phage PBC5] | | | |
| 16789, 16790 | 20807875 | 48 | 9.00E-18 | MB4 | Thermoanaerobacter tengcongensis | CheY-like receiver domains [Thermoanaerobacter tengcongensis MB4] gb AAM24650.1 CheY-like receiver domains [Thermoanaerobacter tengcongensis MB4] | | | 3.1.1.61 |
| 16791, 16792 | 53729414 | 38 | 1.00E-30 | aromatica RCB | Dechloromonas | COG0515: Serine/threonine protein kinase [Dechloromonas aromatica RCB] | | | 2.7.1.37 |
| 16793, 16794 | 33284889 | 39 | 2.00E-21 | Danio rerio | Danio rerio | novel protein similar to human telomerase-associated protein 1 (TEP1) [Danio rerio] | | | |
| 16795, 16796 | 24372449 | 46 | 2.00E-19 | Shewanella oneidensis MR-1 | Shewanella oneidensis MR-1 | response regulator [Shewanella oneidensis MR-1] gb AAN53936.1 response regulator [Shewanella oneidensis MR-1] | | | |
| 16799, 16800 | 53715569 | 37 | 4.00E-35 | YCH46 | Bacteroides fragilis | hypothetical protein BF4287 [Bacteroides fragilis YCH46] dbj BAD51027.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 16801, 16802 | 17232096 | 47 | 1.00E-62 | 7120 | Nostoc sp. PCC | type I site-specific deoxyribonuclease chain R [Nostoc sp. PCC 7120] dbj BAB76303.1 type I site-specific deoxyribonuclease chain R [Nostoc sp. PCC 7120] pir AD2381 type I site-specific deoxyribonuclease chain R [Imported] - Nostoc sp. (strain PCC 7120) | | | 3.1.21.3 |
| 16805, 16806 | 57241016 | 28 | 4.00E-26 | RM2100 | Campylobacter lari | methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100] gb EAL54712.1 methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100] | | | |
| 16807, 16808 | 20089643 | 30 | 9.00E-23 | acetivorans C2A | Methanosarcina | sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AAM04198.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A] | | | 2.7.3.- |
| 16811, 16812 | 57242712 | 29 | 2.00E-09 | RM3195 | Campylobacter upsallensis | probable transmembrane protein Cj0352 [Campylobacter upsallensis RM3195] gb EAL53425.1 probable transmembrane protein Cj0352 [Campylobacter upsallensis RM3195] | | | |
| 16815, 16816 | 53735986 | 36 | 5.00E-42 | WH 8501 | Crocospaera | COG3347: Uncharacterized conserved protein [Crocospaera watsonii WH 8501] | | | 1.2.1.1 |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---------------|--|---|--|--|----|------------------|
| 16817, 16818 | 34557562 | 38 | 3.00E-22 | 1740 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10277.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes] | | | | |
| 16821, 16822 | 20806576 | 37 | 3.00E-26 | MB4 | Thermoanaerobact er tengcongensis MB4 | Response regulators consisting of a CheY-like receiver domain and an HD- GYP domain [Thermoanaerobacter tengcongensis MB4] gb AAM23351.1 Response regulators consisting of a CheY-like receiver domain and an HD- GYP domain [Thermoanaerobacter tengcongensis MB4] | | | | 2.7.3.- |
| 16823, 16824 | 21229428 | 24 | 3.00E-09 | mazei Go1 | Methanosarcha mazei Go1 | aldehyde ferredoxin oxidoreductase [Methanosarcha mazei Go1] gb AAM33022.1 aldehyde ferredoxin oxidoreductase [Methanosarcha mazei Go1] | | | | 1.2.7.- |
| 16825, 16826 | 48860413 | 57 | 6.00E-50 | ATCC 27405 | Clostridium thermocellum ATCC 27405 | COG1331: Highly conserved protein containing a thioredoxin domain [Clostridium thermocellum ATCC 27405] | | | 84 | 7.00E-12 2.7.4.9 |
| 16827, 16828 | 20807051 | 41 | 6.00E-14 | MB4 | Thermoanaerobact er tengcongensis MB4 | NtrC family Transcriptional regulator, ATPase domain [Thermoanaerobacter tengcongensis MB4] gb AAM23826.1 NtrC family Transcriptional regulator, ATPase domain [Thermoanaerobacter tengcongensis MB4] | | | | |
| 1683, 1684 | 51891955 | 43 | 3.00E-54 | 14863 | Symbiobacterium thermophilum IAM 14863 | hypothetical protein STH817 [Symbiobacterium thermophilum IAM 14863] dbj BAD39802.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863] | | | | 2.8.1.6 |
| 16833, 16834 | 29349667 | 46 | 2.00E-72 | VPI-5482 | Bacteroides thetaiotaomicron VPI-5482 | carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79364.1 carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.4.21.- |
| 16837, 16838 | 15644333 | 32 | 3.00E-37 | maritima MSB8 | Thermotoga maritima MSB8 | glycerate kinase, putative [Thermotoga maritima MSB8] gb AAD36652.1 glycerate kinase, putative [Thermotoga maritima MSB8] pir A72236 hypothetical protein TM1585 - Thermotoga maritima (strain MSB8) | | | | 1.1.1.81 |
| 16839, 16840 | 29347128 | 35 | 2.00E-38 | VPI-5482 | Bacteroides thetaiotaomicron VPI-5482 | putative 2-aminoethylphosphonate pyruvate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76825.1 putative 2- aminoethylphosphonate pyruvate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.6.1.- |
| 16841, 16842 | 29346727 | 70 | 8.00E-21 | VPI-5482 | Bacteroides thetaiotaomicron VPI-5482 | riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76424.1 riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.5.1.9 |

| | | | | | | | | | |
|--------|----------|----|-----------|---------------------------------------|--|---|----|----------|----------|
| 16843, | 57167730 | 71 | 1.00E-114 | Campylobacter coli RM2228 | DNA polymerase III, alpha subunit [Campylobacter coli RM2228] gb EAL57516.1 DNA polymerase III, alpha subunit [Campylobacter coli RM2228] | Clostridium tetani E88, section 9 of 10 of the complete genome | 84 | 5.00E-11 | 2.7.7.7 |
| 16844, | 13123741 | 42 | 1.00E-47 | Campylobacter jejuni | WaaF [Campylobacter jejuni] | | | | |
| 16848 | 56677131 | 32 | 3.00E-14 | Silicibacter pomeroi DSS-3 | SSpo8, transposase [Silicibacter pomeroi DSS-3] ref YP_165742.1 SSpo8, transposase [Silicibacter pomeroi DSS-3] | | | | |
| 16849, | | | | | | | | | |
| 16850 | | | | | hypothetical protein PAE1163 [Pyrobaculum aerophilum str. IM2] gb AAL63294.1 conserved hypothetical protein [Pyrobaculum aerophilum str. IM2] | | | | |
| 1685, | 18312445 | 44 | 1.00E-33 | Pyrobaculum aerophilum str. IM2 | | | | | |
| 1686 | | | | Clostridium thermocellum | COG0324: tRNA delta(2)-isopentenylpyrophosphate transferase [Clostridium thermocellum ATCC 27405] | | | | 2.5.1.8 |
| 16851, | 48857812 | 48 | 4.00E-38 | ATCC 27405 | COG2518: Protein-L-isoaspartate carboxylmethyltransferase [Cytophaga hutchinsonii] | | | | 2.1.1.77 |
| 16853, | 48856515 | 42 | 4.00E-24 | Cytophaga hutchinsonii | hypothetical protein CT1335 [Chlorobium tepidum TLS] gb AAM72564.1 hypothetical protein [Chlorobium tepidum TLS] | | | | |
| 16854 | | | | Chlorobium tepidum TLS | | | | | |
| 16855, | 21674157 | 34 | 2.00E-13 | Wolinella succinogenes DSM | hypothetical protein WS2098 [Wolinella succinogenes DSM 1740] emb CAE11096.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 16856 | 34558381 | 46 | 3.00E-26 | 1740 | | | | | |
| 16857, | | | | Microbulbifer degradans 2-40 | COG0308: Aminopeptidase N [Microbulbifer degradans 2-40] DNA polymerase III delta prime subunit (holB) [Campylobacter coli RM2228] gb EAL57223.1 DNA polymerase III delta prime subunit (holB) [Campylobacter coli RM2228] | | | 3.4.11.2 | |
| 16861, | 48862107 | 47 | 8.00E-31 | Campylobacter coli RM2228 | | | | | |
| 16862 | | | | | | | | | |
| 16863, | 57168180 | 48 | 1.00E-16 | Wolinella succinogenes DSM | hypothetical protein WS1730 [Wolinella succinogenes DSM 1740] emb CAE10755.1 conserved hypothetical protein [Wolinella succinogenes] probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195] gb EAL53524.1 probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195] | | | 2.7.7.7 | |
| 16864 | | | | | | | | | |
| 16865, | 34558040 | 44 | 4.00E-42 | 1740 | | | | | |
| 16866 | | | | Campylobacter upsaliensis | | | | | |
| 16867, | 57242456 | 27 | 2.00E-26 | RM3195 | | | | | |
| 16868 | | | | | | | | | |
| 16869, | 53757202 | 38 | 2.00E-33 | Methylococcus capsulatus str. Bath | cell division protein FtsA [Methylococcus capsulatus str. Bath] ref YP_114838.1 cell division protein FtsA [Methylococcus capsulatus str. Bath] | | | | |
| 16870 | | | | | | | | | |
| 1687, | | | | Nostoc punctiforme | | | | | |
| 1688 | 23128539 | 30 | 6.00E-14 | PCC 73102 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] hypothetical protein TTC1571 [Thermus thermophilus HB27] gb AAS81913.1 hypothetical conserved protein [Thermus thermophilus HB27] | | | 2.7.3.- | |
| 16873, | | | | Thermus | | | | | |
| 16874 | 46199873 | 31 | 2.00E-13 | thermophilus HB27 | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|---------------------|---------------|
| 16875, 16876 | 34558498 | 60 | 5.00E-51 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2225 [Wolinella succinogenes DSM 1740] emb CAE11213.1 conserved hypothetical protein [Wolinella succinogenes] | | | 2.7.3.- |
| 16877, 16878 | 57240555 | 37 | 6.00E-27 | Campylobacter lari RM2100 | transformation system protein [Campylobacter lari RM2100] gb EAL55669.1 transformation system protein [Campylobacter lari RM2100] | | | |
| 16879, 16880 | 34397664 | 35 | 3.00E-46 | Porphyromonas gingivalis W83 | ABC transporter, ATP-binding protein, MsbA family [Porphyromonas gingivalis W83] ref NP_905827.1 ABC transporter, ATP-binding protein, MsbA family [Porphyromonas gingivalis W83] | | | |
| 16881, 16882 | 49524759 | 27 | 5.00E-13 | Candida glabrata CBS138 | unnamed protein product [Candida glabrata CBS138] ref XP_445454.1 unnamed protein product [Candida glabrata] | | | 3.1.3.3 |
| 16883, 16884 | 57238095 | 46 | 3.00E-49 | Campylobacter jejuni RM1221 | DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW35678.1 DNA-binding response regulator [Campylobacter jejuni RM1221] emb CAB73477.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282370.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81329 probable two-component regulator Cj1223c [imported] - Campylobacter jejuni (strain NCTC 11168) | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 4/6 | 87 8.00E-12 2.7.3.- | |
| 16885, 16886 | AAW9831 | 32 | 3.00E-16 | | Desc:H. pylori GHPO 881 protein. Org:Helicobacter pylori | | | |
| 16887, 16888 | 48856048 | 37 | 4.00E-11 | Cytophaga hutchinsonii | COG1597: Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase [Cytophaga hutchinsonii] | | | |
| 16889, 16890 | 34557780 | 37 | 4.00E-21 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10495.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes] | | | 2.7.3.- |
| 16891, 16892 | 51244370 | 42 | 6.00E-25 | Desulfotalea psychrophila LSV54 | hypothetical protein DP0518 [Desulfotalea psychrophila LSV54] emb CAG35247.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 16893, 16894 | 54028700 | 22 | 2.00E-10 | Polaromonas sp. JS666 | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Polaromonas sp. JS666] | | | |
| 16895, 16896 | 45656429 | 33 | 1.00E-16 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | tetraacyldisaccharide 4'-kinase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69152.1 tetraacyldisaccharide 4'- kinase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.7.1.13 0 |
| 16899, 16900 | 23130537 | 38 | 5.00E-44 | Nostoc punctiforme PCC 73102 | COG0778: Nitroreductase [Nostoc punctiforme PCC 73102] | | | |

| | | | | | | | | | |
|--------------|----------|----|----------|---------------------------------------|---|--|----|----------|----------|
| 169, 170 | 3282095 | 45 | 7.00E-30 | Thermotoga neapolitana | hypothetical protein [Thermotoga neapolitana] sp O86953 PANC_THENIE Pantoate-beta-alanine ligase (Pantothenate synthetase) (Pantoate activating enzyme) | | | | 6.3.2.1 |
| 16901, 16902 | 34557978 | 40 | 1.00E-53 | Wolinella succinogenes DSM 1740 | PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10693.1 PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes] | | | | 2.3.2.- |
| 16905, 16906 | 57242230 | 53 | 1.00E-70 | Campylobacter upsaliensis RM3195 | ribosomal protein S1, putative [Campylobacter upsaliensis RM3195] gb EAL53692.1 ribosomal protein S1, putative [Campylobacter upsaliensis RM3195] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 90 | 6.00E-07 | |
| 16907, 16908 | 48854003 | 41 | 1.00E-40 | Cytophaga hutchinsonii | hypothetical protein Chut02003091 [Cytophaga hutchinsonii] collagenase precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO78178.1 collagenase precursor [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 16909, 16910 | 29348481 | 62 | 2.00E-88 | Bacteroides thetaiotaomicron VPI-5482 | COG3604: Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains [Cytophaga hutchinsonii] | | | | 3.4.-.- |
| 16911, 16912 | 48856412 | 41 | 7.00E-22 | Cytophaga hutchinsonii | hypothetical protein BT1057 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76164.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 16915, 16916 | 29346467 | 31 | 5.00E-15 | Plasmodium falciparum 3D7 | hypothetical protein PF14_0667 [Plasmodium falciparum 3D7] gb AAN37280.1 hypothetical protein [Plasmodium falciparum 3D7] | | | | |
| 16919, 16920 | 23509889 | 26 | 3.00E-07 | Wolinella succinogenes DSM 1740 | RIBONUCLEASE [Wolinella succinogenes DSM 1740] emb CAE10885.1 RIBONUCLEASE [Wolinella succinogenes] | | | | 3.1.-.- |
| 16921, 16922 | 34558170 | 42 | 9.00E-41 | Alvinella pompejana epibiont | DNA-binding response regulator RprY [Alvinella pompejana epibiont 6C6] ARGINYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE09347.1 ARGINYL-TRNA SYNTHETASE [Wolinella succinogenes] | | | | 2.7.3.- |
| 16925, 16926 | 34558806 | 36 | 8.00E-35 | Wolinella succinogenes DSM 1740 | COG1555: DNA uptake protein and related DNA-binding proteins [Moorella thermoacetica ATCC 39073] | | | | 6.1.1.19 |
| 16929, 16930 | 34556632 | 59 | 5.00E-82 | Moorella thermoacetica ATCC 39073 | mannosyltransferase A (mtfA) [Archaeoglobus fulgidus DSM 4304] gb AAB91182.1 mannosyltransferase A (mtfA) [Archaeoglobus fulgidus DSM 4304] pir E69255 mannosyltransferase A (mtfA) homolog - Archaeoglobus fulgidus | | | | 2.4.1.- |
| 1693, 1694 | 49235971 | 54 | 6.00E-14 | Archaeoglobus fulgidus DSM 4304 | | | | | |
| 16931, 16932 | 11497665 | 28 | 1.00E-12 | Archaeoglobus fulgidus DSM 4304 | | | | | |

| | | | | | | | |
|-------------------------------------|-----------------------------------|----------------------------|--|--|--|--|----------|
| 16933, 16934, 16937, 16938 | 34556520 65 16937, 16938 | 3.00E-98 65 3.00E-13 | Wollinella succinogenes DSM 1740 Cytophaga hutchinsonii | hypothetical protein WS0066 [Wollinella succinogenes DSM 1740] emb CAE09235.1 conserved hypothetical protein [Wollinella succinogenes] | | | 3.1.1.1 |
| 16939, 16940 | 48854887 31 32261577 40 | 6.00E-13 31 1.00E-16 | Helicobacter hepaticus ATCC 51449 Geobacter metallireducens GS 15 | COG0538: Isocitrate dehydrogenases [Cytophaga hutchinsonii] conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859561.1 hypothetical protein HH0030 [Helicobacter hepaticus ATCC 51449] | | | |
| 16941, 16942 | 48944818 34 | 7.00E-10 | Geobacter metallireducens GS 15 | COG0500: SAM-dependent methyltransferases [Geobacter metallireducens GS-15] | | | |
| 16943, 16944, 16945, 16946 | 38505877 35 48853770 59 | 3.00E-07 35 8.00E-93 | Synechocystis sp. PCC 6803 Cytophaga hutchinsonii | hypothetical protein [Synechocystis sp. PCC 6803] dbj BAD02109.1 sl 6052 [Synechocystis sp. PCC 6803] COG0046: Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Cytophaga hutchinsonii] | | | 6.3.5.3 |
| 16947, 16948 | 57240288 50 | 2.00E-32 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55402.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 1695, 1696 | 5123897 42 | 4.00E-24 | Streptomyces coelicolor A3(2) | putative aminotransferase [Streptomyces coelicolor A3(2)] ref NP_627817.1 putative aminotransferase [Streptomyces coelicolor A3(2)] pir T35390 probable aminotransferase - Streptomyces coelicolor | | | 2.6.1.- |
| 16951, 16952 | 21283478 28 | 4.00E-11 | Staphylococcus aureus subsp. aureus MW2 | hypothetical protein MW1749 [Staphylococcus aureus subsp. aureus MW2] dbj BAB95614.1 hypothetical protein [Staphylococcus aureus subsp. aureus MW2] | | | |
| 16953, 16954 | 16125586 42 | 8.00E-28 | Caulobacter crescentus CB15 | peptidyl-prolyl cis-trans isomerase A [Caulobacter crescentus CB15] gb AAK23318.1 peptidyl-prolyl cis-trans isomerase A [Caulobacter crescentus CB15] pir B87415 peptidyl-prolyl cis-trans isomerase A [imported] - Caulobacter crescentus | | | 5.2.1.8 |
| 16955, 16956 | 46580489 41 | 3.00E-22 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96557.1 oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 16957, 16958 | 57240920 52 | 1.00E-33 | Campylobacter lari RM2100 | hydrolase, haloacid dehalogenase-like family, putative [Campylobacter lari RM2100] gb EAL55313.1 hydrolase, haloacid dehalogenase-like family, putative [Campylobacter lari RM2100] | | | 3.1.3.18 |
| 16959, 16960 | 34558414 57 | 5.00E-31 | Wollinella succinogenes DSM 1740 | PYRUVATE:FERREDOXIN OXIDOREDUCTASE GAMMA SUBUNIT [Wollinella succinogenes DSM 1740] emb CAE11129.1 PYRUVATE:FERREDOXIN OXIDOREDUCTASE GAMMA SUBUNIT [Wollinella succinogenes] | | | |
| 16961, 16962 | 20090834 34 | 2.00E-24 | Methanosarcina acetivorans C2A | transposase [Methanosarcina acetivorans C2A] gb AAM05389.1 transposase [Methanosarcina acetivorans str. C2A] | | | 1.2.7.1 |

| | | | | | | | | |
|---|----------------------|----------|----------------------|--|---|--|---------|----------|
| 16965, 16966 | 24375997 | 42 | 2.00E-08 | Shewanella oneidensis MR-1 | oxygen-independent coproporphyrinogen III oxidase, putative [Shewanella oneidensis MR-1] gb AA57484.1 oxygen-independent coproporphyrinogen III oxidase, putative [Shewanella oneidensis MR-1] | | | |
| 16969, 16970 1697, 1698 16971, 16972 | 27807025 46131192 | 50 24 | 3.00E-38 1.00E-09 | ubiquinone Ralstonia eutropha JMP134 | NADH dehydrogenase flavoprotein 2 (24kD) [ubiquinone] [NADH-ubiquinone reductase 24 kDa mitochondrial] [Bos taurus] sp P04394 NUHM_BOVIN NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor (Polypeptide II) pir B30113 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) 24K chain precursor - bovine gb AAA87358.1 NADH-ubiquinone reductase 24 kDa subunit [Bos taurus] COG0859: ADP-heptose:LPS heptosyltransferase [Ralstonia eutropha JMP134] | | 1.6.5.3 | |
| 16973, 16974 | 48854899 34558362 | 56 43 | 2.00E-26 1.00E-31 | Cytophaga hutchinsonii Wolinella succinogenes DSM 1740 | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] PEPTIDYL-TRNA HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE11077.1 PEPTIDYL-TRNA HYDROLASE [Wolinella succinogenes] sp Q7M7U8 PTH_WOLSU Peptidyl-tRNA hydrolase (PTH) | | 2.1.1.- | 3.1.1.29 |
| 16975, 16976 | 57169449 | 33 | 2.00E-33 | Campylobacter coli RM2228 | probable integral membrane protein Cj0313 [Campylobacter coli RM2228] gb EAL56931.1 probable integral membrane protein Cj0313 [Campylobacter coli RM2228] | | | |
| 16979, 16980 | 34557405 | 25 | 7.00E-07 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1018 [Wolinella succinogenes DSM 1740] emb CAE10120.1 hypothetical protein [Wolinella succinogenes] | | | |
| 16981, 16982 | 34558264 | 55 | 2.00E-36 | Wolinella succinogenes DSM 1740 | TRNA DELTA-2-ISOPENTENYL PYROPHOSPHATE [Wolinella succinogenes DSM 1740] emb CAE10979.1 TRNA DELTA-2-ISOPENTENYL PYROPHOSPHATE [Wolinella succinogenes] | | 2.5.1.8 | |
| 16985, 16986 | 48846313 | 45 | 3.00E-37 | Geobacter metallireducens GS-15 | COG1450: Type II secretory pathway, component Puid [Geobacter metallireducens GS-15] | | | |
| 16989, 16990 | 3455574 | 23 | 3.00E-15 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09289.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | |
| 1699, 1700 | 21226642 | 31 | 1.00E-11 | Methanosarcina mazel Go1 | hypothetical protein MM0540 [Methanosarcina mazel Go1] gb AAM30236.1 conserved protein [Methanosarcina mazel Go1] | | | |
| 16991, 16992 | 57169076 | 28 | 1.00E-13 | Campylobacter coli RM2228 | signal-transducing histidine kinase, putative [Campylobacter coli RM2228] gb EAL56225.1 signal-transducing histidine kinase, putative [Campylobacter coli RM2228] | | 2.7.3.- | |
| 16993, 16994 | 13475786 | 38 | 9.00E-09 | Mesorhizobium loti MAFF303099 | hypothetical protein ml6953 [Mesorhizobium loti MAFF303099] db BAB53139.1 ml6953 [Mesorhizobium loti MAFF303099] | | | |

| | | | | | | | | |
|--------|----------|----|----------|-------------------------------------|---|--|--|----------|
| 16995, | 51209987 | 33 | 2.00E-09 | Gracilaria tenuistipitata var. liui | sec-independent protein translocase-like protein [Gracilaria tenuistipitata var. liui] gb AA79706.1 sec-independent protein translocase-like protein | | | |
| 16996 | | | | | [Gracilaria tenuistipitata var. liui] | | | |
| 16999, | 53714650 | 26 | 3.00E-20 | Bacteroides fragilis YCH46 | aminopeptidase C [Bacteroides fragilis YCH46] dbj BAD50108.1 | | | |
| 17000 | | | | | aminopeptidase C [Bacteroides fragilis YCH46] | | | |
| 17001, | | | | | hypothetical protein PH0872 [Pyrococcus horikoshii OT3] dbj BAA29966.1 | | | |
| 17002 | 14590731 | 32 | 2.00E-12 | Pyrococcus horikoshii OT3 | 500aa long hypothetical protein [Pyrococcus horikoshii OT3] pir H71075 | | | |
| 17003, | | | | | hypothetical protein PH0872 - Pyrococcus horikoshii | | | |
| 17004 | 57167790 | 28 | 3.00E-11 | Campylobacter coli RM2228 | IRNA nucleotidyltransferase [Campylobacter coli RM2228] gb EAL57576.1 | | | 2.7.7.25 |
| 17005, | | | | | IRNA nucleotidyltransferase [Campylobacter coli RM2228] | | | |
| 17006 | 23474422 | 34 | 3.00E-34 | Desulfovibrio desulfuricans G20 | COG0840: Methyl-accepting chemotaxis protein [Desulfovibrio desulfuricans G20] | | | |
| 17009, | | | | | peptide deformylase [Helicobacter pylori] | | | 3.5.1.88 |
| 17010 | 49089808 | 57 | 3.00E-51 | Helicobacter pylori | COG0673: Predicted dehydrogenases and related proteins [Magnetococcus sp. MC-1] | | | 1.1.1.18 |
| 1701, | 48833968 | 47 | 3.00E-56 | Magnetococcus sp. MC-1 | | | | |
| 1702 | | | | | Mg chelatase-related protein [Campylobacter lari RM2100] gb EAL54444.1 | | | |
| 17011, | | | | | Mg chelatase-related protein [Campylobacter lari RM2100] | | | |
| 17012 | 57241774 | 49 | 1.00E-30 | Campylobacter lari RM2100 | | | | |
| 17015, | | | | | COG4122: Predicted O-methyltransferase [Cytophaga hutchinsonii] | | | 2.1.1.- |
| 17016 | 48853625 | 49 | 1.00E-55 | Cytophaga hutchinsonii | pxo1-96 [Bacillus anthracis] gb AAD32400.1 pxo1-96 [Bacillus anthracis] | | | |
| | | | | | gb AAA74029.1 ORFB [Bacillus anthracis] gb AAA74027.1 ORFB [Bacillus anthracis] pir H59102 hypothetical protein pxo1-96 - Bacillus anthracis virulence plasmid pxo1 | | | |
| 17017, | 10956343 | 41 | 2.00E-29 | Bacillus anthracis | Desc:Helicobacter pylori cellular proliferation protein #241. Org:Helicobacter pylori | | | 4.6.1.4 |
| 17018 | | | | | putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD48085.1 putative RNA polymerase ECF-type sigma factor | | | |
| 17019, | AAU3592 | 62 | 6.00E-46 | Bacteroides fragilis YCH46 | [Bacteroides fragilis YCH46] | | | |
| 17020 | | | | | hypothetical protein glr0227 [Gloeobacter violaceus PCC 7421] dbj BAC88168.1 glr0227 [Gloeobacter violaceus PCC 7421] | | | |
| 17021, | 53712627 | 38 | 9.00E-13 | Gloeobacter violaceus PCC 7421 | REGULATORY PROTEIN DNIR [Wolinella succinogenes DSM 1740] emb CAE11071.1 REGULATORY PROTEIN DNIR [Wolinella succinogenes] | | | 3.2.1.- |
| 17022 | | | | | penicillin-binding protein, 1A family [Geobacter sulfurreducens PCA] gb AAR36524.1 penicillin-binding protein, 1A family [Geobacter sulfurreducens PCA] | | | 2.4.2.- |
| 17023, | | | | | | | | |
| 17024 | 37519796 | 28 | 2.00E-11 | Wolinella succinogenes DSM 1740 | | | | |
| 17025, | | | | | | | | |
| 17026 | 34558356 | 45 | 7.00E-26 | Geobacter sulfurreducens PCA | | | | |
| 17027, | | | | | | | | |
| 17028 | 39998223 | 48 | 5.00E-18 | PCA | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---|--------------------------------------|--|--|--|--|----------|
| 17029, 17030 | 27377226 | 45 | 8.00E-31 | 110 | Bradyrhizobium japonicum USDA | hypothetical protein b1r2115 [Bradyrhizobium japonicum USDA 110] dbj BAC47380.1 b1r2115 [Bradyrhizobium japonicum USDA 110] | | | | |
| 17033, 17034 | 34558237 | 39 | 2.00E-43 | 1740 | Wolonia succinogenes DSM | hypothetical protein WS1946 [Wolonia succinogenes DSM 1740] emb CAE10952.1 hypothetical protein [Wolonia succinogenes] | | | | |
| 17035, 17036 | 52008197 | 30 | 4.00E-18 | 25259 | Thiobacillus denitrificans ATCC | COG3528: Uncharacterized protein conserved in bacteria [Thiobacillus denitrificans ATCC 25259] | | | | |
| 17037, 17038 | 53712193 | 32 | 7.00E-14 | YCH46 | Bacteroides fragilis | hypothetical protein BF0900 [Bacteroides fragilis YCH46] hypothetical protein [Bacteroides fragilis YCH46] | | | | 2.7.3.- |
| 17039, 17040 | 15838587 | 25 | 2.00E-10 | 9a5c | Xylella fastidiosa | hypothetical protein XF1993 [Xylella fastidiosa 9a5c] gb AAF84795.1 hypothetical protein XF1993 [Xylella fastidiosa 9a5c] pir C82611 hypothetical protein XF1993 [imported] - Xylella fastidiosa (strain 9a5c) | | | | |
| 17041, 17042 | 21673056 | 46 | 2.00E-68 | Chlorobium tepidum TLS | Chlorobium | ABC transporter, ATP-binding protein [Chlorobium tepidum TLS] gb AAM71463.1 ABC transporter, ATP-binding protein [Chlorobium tepidum TLS] | | | | 3.4.21.- |
| 17043, 17044 | 15643327 | 42 | 2.00E-46 | Thermotoga maritima MSB8 | Thermotoga | divalent cation transport-related protein [Thermotoga maritima MSB8] gb AAD35646.1 divalent cation transport-related protein [Thermotoga maritima MSB8] pir H72360 divalent cation transport-related protein - Thermotoga maritima (strain MSB8) | | | | |
| 17047, 17048 | 52140234 | 35 | 3.00E-34 | Bacillus cereus ZK | Bacillus cereus ZK | modification methylase, HemK family [Bacillus cereus ZK] gb AAU15253.1 modification methylase, HemK family [Bacillus cereus ZK] | | | | 2.1.1.- |
| 17051, 17052 | 20808143 | 45 | 2.00E-21 | Thermoanaerobacter tengcongensis MB4 | Thermoanaerobacter tengcongensis MB4 | Thiol-disulfide isomerase and thioredoxins [Thermoanaerobacter tengcongensis MB4] | | | | |
| 17053, 17054 | 21673718 | 29 | 7.00E-23 | Chlorobium tepidum TLS | Chlorobium tepidum TLS | methyltransferase, putative [Chlorobium tepidum TLS] gb AAM72125.1 methyltransferase, putative [Chlorobium tepidum TLS] | | | | 1.-.- |
| 17057, 17058 | 57242467 | 29 | 3.00E-24 | Campylobacter upsaliensis RM3195 | Campylobacter upsaliensis RM3195 | restriction and modification enzyme CjeI [Campylobacter upsaliensis RM3195] gb EAL53535.1 restriction and modification enzyme CjeI [Campylobacter upsaliensis RM3195] | | | | 3.1.21.3 |
| 17059, 17060 | 48853400 | 52 | 1.00E-39 | Cytophaga hutchinsonii | Cytophaga hutchinsonii | COG0732: Restriction endonuclease S subunits [Cytophaga hutchinsonii] | | | | 3.1.21.3 |
| 17061, 17062 | 53613391 | 31 | 2.00E-29 | Azotobacter vinelandii | Azotobacter vinelandii | COG1357: Uncharacterized low-complexity proteins [Azotobacter vinelandii] | | | | |
| 17065, 17066 | 34556739 | 32 | 3.00E-34 | Wolonia succinogenes DSM | Wolonia succinogenes DSM 1740 | hypothetical protein WS0303 [Wolonia succinogenes DSM 1740] emb CAE09454.1 hypothetical protein [Wolonia succinogenes] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|---------------|
| 17067, 17068 | 12517728 | 42 | 2.00E-28 | Escherichia coli O157:H7 | putative tagatose 6-phosphate kinase 2 [Escherichia coli ref NP_289703.1 putative tagatose 6-phosphate kinase 2 [Escherichia coli O157:H7 EDL933] pir B55975 probable tagatose 6-phosphate kinase 2 agaZ [imported] - Escherichia coli (strain O157:H7, substrain EDL933) | | | 2.7.1.14 4 |
| 17069, 17070 | 15643576 | 27 | 1.00E-17 | Thermotoga maritima MSB8 | hypothetical protein TM0813 [Thermotoga maritima MSB8] gb AAD35895.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir F72331 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | 2.6.1.16 |
| 17071, 17072 | 51246243 | 43 | 2.00E-35 | Desulfotalea psychrophila Lsv54 | probable two-component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila Lsv54] emb CAG37120.1 probable two- component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila Lsv54] | | | 2.7.3.- |
| 17075, 17076 | 48865290 | 36 | 3.00E-37 | Oenococcus oeni PSU-1 | COG1609: Transcriptional regulators [Oenococcus oeni PSU-1] nucleotidyltransferase PLUS glutamate rich protein GrpB PLUS ribosomal protein alanine acetyltransferase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27174.1 nucleotidyltransferase PLUS glutamate rich protein GrpB PLUS ribosomal protein alanine acetyltransferase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | 2.3.1.12 8 |
| 17077, 17078 | 52841322 | 33 | 3.00E-20 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | SAM (and some other nucleotide) binding motif [Nitrosomonas europaea ATCC 19718] emb CAD86083.1 SAM (and some other nucleotide) binding motif [Nitrosomonas europaea ATCC 19718] | | | |
| 17079, 17080 | 30250106 | 35 | 3.00E-09 | Nitrosomonas europaea ATCC 19718 | dTDP-4-dehydrothiamine reductase [Bacillus clausii KSM-K16] dbj BAD66221.1 dTDP-4-dehydrothiamine reductase [Bacillus clausii KSM- K16] | | | 1.1.1.13 3 |
| 17081, 17082 | 56965450 | 30 | 1.00E-14 | Bacillus clausii KSM-K16 | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | |
| 17083, 17084 | 48853395 | 46 | 4.00E-26 | Cytophaga hutchinsonii | glycosyltransferase WbaZ [Escherichia coli] transposase, similar to IS240 [Methanocaldococcus jannaschii DSM 2661] gb AAB99474.1 transposase, similar to IS240 [Methanocaldococcus jannaschii DSM 2661] pir A64483 hypothetical protein MJ1466 - Methanococcus jannaschii sp Q58861 YE66_METJA Hypothetical protein MJ1466 | | | 2.4.1.- |
| 17085, 17086 | 4512014 | 51 | 4.00E-77 | Escherichia coli | COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii] | | | |
| 1709, 1710 | 15669657 | 34 | 7.00E-21 | Methanocaldococ- us jannaschii DSM 2661 | | | | |
| 17091, 17092 | 48853585 | 35 | 4.00E-30 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---------------------------------|---------------------------------|---|--|----|----------------------|
| 17093, 17094 | 34557033 | 58 | 1.00E-64 | 1740 | Wolinella succinogenes DSM | GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09748.1 GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes] sp Q7M9X0 HIS5_WOLSU lmidazole glycerol phosphate synthase subunit hisH (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (mGP synthase subunit hisH) (IGP subunit hisH) | | | 2.4.2.- |
| 17095, 17096 | 15896194 | 26 | 1.00E-08 | ATCC 824 | Clostridium acetobutylicum | HAD superfamily hydrolase [Clostridium acetobutylicum ATCC 824] gb AAK80883.1 HAD superfamily hydrolase [Clostridium acetobutylicum ATCC 824] pir j497261 HAD superfamily hydrolase [imported] - Clostridium acetobutylicum | | | |
| 17097, 17098 | 57240961 | 63 | 3.00E-64 | RM2100 | Campylobacter lari | conserved hypothetical protein TIGR00423 [Campylobacter lari RM2100] gb EAL55354.1 conserved hypothetical protein TIGR00423 [Campylobacter lari RM2100] | | | 2.8.1.6 |
| 17099, 17100 | 48854814 | 79 | 1.00E-108 | Cytophaga hutchinsonii | | COG0396: ABC-type transport system involved in Fe-S cluster assembly, ATPase component [Cytophaga hutchinsonii] | Desc:Enterococcus faecalis contig sequence #929. Org:Enterococcus faecalis | 81 | 6.00E-07 1.8.- |
| 171, 172 | 48855001 | 31 | 1.00E-14 | Cytophaga hutchinsonii | | COG2849: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | 2.7.1.68 |
| 17105, 17106 | 48856573 | 41 | 2.00E-61 | Cytophaga hutchinsonii | | COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii] | | | |
| 17109, 17110 | 34556843 | 40 | 8.00E-44 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS0414 [Wolinella succinogenes DSM 1740] emb CAE09558.1 conserved hypothetical protein [Wolinella succinogenes] putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79084.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.3.- |
| 1711, 1712 | 29349387 | 50 | 1.00E-28 | VPI-5482 | Bacteroides thetaiotaomicron | rod shape-determining protein (mreC), putative [Campylobacter coli RM2228] gb EAL56879.1 rod shape-determining protein (mreC), putative [Campylobacter coli RM2228] | | | 2.1.1.- |
| 17111, 17112 | 57168397 | 31 | 3.00E-23 | RM2228 | Campylobacter coli | phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] gb AAD35904.1 phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] pir j472330 phenylalanyl-tRNA ligase (EC 6.1.1.20) beta chain - Thermotoga maritima (strain MSB8) sp Q9WZS9 SYFB_THEME Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS) | | | |
| 17113, 17114 | 15643585 | 44 | 1.00E-54 | Thermotoga maritima MSB8 | | hypothetical NosD, Nitrous oxidase accessory protein [Photobacterium profundum SS9] emb CAG22720.1 hypothetical NosD, Nitrous oxidase accessory protein [Photobacterium profundum] | Photobacterium profundum SS9 chromosome 2; segment 3/7 | 79 | 6.1.1.20 3.00E-08 |
| 17115, 17116 | 54302527 | 73 | 6.00E-86 | Photobacterium profundum SS9 | | | | | |

| | | | | | | | | | |
|-------------------------------------|----------------------|----------|----------------------|--|---|--|--|--|--------------------|
| 17119, 17120, 17127, 17128 | 15644023 46131517 | 68 36 | 2.00E-48 8.00E-13 | Thermotoga maritima MSB8 Ralstonia eutropha JMP134 | thiH protein, putative [Thermotoga maritima MSB8] gb AAD36342.1 thiH protein, putative [Thermotoga maritima MSB8] pir B72274 hypothetical protein TM1267 - Thermotoga maritima (strain MSB8) COG1629: Outer membrane receptor proteins, mostly Fe transport [Ralstonia eutropha JMP134] | | | | 2.8.1.6 |
| 1713, 1714, 17131, 17132 | 29349387 48855487 | 50 73 | 1.00E-28 2.00E-37 | Bacteroides thetaiotaomicron VPI-5482 Cytophaga hutchinsonii | putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79084.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] COG1048: Aconitase A [Cytophaga hutchinsonii] | | | | 2.1.1.- 4.2.1.3 |
| 17133, 17134 | 6459446 | 29 | 1.00E-21 | Deinococcus radiodurans | hypothetical protein [Deinococcus radiodurans] pir G75368 hypothetical protein - Deinococcus radiodurans (strain R1) ref NP_295399.1 hypothetical protein DR1676 [Deinococcus radiodurans R1] | | | | |
| 17135, 17136 | 9947043 | 53 | 1.00E-45 | Pseudomonas aeruginosa PAO1 | deoxyguanosinetriphosphate triphosphohydrolase [Pseudomonas aeruginosa PAO1] pir H83505 deoxyguanosinetriphosphate triphosphohydrolase PA1124 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_249815.1 deoxyguanosinetriphosphate triphosphohydrolase [Pseudomonas aeruginosa PAO1] sp Q914L1 DGTP_PSEAE Probable deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase) | | | | 3.1.5.1 |
| 17137, 17138 | 17229920 | 26 | 3.00E-13 | Nostoc sp. PCC 7120 | two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] pir AE2109 two-component hybrid sensor and regulator alr2428 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB74127.1 two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] | | | | 2.7.3.- |
| 17139, 17140 | 29348537 | 58 | 2.00E-59 | Bacteroides thetaiotaomicron VPI-5482 | putative xanthosine triphosphate pyrophosphatase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78234.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.7.56 |
| 17141, 17142 | 18309624 | 40 | 9.00E-40 | Clostridium perfringens str. 13 | two-component response regulator [Clostridium perfringens str. 13] dbj BAB80348.1 two-component response regulator [Clostridium perfringens str. 13] | | | | 2.7.3.- |
| 17145, 17146 | 38638619 | 44 | 1.00E-36 | Burkholderia cenocepacia phage Bcep1 | gp12 [Burkholderia cenocepacia phage Bcep1] gb AAQ73358.1 gp12 [Burkholderia cenocepacia phage Bcep1] | | | | |
| 17147, 17148 | 9654468 | 44 | 6.00E-35 | Vibrio cholerae O1 biovar eltor str. N16961 | sensory box/GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229731.1 sensory box/GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961] pir H82367 sensory box/GGDEF family protein VC0072 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 17149, 17150 | 51209539 | 51 | 6.00E-40 | Campylobacter jejuni | cgp27 [Campylobacter jejuni] gb AAR29560.1 cgp27 [Campylobacter jejuni] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|----------|
| 1715, 1716 | 53731132 | 40 | 3.00E-12 | Methanococcoides burtonii DSM 6242 | COG2097: Ribosomal protein L31E [Methanococcoides burtonii DSM 6242] | | | | |
| 17151, 17152 | 24214120 | 37 | 4.00E-14 | Leptospira interrogans serovar Lai str. 56601 | hypothetical protein LA1420 [Leptospira Interrogans serovar Lai str. 56601] gb AA48619.1 unknown protein [Leptospira interrogans serovar lai str. 56601] | | | | |
| 17157, 17158 | 34557543 | 36 | 4.00E-39 | Wolinella succinogenes DSM 1740 | PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10258.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] emb CAD5552.1 NapL protein [Wolinella succinogenes] | | | | |
| 17163, 17164 | 34557640 | 49 | 8.00E-61 | Wolinella succinogenes DSM 1740 | POSSIBLE TRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10355.1 POSSIBLE TRANSFERASE [Wolinella succinogenes] | | | | 2.3.2.8 |
| 17165, 17166 | 57241121 | 39 | 3.00E-47 | Campylobacter lari RM2100 | DNA repair protein RecN, putative [Campylobacter lari RM2100] gb EAL54817.1 DNA repair protein RecN, putative [Campylobacter lari RM2100] | | | | |
| 17167, 17168 | 19338425 | 41 | 9.00E-08 | Rhizobium leguminosarum bv. viciae | two-component response regulator [Rhizobium leguminosarum bv. viciae] | | | | |
| 17169, 17170 | 57241290 | 61 | 1.00E-40 | Campylobacter lari RM2100 | Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100] gb EAL54986.1 Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100] | Campylobacter lari subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 97 | 3.00E-11 | 4.--- |
| 1717, 1718 | 48855091 | 42 | 3.00E-40 | Cytophaga hutchinsonii | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii] | | | | 3.1.1.61 |
| 17171, 17172 | 42527788 | 41 | 4.00E-50 | Treponema denticola ATCC 35405 | MazG family protein [Treponema denticola ATCC 35405] gb AAS12805.1 MazG family protein [Treponema denticola ATCC 35405] | | | | |
| 17173, 17174 | 51246665 | 37 | 3.00E-29 | Desulfotalea psychrophila LSv54 | hypothetical protein DP2813 [Desulfotalea psychrophila LSv54] emb CAG37542.1 conserved hypothetical protein [Desulfotalea psychrophila LSv54] | | | | |
| 17175, 17176 | 45523887 | 27 | 5.00E-09 | Crocospira watsonii WH 8501 | COG5433: Transposase [Crocospira watsonii WH 8501] | | | | |
| 17179, 17180 | 50304149 | 25 | 6.00E-08 | Kluyveromyces lactis | unnamed protein product [Kluyveromyces lactis] emb CAH02417.1 unnamed protein product [Kluyveromyces lactis NRRL Y-1140] | | | | |
| 17185, 17186 | 21241245 | 25 | 6.00E-07 | Xanthomonas axonopodis pv. citri str. 306 | membrane protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM35363.1 membrane protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|-------------------------------------|--|--|--|--|---------|
| 17187, 17188 | 17228167 | 30 | 2.00E-08 | Nostoc sp. PCC 7120 | WD-repeat protein [Nostoc sp. PCC 7120] dbj BAB72629.1 WD-repeat protein [Nostoc sp. PCC 7120] pir JAF1890 WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) | | | | |
| 17191, 17192 | 57158492 | 31 | 7.00E-11 | Thermococcus kodakaraensis | ribosomal protein-serine acetyltransferase RimL homolog [Thermococcus kodakaraensis] ref YP_182646.1 ribosomal protein-serine acetyltransferase RimL homolog [Thermococcus kodakaraensis] | | | | |
| 17197, 17198 | 15607008 | 32 | 2.00E-17 | Aquifex aeolicus VF5 | hypothetical protein aq_2027 [Aquifex aeolicus VF5] gb AAC07788.1 hypothetical protein [Aquifex aeolicus VF5] pir J70474 conserved hypothetical protein aq_2027 - Aquifex aeolicus sp O67821 YK27_AQUAE Hypothetical protein Aq_2027 | | | | |
| 17199, 17200 | 34556582 | 39 | 4.00E-13 | Wolinella succinogenes DSM 1740 | PUTATIVE INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09297.1 PUTATIVE INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes] | | | | |
| 17201, 17202 | 21674385 | 30 | 4.00E-14 | Chlorobium tepidum TLS | BmrU protein [Chlorobium tepidum TLS] gb AAM72792.1 BmrU protein [Chlorobium tepidum TLS] | | | | |
| 17203, 17204 | 48853894 | 44 | 9.00E-49 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | | |
| 17209, 17210 | 48860014 | 40 | 8.00E-30 | thermocellum ATCC 27405 | COG3321: Polyketide synthase modules and related proteins [Clostridium thermocellum ATCC 27405] | | | | |
| 17213, 17214 | 34557352 | 42 | 8.00E-28 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0964 [Wolinella succinogenes DSM 1740] emb CAE10067.1 conserved hypothetical protein [Wolinella succinogenes] | | | | 2.7.3.- |
| 17215, 17216 | 34558806 | 33 | 3.00E-07 | Alvinella pompejana epibiont 6C6 | DNA-binding response regulator RprY [Alvinella pompejana epibiont 6C6] DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | | |
| 17217, 17218 | 34557665 | 42 | 4.00E-36 | Wolinella succinogenes DSM 1740 | ENSANGP00000019035 [Anopheles gambiae] | | | | 2.7.3.- |
| 17219, 17220 | 31204521 | 32 | 5.00E-14 | Anopheles gambiae | COG2770: FOG: HAMP domain [Nostoc punctiforme PCC 73102] | | | | 4.6.1.1 |
| 17221, 17222 | 23123968 | 25 | 1.00E-18 | Nostoc punctiforme PCC 73102 | Methyl-accepting chemotaxis protein, contain HAMP domain [Clostridium acetobutylicum ATCC 824] gb AAK78885.1 Methyl-accepting chemotaxis protein, contain HAMP domain [Clostridium acetobutylicum ATCC 824] pir B97012 methyl-accepting chemotaxis protein, contain HAMP domain [imported] - Clostridium acetobutylicum | | | | 2.7.3.- |
| 17223, 17224 | 15894196 | 24 | 1.00E-06 | Clostridium acetobutylicum ATCC 824 | | | | | 2.7.3.- |

| | | | | | | | | |
|-----------------|--------------|----|----------|--|--|--|--|----------|
| 17225, 17226 | 34396333 | 44 | 6.00E-36 | Porphyromonas gingivalis W83 | conserved domain protein [Porphyromonas gingivalis W83] ref NP_904501.1 hypothetical protein PG0160 [Porphyromonas gingivalis W83] | | | |
| 17229, 17230 | 57242241 | 43 | 4.00E-48 | NiFe | [NiFe] hydrogenase maturation protein HypF [Campylobacter upsallensis RM3195] gb EAL53703.1 [NiFe] hydrogenase maturation protein HypF [Campylobacter upsallensis RM3195] | | | |
| 1723, 1724 | 53711817 | 28 | 2.00E-20 | Bacteroides fragilis YCH46 | hypothetical protein BF0526 [Bacteroides fragilis YCH46] dbj BAD47275.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 17231, 17232 | 15606085 | 40 | 3.00E-35 | Aquifex aeolicus VF5 | transcriptional regulatory protein HypF [Aquifex aeolicus VF5] gb AAC06863.1 transcriptional regulatory protein HypF [Aquifex aeolicus VF5] pir B70359 transcription regulator HypF - Aquifex aeolicus | | | |
| 17233, 17234 | 34558196 | 33 | 2.00E-28 | Wolinella succinogenes DSM 1740 | DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes] | | | 2.7.7.- |
| 17235, 17236 | 34558196 | 56 | 5.00E-80 | Wolinella succinogenes DSM 1740 | DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes] | | | 2.7.7.- |
| 17239, 17240 | 32469876 | 33 | 4.00E-26 | Campylobacter jejuni | VirB4 [Campylobacter jejuni] gb AAN46946.1 VirB4 [Campylobacter jejuni] | | | |
| 17241, 17242 | 48846045 | 36 | 3.00E-27 | Geobacter metallireducens GS 15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 17243, 17244 | 30249663 | 39 | 2.00E-49 | Nitrosomonas europaea ATCC 19718 | possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718] emb CAD85612.1 possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718] | | | 1.8.4.6 |
| 17245, 17246 | ABB4813 5 | 34 | 1.00E-17 | | Desc:Listeria monocytogenes protein #839. Org:Listeria monocytogenes COG1197: Transcription-repair coupling factor (superfamily II helicase) | | | |
| 17247, 17248 | 48853984 | 49 | 4.00E-62 | Cytophaga hutchinsonii | [Cytophaga hutchinsonii] | | | |
| 17249, 17250 | 48855632 | 36 | 4.00E-13 | Cytophaga hutchinsonii | COG0712: F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein) [Cytophaga hutchinsonii] | | | 3.6.3.14 |
| 1725, 1726 | 53711742 | 33 | 5.00E-11 | Bacteroides fragilis YCH46 | UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate-D-alanyl-D- alanyl ligase [Bacteroides fragilis YCH46] dbj BAD47200.1 UDP-N- acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides fragilis YCH46] | | | 6.3.2.15 |
| 17251, 17252 | 48855632 | 35 | 1.00E-25 | Cytophaga hutchinsonii | COG0712: F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein) [Cytophaga hutchinsonii] | | | 3.6.3.15 |

| | | | | | | | | | | |
|-----------------|----------|----|-----------|--|---|--|----|----------|----------|----------|
| 17257, 17258 | 34558383 | 45 | 4.00E-68 | Wollinella succinogenes DSM 1740 | RNA POLYMERASE SIGMA-54 FACTOR [Wollinella succinogenes DSM 1740] emb CAE11098.1 RNA POLYMERASE SIGMA-54 FACTOR [Wollinella succinogenes] | | | | | |
| 17261, 17262 | 57168943 | 59 | 2.00E-62 | Campylobacter coli RM2228 | glyceraldehyde-3-phosphate dehydrogenase, type I [Campylobacter coli RM2228] gb EAL56298.1 glyceraldehyde-3-phosphate dehydrogenase, type I [Campylobacter coli RM2228] | | | | | 1.2.1.12 |
| 17263, 17264 | 53688490 | 31 | 2.00E-20 | Nostoc punctiforme PCC 73102 | COG1100: GTPase SAR1 and related small G proteins [Nostoc punctiforme PCC 73102] | | | | | |
| 17265, 17266 | 34557419 | 40 | 4.00E-30 | Wollinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes] | | | | | 2.7.3.- |
| 17269, 17270 | 46140379 | 44 | 5.00E-25 | Dechloromonas aromatica RCB | COG0835: Chemotaxis signal transduction protein [Dechloromonas aromatica RCB] | | | | | 2.7.3.- |
| 1727, 1728 | 48854018 | 65 | 1.00E-120 | Cytophaga hutchinsonii | COG0423: Glycyl-tRNA synthetase (class II) [Cytophaga hutchinsonii] | Bacteroides thetaiotaomicron VPI-5482, section 16 of 21 of the complete genome | 82 | 8.00E-16 | 6.1.1.14 | |
| 17271, 17272 | 48856870 | 31 | 6.00E-37 | Cytophaga hutchinsonii | COG1555: DNA uptake protein and related DNA-binding proteins [Cytophaga hutchinsonii] | | | | | |
| 17273, 17274 | 34555688 | 59 | 9.00E-98 | Wollinella succinogenes DSM 1740 | ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09403.1 ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wollinella succinogenes] | | | | | 1.8.- |
| 17275, 17276 | 56460917 | 54 | 9.00E-29 | Idiomarina loihensis L2TR | hypothetical protein IL1817 [Idiomarina loihensis L2TR] gb AAV82649.1 Uncharacterized conserved protein [Idiomarina loihensis L2TR] | Vibrio salmonicida partial plasmid pRVS1 | 82 | 1.00E-33 | | |
| 17277, 17278 | 46401632 | 42 | 3.00E-43 | Enterobacteria phage P1 | Res [Enterobacteria phage P1] gb AAQ14090.1 Res [Enterobacteria phage P1] gb AAQ13982.1 Res [Enterobacteria phage P1] emb CAA29615.1 unnamed protein product [Enterobacteria phage P1] sp P08764 T3RE_BPP1 Type III restriction-modification system EcoPI enzyme res pir S01352 type III site-specific deoxyribonuclease (EC 3.1.21.5) EcoP1 chain res - phage P1 | | | | | 3.1.21.5 |
| 17281, 17282 | 34557246 | 30 | 6.00E-33 | Wollinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes] | | | | | |
| 17283, 17284 | 48846045 | 37 | 1.00E-24 | Geobacter metallireducens GS-15 | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | | | 2.7.3.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|----------|
| 17285, 17286 | 288221 | 38 | 1.00E-61 | Myxococcus xanthus | ORF2 [Myxococcus xanthus] p[ri]S32169 hypothetical protein 2 - Myxococcus xanthus sp[P54979]CRTJ_MYXXA Phytoene dehydrogenase (Phytoene desaturase) | | | | |
| 17289, 17290 | 34556985 | 38 | 4.00E-42 | Wolinella succinogenes DSM 1740 | EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT [Wolinella succinogenes DSM 1740] emb[CAE09700.1] EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT [Wolinella succinogenes] | | | | 3.1.11.6 |
| 17291, 17292 | 56707780 | 57 | 2.00E-73 | Francisella tularensis subsp. tularensis Schu 4 | DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb[CAG45292.1] DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis] | | | | |
| 17295, 17296 | 39997909 | 34 | 2.00E-16 | Geobacter sulfurreducens PCA | sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gbJAAR36210.1] sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] | | | | |
| 17297, 17298 | 57237364 | 33 | 3.00E-40 | Campylobacter jejuni RM1221 | membrane protein, putative [Campylobacter jejuni RM1221] gbJAAW34947.1] membrane protein, putative [Campylobacter jejuni RM1221] | | | | |
| 17299, 17300 | 29348366 | 41 | 8.00E-59 | Bacteroides thetaiotaomicron VPI-5482 | transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] gbJAAO78063.1] transcriptional regulator [Bacteroides thetaiotaomicron VPI- 5482] | | | | |
| 173, 174 | 21242456 | 41 | 1.00E-24 | Xanthomonas axonopodis pv. citri str. 306 | general stress protein [Xanthomonas axonopodis pv. citri str. 306] gbJAAW36574.1] general stress protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 17301, 17302 | 48853414 | 40 | 1.00E-64 | Cytophaga hutchinsonii | COG0686: Alanine dehydrogenase [Cytophaga hutchinsonii] | | | | 1.5.1.7 |
| 17303, 17304 | 48855884 | 40 | 4.00E-22 | Cytophaga hutchinsonii | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | | |
| 17305, 17306 | 48856096 | 57 | 4.00E-70 | Cytophaga hutchinsonii | COG3129: Predicted SAM-dependent methyltransferase [Cytophaga hutchinsonii] | | | | |
| 17307, 17308 | 48846045 | 37 | 1.00E-29 | Geobacter metallireducens GS | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | | 2.7.3.- |
| 17309, 17310 | 46143327 | 42 | 2.00E-39 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | COG0514: Superfamily II DNA helicase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | | 3.6.1.- |
| 1731, 1732 | 53715782 | 59 | 7.00E-91 | Bacteroides fragilis YCH46 | methionyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj[BAD51240.1] methionyl-tRNA synthetase [Bacteroides fragilis YCH46] | Mus musculus cDNA clone IMAGE:30025832 | 80 | 8.00E-25 | 6.1.1.10 |
| 17313, 17314 | 48895665 | 48 | 5.00E-30 | Trichodesmium erythraeum IMS101 | COG0286: Type I restriction-modification system methyltransferase subunit [Trichodesmium erythraeum IMS101] | | | | 2.1.1.72 |

| | | | | | | | | | |
|-----------------|--------------|----|-----------|---|--|----|----------|----------|--|
| 17315, 17316 | 34556743 | 50 | 4.00E-52 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0307 [Wolinella succinogenes DSM 1740] emb CAE09458.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 17317, 17318 | 48892769 | 34 | 6.00E-08 | Trichodesmium erythraeum IMS101 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] hypothetical protein BT3853 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78958.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 17319, 17320 | 29349261 | 35 | 1.00E-38 | Bacteroides thetaitaomicron VPI-5482 | | | | | |
| 17321, 17322 | 46142296 | 61 | 1.00E-109 | Methanococcoides burtonii DSM 6242 | COG4804: Uncharacterized conserved protein [Methanococcoides burtonii DSM 6242] | | | | |
| 17327, 17328 | 48833879 | 26 | 2.00E-17 | Magnetococcus sp. MC-1 | COG0525: Valyl-tRNA synthetase [Magnetococcus sp. MC-1] | | | | |
| 17329, 17330 | ABB4802 6 | 51 | 4.00E-46 | | Clostridium acetobutylicum ATCC 824 section 254 of 356 of the complete genome | 87 | 1.00E-09 | 2.4.1.8 | |
| 1733, 1734 | AAU3655 0 | 30 | 4.00E-19 | | Desc:Listeria monocytogenes protein #730. Org:Listeria monocytogenes Desc:Staphylococcus aureus cellular proliferation protein #720. Org:Staphylococcus aureus | | | | |
| 17331, 17332 | 23472835 | 37 | 3.00E-16 | Pseudomonas syringae pv. syringae B728a | hypothetical protein Psyr03004990 [Pseudomonas syringae pv. syringae B728a] | | | | |
| 17333, 17334 | 48859668 | 30 | 2.00E-24 | Clostridium thermocellum ATCC 27405 | COG1451: Predicted metal-dependent hydrolase [Clostridium thermocellum ATCC 27405] | | | 3.4.24.- | |
| 17335, 17336 | 57240288 | 48 | 2.00E-59 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55402.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 17337, 17338 | 46142567 | 51 | 8.00E-30 | Methanococcoides burtonii DSM 6242 | COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242] | | | 2.1.1.73 | |
| 17339, 17340 | 46142567 | 38 | 3.00E-31 | Methanococcoides burtonii DSM 6242 | COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242] | | | 2.1.1.73 | |
| 17343, 17344 | 34556481 | 27 | 1.00E-18 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 17345, 17346 | 34556481 | 43 | 1.00E-41 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes] | | | 2.7.3.- |
| 17349, 17350 | 51245709 | 40 | 6.00E-10 | Desulfotalea psychrophila LSV54 | hypothetical protein DP1857 [Desulfotalea psychrophila LSV54] emb CAG36586.1 hypothetical protein [Desulfotalea psychrophila LSV54] | | | 2.3.1.51 |
| 1735, 1736 | 48847199 | 50 | 5.00E-55 | Geobacter metallireducens GS-15 | COG0861: Membrane protein TerC, possibly involved in tellurium resistance [Geobacter metallireducens GS-15] | | | |
| 17351, 17352 | 48859385 | 24 | 9.00E-18 | Clostridium thermocellum ATCC 27405 | COG0658: Predicted membrane metal-binding protein [Clostridium thermocellum ATCC 27405] | | | |
| 17353, 17354 | 29347784 | 44 | 2.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2374 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77481.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 17355, 17356 | 4234793 | 27 | 1.00E-09 | Leptospira borgpetersenii | unknown [Leptospira borgpetersenii] | | | |
| 17357, 17358 | 45657982 | 49 | 5.00E-20 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | sugar transferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711831.1 hemolysin hemolytic protein hlpA [Leptospira interrogans serovar Lai str. 56601] gb AA448849.1 hemolysin hemolytic protein hlpA [Leptospira interrogans serovar lai str. 56601] gb AAK19900.1 unknown [Leptospira interrogans] gb AAD52178.1 unknown [Leptospira interrogans] gb AAS70705.1 sugar transferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 17359, 17360 | 48855350 | 32 | 3.00E-19 | Cytophaga hutchinsonii | COG2849: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 17361, 17362 | 15605941 | 48 | 3.00E-52 | Aquifex aeolicus VF5 | hypothetical protein aq_321 [Aquifex aeolicus VF5] gb AAC06618.1 putative protein [Aquifex aeolicus VF5] pir [F70328 hypothetical protein aq_321 - Aquifex aeolicus] | | | |
| 17363, 17364 | 20806660 | 49 | 1.00E-50 | Thermoanaerobact er tengcongensis MB4 | Hydrogenase maturation factor [Thermoanaerobacter tengcongensis MB4] gb AAM23435.1 Hydrogenase maturation factor [Thermoanaerobacter tengcongensis MB4] | | | 3.6.1.7 |
| 17365, 17366 | 46580951 | 39 | 3.00E-26 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | transcriptional regulator, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97019.1 transcriptional regulator, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 17367, 17368 | 31615651 | 33 | 1.00E-06 | | Chain B, Design Of Stable Alpha-Helical Arrays From An Idealized Tpr Motif pdb 1NA0 A Chain A, Design Of Stable Alpha-Helical Arrays From An Idealized Tpr Motif | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|---|--|--|----------|
| 17369, 17370 | 48855217 | 37 | 2.00E-39 | Cytophaga hutchinsonii | COG5635: Predicted NTPase (NACHT family) [Cytophaga hutchinsonii] | | | |
| 1737, 1738 | 48847199 | 46 | 2.00E-48 | Geobacter metallireducens GS-15 | COG0861: Membrane protein TerC, possibly involved in tellurium resistance [Geobacter metallireducens GS-15] | | | |
| 17371, 17372 | 23506369 | 31 | 6.00E-10 | Francisella tularensis subsp. novicida | galactose epimerase [Francisella tularensis subsp. novicida] | | | 5.1.3.2 |
| 17373, 17374 | 17940062 | 42 | 2.00E-32 | Leptospira interrogans | unknown [Leptospira interrogans] | | | 2.4.1.- |
| 17375, 17376 | 39996515 | 41 | 2.00E-57 | Geobacter sulfurreducens PCA | sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gblAAR34789.1] sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] | | | 2.7.3.- |
| 17377, 17378 | 52548677 | 37 | 5.00E-07 | uncultured archaeon GZfos18C8 | hypothetical protein GZ18C8_3 [uncultured archaeon GZfos18C8] | | | |
| 17379, 17380 | 48858932 | 43 | 2.00E-41 | Clostridium thermocellum ATCC 27405 | COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | 2.7.3.- |
| 17381, 17382 | 34556868 | 28 | 5.00E-23 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0441 [Wolinella succinogenes DSM 1740] embjCAE09583.1] conserved hypothetical protein [Wolinella succinogenes] PUTATIVE HOLLIDAY JUNCTION DNA HELICASE [Wolinella succinogenes DSM 1740] embjCAE09582.1] PUTATIVE HOLLIDAY JUNCTION DNA HELICASE [Wolinella succinogenes] spjQ7MA70 RUVA_WOLSU Holliday junction DNA helicase ruva | | | |
| 17383, 17384 | 34556867 | 50 | 2.00E-38 | Wolinella succinogenes DSM 1740 | rfbL protein [Vibrio cholerae O1 biovar eltor str. N16961] refjNP_229906.1] rfbL protein [Vibrio cholerae O1 biovar eltor str. N16961] embjCAA42142.1] rfbL [Vibrio cholerae] pirjS28476 rfbL protein VC0249 [similarity] - Vibrio cholerae (strain N16961 serogroup O1) prfj2203284B rfbL gene | | | 6.2.1.3 |
| 17389, 17390 | 34557200 | 31 | 2.00E-30 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0802 [Wolinella succinogenes DSM 1740] embjCAE09915.1] conserved hypothetical protein [Wolinella succinogenes] probable acylaminoacyl-peptidase [Rhodopirellula baltica SH 1] embjCAD71387.1] probable acylaminoacyl-peptidase [Pirellula sp.] 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE [Wolinella succinogenes DSM 1740] embjCAE10998.1] 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE [Wolinella succinogenes] spjQ7M7Z0 DXS_WOLSU 1-deoxy-D-xylulose-5-phosphate synthase (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS) | | | 4.1.3.37 |
| 1739, 1740 | 32470723 | 27 | 7.00E-22 | Rhodopirellula baltica SH 1 | | | | |
| 17391, 17392 | 34558283 | 67 | 1.00E-105 | Wolinella succinogenes DSM 1740 | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|--|--|--|--|----------|
| 17393, 17394 | AAU3592 8 | 58 | 6.00E-66 | | | Desc: Helicobacter pylori cellular proliferation protein #241. Org: Helicobacter pylori | | | 4.6.1.4 |
| 17395, 17396 | 57240635 | 41 | 2.00E-36 | Campylobacter lari RM2100 | | peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL55749.1 peptidase, M23/M37 family [Campylobacter lari RM2100] | | | |
| 17397, 17398 | 20808841 | 47 | 2.00E-59 | Thermoanaerobact er tengcongensis MB4 | | NADH dehydrogenase, FAD-containing subunit [Thermoanaerobacter tengcongensis MB4] NADH dehydrogenase, FAD-containing subunit [Thermoanaerobacter tengcongensis MB4] | | | 1.6.99.3 |
| 17399, 17400 | 53715372 | 67 | 1.00E-45 | Bacteroides fragilis YCH46 | | putative GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD50830.1 putative GTP-binding protein [Bacteroides fragilis YCH46] | | | |
| 17401, 17402 | 48845271 | 43 | 4.00E-43 | Geobacter metallireducens GS-15 | | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 17403, 17404 | 55822185 | 49 | 1.00E-37 | Streptococcus thermophilus CNRZ1066 | | undecaprenyl pyrophosphate synthetase [Streptococcus thermophilus CNRZ1066] ref YP_138737.1 undecaprenyl pyrophosphate synthetase [Streptococcus thermophilus LMG 18311] gb AAV61811.1 undecaprenyl pyrophosphate synthetase [Streptococcus thermophilus CNRZ1066] gb AAV59922.1 undecaprenyl pyrophosphate synthetase [Streptococcus thermophilus LMG 18311] | | | 2.5.1.31 |
| 17411, 17412 | 37519590 | 36 | 6.00E-44 | Geobacter violaceus PCC 7421 | | HlyB/MsbA family ABC transporter [Geobacter violaceus PCC 7421] dbj BAC87962.1 HlyB/MsbA family ABC transporter [Geobacter violaceus PCC 7421] | | | 3.4.21.- |
| 17413, 17414 | 34557946 | 43 | 2.00E-29 | Wolinella succinogenes DSM 1740 | | RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes DSM 1740] emb CAE10681.1 RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes] | | | 2.7.3.- |
| 17415, 17416 | 34557665 | 50 | 4.00E-39 | Wolinella succinogenes DSM 1740 | | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | 2.7.3.- |
| 17417, 17418 | 34558399 | 44 | 9.00E-26 | Wolinella succinogenes DSM 1740 | | 3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE KDTA [Wolinella succinogenes DSM 1740] emb CAE11114.1 3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE KDTA [Wolinella succinogenes] | | | 2.4.99.- |
| 17419, 17420 | 16330004 | 37 | 4.00E-34 | Synechocystis sp. PCC 6803 | | hypothetical protein slr2077 [Synechocystis sp. PCC 6803] dbj BAA17412.1 slr2077 [Synechocystis sp. PCC 6803] pir S77565 hypothetical protein slr2077 - Synechocystis sp. (strain PCC 6803) | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 17421, 17422 | 15895797 | 40 | 2.00E-20 | Clostridium acetobutylicum ATCC 824 | HD_GYP hydrolase domain fused to HD hydrolase domain [Clostridium acetobutylicum ATCC 824] gb AAK80486.1 HD_GYP hydrolase domain fused to HD hydrolase domain [Clostridium acetobutylicum ATCC 824] pir C97212 HD_GYP hydrolase domain fused to HD hydrolase domain [imported] - Clostridium acetobutylicum | | | | |
| 17423, 17424 | 54301944 | 38 | 2.00E-44 | Photobacterium profundum SS9 | putative response regulator protein [Photobacterium profundum SS9] emb CAG22137.1 putative response regulator protein [Photobacterium profundum] | | | | 2.7.3.- |
| 17427, 17428 | 46202456 | 36 | 2.00E-58 | Magnetospirillum magnetotacticum MS-1 | COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1] | | | | 2.7.3.- |
| 17429, 17430 | 48853400 | 53 | 7.00E-44 | Cytophaga hutchinsonii | COG0732: Restriction endonuclease S subunits [Cytophaga hutchinsonii] | | | | 3.1.21.- |
| 1743, 1744 | 22797876 | 45 | 2.00E-62 | uncultured crenarchaeote | putative alpha/beta hydrolase [uncultured crenarchaeote] | | | | 3.7.1.- |
| 17431, 17432 | 48853400 | 56 | 5.00E-33 | Cytophaga hutchinsonii | COG0732: Restriction endonuclease S subunits [Cytophaga hutchinsonii] | | | | 3.1.21.3 |
| 17433, 17434 | 17938569 | 37 | 3.00E-12 | Agrobacterium tumefaciens str. C58 | transcriptional regulator, AraC family [Agrobacterium tumefaciens str. C58] gb AAL45674.1 transcriptional regulator, AraC family [Agrobacterium tumefaciens str. C58] pir AD3157 transcription regulator, AraC family Au4880 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) PUTATIVE TWO-COMPONENT SENSOR [Wolnella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolnella succinogenes] | | | | 2.7.3.- |
| 17437, 17438 | 34557782 | 39 | 4.00E-41 | Wolnella succinogenes DSM 1740 | putative protease [Bacteroides fragilis YCH46] dbj BAD49186.1 putative protease [Bacteroides fragilis YCH46] | | | | 3.4.21.- |
| 17439, 17440 | 53713728 | 40 | 2.00E-21 | Bacteroides fragilis YCH46 | COG1355: Predicted dioxygenase [Magnetococcus sp. MC-1] | | | | |
| 17443, 17444 | 48833126 | 35 | 3.00E-25 | Magnetococcus sp. MC-1 | hypothetical protein bli7506 [Bradyrhizobium japonicum USDA 110] dbj BAC5277.1 bli7506 [Bradyrhizobium japonicum USDA 110] | | | | 3.1.- |
| 17447, 17448 | 27382617 | 34 | 3.00E-30 | Bradyrhizobium japonicum USDA 110 | Methionine sulfoxide reductase C-terminal domain related protein, YPPQ ortholog [Clostridium acetobutylicum ATCC 824] gb AAK79517.1 Methionine sulfoxide reductase C-terminal domain related protein, YPPQ ortholog [Clostridium acetobutylicum ATCC 824] pir B97091 methionine sulfoxide reductase C-terminal domain related protein, YPPQ ortholog [imported] - Clostridium acetobutylicum sp Q971U0 MSRB_CLOAB Peptide methionine sulfoxide reductase msrB | | | | 1.8.4.6 |
| 17449, 17450 | 15894828 | 64 | 3.00E-50 | Clostridium acetobutylicum ATCC 824 | | | | | |

| | | | | | | | | | | |
|--------|----------|----|-----------|----|--|---|--|--|--|----------|
| 1745, | 48847433 | 42 | 2.00E-49 | 15 | Geobacter metallireducens GS | COG0058: Glucan phosphorylase [Geobacter metallireducens GS-15] | | | | 2.4.1.1 |
| 1746 | | | | | | probable phosphate acetyltransferase [Desulfotalea psychrophila LSV54] | | | | |
| 17451, | 51244410 | 32 | 1.00E-35 | | Desulfotalea psychrophila LSV54 | emb CAG35287.1 probable phosphate acetyltransferase [Desulfotalea psychrophila LSV54] | | | | 2.3.1.8 |
| 17452 | | | | | | probable phosphate acetyltransferase [Desulfotalea psychrophila LSV54] | | | | |
| 17453, | 51244410 | 29 | 3.00E-26 | | Desulfotalea psychrophila LSV54 | emb CAG35287.1 probable phosphate acetyltransferase [Desulfotalea psychrophila LSV54] | | | | 2.3.1.8 |
| 17454 | | | | | | rubredoxin:oxygen oxidoreductase, putative [Chlorobium tepidum TLS] | | | | |
| 17457, | 21675091 | 54 | 1.00E-85 | | Chlorobium tepidum TLS | gb AAM73498.1 rubredoxin:oxygen oxidoreductase, putative [Chlorobium tepidum TLS] | | | | |
| 17458 | | | | | | probable flagellar protein Cj1312 [Campylobacter coli RM2228] | | | | |
| 17459, | 57168227 | 41 | 2.00E-31 | | Campylobacter coli RM2228 | gb EAL57270.1 probable flagellar protein Cj1312 [Campylobacter coli RM2228] | | | | |
| 17460 | | | | | | COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii] | | | | 3.4.--- |
| 17461, | 48855342 | 64 | 1.00E-105 | | Cytophaga hutchinsonii | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | | |
| 17462 | | | | | | threonine synthase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 17463, | 48854183 | 66 | 2.00E-94 | | Cytophaga hutchinsonii | gb AAO77508.1 threonine synthase [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.2.99.2 |
| 17464 | | | | | | threonine synthase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 17469, | 29347811 | 58 | 7.00E-81 | | Bacteroides thetaiotaomicron VPI-5482 | threonine synthase [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.2.99.2 |
| 17470 | | | | | | glycerophosphoryl diester phosphodiesterase family protein [Desulfovibrio vulgaris subsp. vulgare str. Hildenborough] | | | | 3.1.4.46 |
| 17471, | 29347811 | 44 | 7.00E-41 | | Bacteroides thetaiotaomicron VPI-5482 | COG1905: NADH:ubiquinone oxidoreductase 24 kD subunit [Clostridium thermocellum ATCC 27405] | | | | 1.6.5.3 |
| 17472 | | | | | | COG0095: Lipote-protein ligase A [Desulfitobacterium hafnense DCB-2] | | | | 6.--- |
| 17473, | 46578593 | 34 | 2.00E-32 | | Desulfovibrio vulgaris subsp. vulgare str. Hildenborough | transposase [Thermoanaerobacter tengcongensis MB4] | | | | |
| 17474 | | | | | | transposase [Thermoanaerobacter tengcongensis MB4] | | | | |
| 17475, | 48858102 | 46 | 4.00E-37 | | Clostridium thermocellum ATCC 27405 | COG0058: Glucan phosphorylase [Cytophaga hutchinsonii] | | | | 2.4.1.1 |
| 17476 | | | | | | | | | | |
| 17477, | 53685137 | 59 | 1.00E-66 | | Desulfitobacterium hafnense DCB-2 | | | | | |
| 17478 | | | | | | | | | | |
| 17479, | 20808205 | 29 | 2.00E-21 | | Thermoanaerobacter tengcongensis MB4 | | | | | |
| 17480 | | | | | | | | | | |
| 17481, | 48855753 | 47 | 1.00E-33 | | Cytophaga hutchinsonii | | | | | |
| 17482 | | | | | | | | | | |

| | | | | | | | | | | |
|---|----------------------------------|----------------|----------------------------------|--|---|--|---|----|---------------|---------|
| 17483, 17484 | 34557416 | 62 | 3.00E-31 | 1740 | Wolonia succinogenes DSM 1740 | PHOSPHOGLYCERATE KINASE [Wolonia succinogenes DSM 1740] emb CAE10131.1 PHOSPHOGLYCERATE KINASE [Wolonia succinogenes] sp Q7M9C1 PGK_WOLSU Phosphoglycerate kinase | Dictyostellum discoideum phosphoglycerate kinase (pgkA) mRNA, complete cds | 91 | 1.00E-09 | 2.7.2.3 |
| 17485, 17486 | 52841303 | 39 | 2.00E-49 | 1740 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | AbiD phage protein-like [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27155.1 AbiD phage protein-like [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | |
| 17487, 17488 | 53729000 | 27 | 1.00E-10 | 4074 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | hypothetical protein Aple02000727 [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | | |
| 17491, 17492 | 46580427 | 27 | 2.00E-25 | 1740 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | hypothetical protein DVU2020 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96495.1 conserved hypothetical protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | |
| 17493, 17494 17497, 17498 | 20807204 48855019 | 44 43 | 3.00E-62 1.00E-35 | MB4 hutchinsonii | Thermoanaerobact er tengcongensis MB4 Cytophaga hutchinsonii | NtrC family Transcriptional regulator, ATPase domain [Thermoanaerobacter tengcongensis MB4] gb AAM23979.1 NtrC family Transcriptional regulator, ATPase domain [Thermoanaerobacter tengcongensis MB4] COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii] | | | 2.4.1.18 2 | |
| 17499, 17500 175, 176 17503, 17504 | 48853636 48853385 37680074 | 48 45 35 | 4.00E-35 2.00E-18 2.00E-09 | hutchinsonii hutchinsonii Vibrio vulnificus YJ016 | Cytophaga hutchinsonii Vibrio vulnificus YJ016 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] hypothetical protein Chut02003884 [Cytophaga hutchinsonii] hypothetical protein VV1890 [Vibrio vulnificus YJ016] db BAC94654.1 hypothetical protein [Vibrio vulnificus YJ016] | | | 2.7.3.- | |
| 17505, 17506 | 57240635 | 48 | 3.00E-68 | RM2100 | Campylobacter lari RM2100 | peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL55749.1 peptidase, M23/M37 family [Campylobacter lari RM2100] | | | 3.5.1.- | |
| 17507, 17508 | 57240635 | 42 | 1.00E-49 | RM2100 | Campylobacter lari RM2100 | peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL55749.1 peptidase, M23/M37 family [Campylobacter lari RM2100] | | | | |
| 17509, 17510 | 34556616 | 44 | 2.00E-35 | 1740 | Wolonia succinogenes DSM 1740 | CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolonia succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolonia succinogenes] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|--|---|--|----------|----------|
| 1751, | AAU3668 | 50 | 3.00E-69 | | | Desc: Staphylococcus aureus cellular proliferation protein #857. Org: Staphylococcus aureus | | | 4.1.1.49 |
| 1752 | 7 | | | | | | | | |
| 17513, | | | | | | | | | |
| 17514 | 34557339 | 43 | 5.00E-18 | Wollinella succinogenes DSM 1740 | | SENSORY TRANSDUCTION REGULATOR [Wollinella succinogenes DSM 1740] emb CAE10054.1 SENSORY TRANSDUCTION REGULATOR [Wollinella succinogenes] | | | |
| 17515, | | | | | | | | | |
| 17516 | 48844440 | 24 | 4.00E-18 | Geobacter metallireducens GS-15 | | COG0859: ADP-heptose:LPS heptosyltransferase [Geobacter metallireducens GS-15] | | | |
| 17517, | | | | | | | | | |
| 17518 | 42527456 | 58 | 8.00E-76 | Treponema denticola ATCC 35405 | | metallo-beta-lactamase family protein [Treponema denticola ATCC 35405] gb AAS12465.1 metallo-beta-lactamase family protein [Treponema denticola ATCC 35405] sp Q73LB4 RNZ_TREDE Ribonuclease Z (RNase Z) (RNase Z) (RNA 3 endonuclease) | | | |
| 17519, | | | | | | | | | |
| 17520 | 53713699 | 30 | 3.00E-37 | Bacteroides fragilis YCH46 | | putative patatin-like phospholipase [Bacteroides fragilis YCH46] dbj BAD49157.1 putative patatin-like phospholipase [Bacteroides fragilis YCH46] | | | |
| 17521, | | | | | | | | | |
| 17522 | 53731000 | 92 | 2.00E-67 | Methanococcoides burtonii DSM 6242 | | COG0661: Predicted unusual protein kinase [Methanococcoides burtonii DSM 6242] | | | |
| 17523, | | | | | | | | | |
| 17524 | 45358779 | 34 | 1.00E-31 | Methanococcus maripaludis S2 | | Histidinol-phosphate aminotransferase [Methanococcus maripaludis S2] emb CAF30772.1 Histidinol-phosphate aminotransferase [Methanococcus maripaludis S2] sp P61003 HIS8_METMP Histidinol-phosphate aminotransferase (imidazole acetol-phosphate transaminase) | | 2.6.1.9 | |
| 17525, | | | | | | | | | |
| 17526 | 27525016 | 31 | 2.00E-13 | Bacillus circulans Wollinella | | BtrN protein [Bacillus circulans] dbj BAC41205.1 BtrN [Bacillus circulans] | | | |
| 17527, | | | | | | | | | |
| 17528 | 34557232 | 37 | 8.00E-16 | succinogenes DSM 1740 | | NIFS PROTEIN (FRAGMENT) [Wollinella succinogenes DSM 1740] emb CAE09947.1 NIFS PROTEIN (FRAGMENT) [Wollinella succinogenes] | | 4.4.1.- | |
| 1753, | | | | | | | | | |
| 1754 | 53712185 | 41 | 2.00E-49 | Bacteroides fragilis YCH46 | | alanine racemase [Bacteroides fragilis YCH46] dbj BAD47643.1 alanine racemase [Bacteroides fragilis YCH46] | | 6.3.2.15 | |
| 17531, | | | | | | | | | |
| 17532 | 48890454 | 36 | 4.00E-22 | Trichodesmium erythraeum IMS101 | | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] | | | |
| 17533, | | | | | | | | | |
| 17534 | 22960166 | 55 | 2.00E-99 | Rhodobacter sphaeroides 2.4.1 | | COG3825: Uncharacterized protein conserved in bacteria [Rhodobacter sphaeroides 2.4.1] | | | |
| 17535, | | | | | | | | | |
| 17536 | 39996008 | 41 | 6.00E-15 | Geobacter sulfurreducens PCA | | hypothetical protein GSJ0905 [Geobacter sulfurreducens PCA] gb AAR34232.1 hypothetical protein GSJ0905 [Geobacter sulfurreducens PCA] | | | |
| 17539, | | | | | | | | | |
| 17540 | 20809022 | 26 | 5.00E-12 | Thermoanaerobacter tengcongensis MB4 | | hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4] gb AAM25797.1 hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4] | | 4.1.99.- | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|----|----------|----------|
| 17541, 17542 | 28899897 | 46 | 4.00E-37 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA0042 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61385.1 hypothetical protein [Vibrio parahaemolyticus] | | | | |
| 17543, 17544 | 28212141 | 62 | 1.00E-69 | Clostridium tetani E88 | methylaspartate ammonia-lyase [Clostridium tetani E88] gb AAC37022.1 methylaspartate ammonia-lyase [Clostridium tetani E88] | | | | |
| 17545, 17546 | 21242902 | 40 | 1.00E-11 | Xanthomonas axonopodis pv. citri str. 306 | two-component system sensor protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM37020.1 two-component system sensor protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 17549, 17550 | 29346178 | 39 | 4.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482] gb AAO75875.1 putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.--- |
| 1755, 1756 | 42523059 | 57 | 1.00E-55 | Bdellovibrio bacteriovorus HD100 | probable zinc proteinase [Bdellovibrio bacteriovorus HD100] emb CAE79432.1 probable zinc proteinase [Bdellovibrio bacteriovorus HD100] | | | | 3.4.99.- |
| 17555, 17556 | 19705092 | 26 | 1.00E-08 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Tetratricopeptide repeat family protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93886.1 Tetratricopeptide repeat family protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | Homo sapiens BAC clone RP11-457D4 from 2, complete sequence | 97 | 4.00E-07 | |
| 17557, 17558 | 34557437 | 45 | 7.00E-57 | Wolinella succinogenes DSM 1740 | FLAGELLAR BIOSYNTHESIS/REGULATION PROTEIN FLBA [Wolinella succinogenes DSM 1740] emb CAE107152.1 FLAGELLAR BIOSYNTHESIS/REGULATION PROTEIN FLBA [Wolinella succinogenes] | | | | |
| 17559, 17560 | 57240611 | 63 | 5.00E-40 | Campylobacter lari RM2100 | phosphoenolpyruvate carboxykinase (ATP) [Campylobacter lari RM2100] gb EAL55725.1 phosphoenolpyruvate carboxykinase (ATP) [Campylobacter lari RM2100] | | | | 4.1.1.49 |
| 17565, 17566 | 34557324 | 21 | 6.00E-20 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10039.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | |
| 17567, 17568 | 34556675 | 46 | 9.00E-26 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0233 [Wolinella succinogenes DSM 1740] emb CAE09390.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 17569, 17570 | 34556675 | 35 | 2.00E-12 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0233 [Wolinella succinogenes DSM 1740] emb CAE09390.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 17571, 17572 | 48854303 | 32 | 2.00E-12 | Cytophaga hutchinsonii | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|----------|---|----------------------|
| 17573, 17574 | 42525591 | 29 | 5.00E-11 | Treponema denticola ATCC 35405 | methyl-accepting chemotaxis protein [Treponema denticola ATCC 35405] gb AA510570.1 methyl-accepting chemotaxis protein [Treponema denticola ATCC 35405] | | | |
| 17577, 17578 | 34556775 | 67 | 4.00E-89 | Wolinella succinogenes DSM 1740 | UTP-GLUCOSE-1-PHOSPHATE URIDYL TRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09490.1 UTP-GLUCOSE-1- PHOSPHATE URIDYL TRANSFERASE [Wolinella succinogenes] | 2.7.7.9 | | |
| 17579, 17580 | 15920920 | 42 | 6.00E-56 | Sulfolobus tokodaii str. 7 | hypothetical protein ST0692 [Sulfolobus tokodaii str. 7] dbj BAB65698.1 470aa long conserved hypothetical protein [Sulfolobus tokodaii str. 7] | 2.3.1.48 | | |
| 17581, 17582 | 57505845 | 59 | 2.00E-52 | Campylobacter upsaliensis RM3195 | GTP cyclohydrolase II [Campylobacter upsaliensis RM3195] gb EAL52664.1 GTP cyclohydrolase II [Campylobacter upsaliensis RM3195] | 3.5.4.25 | | |
| 17583, 17584 | 34556603 | 39 | 3.00E-21 | Wolinella succinogenes DSM 1740 | DKSA-LIKE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09318.1 DKSA-LIKE PROTEIN [Wolinella succinogenes] | | | |
| 17587, 17588 | 32261568 | 32 | 1.00E-16 | Helicobacter hepaticus ATCC 51449 | two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] | 2.7.3.- | | |
| 17589, 17590 | 34558196 | 34 | 6.00E-33 | Wolinella succinogenes DSM 1740 | DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes] | 2.7.7.- | | |
| 1759, 1760 | 34895012 | 45 | 8.00E-65 | Oryza sativa (japonica cultivar- group) | putative polyprotein [Oryza sativa (japonica cultivar-group)] | 3.4.23.- | | |
| 17591, 17592 | 34558196 | 52 | 2.00E-60 | Wolinella succinogenes DSM 1740 | DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes] | 2.7.7.- | | |
| 17593, 17594 | 48833487 | 50 | 3.00E-32 | Magnetococcus sp. MC-1 | COG2326: Uncharacterized conserved protein [Magnetococcus sp. MC-1] | 2.-.-.- | | |
| 17595, 17596 | 34556523 | 60 | 5.00E-99 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0069 [Wolinella succinogenes DSM 1740] emb CAE09238.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 17597, 17598 | 34397452 | 57 | 5.00E-74 | Porphyromonas gingivalis W83 | type I restriction-modification system, M subunit, putative [Porphyromonas gingivalis W83] ref NP_905615.1 type I restriction-modification system, M subunit, putative [Porphyromonas gingivalis W83] | | Porphyromonas gingivalis W83 section 6 of 8 of the complete genome | 86 1.00E-07 2.1.1.72 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|---|----|----------|----------|
| 17599, 17600 | 12964608 | 56 | 4.00E-78 | Clostridium difficile | formylglycinamide ribonucleotide synthetase (FGAM synthetase) [Clostridium difficile] probable ATP-dependent DNA helicase [Azoarcus sp. EbN1] emb CA109453.1 probable ATP-dependent DNA helicase [Azoarcus sp. EbN1] | Clostridium difficile purL gene for formylglycinamide ribonucleotide synthetase (FGAM synthetase), complete cds | 88 | 3.00E-21 | 6.3.5.3 |
| 17603, 17604 | 56478765 | 54 | 2.00E-39 | Azoarcus sp. EbN1 | aldose 1-epimerase [Rhodopirellula baltica SH 1] emb CAD74867.1 aldose 1-epimerase [Pirellula sp.] | | | | 3.6.1.- |
| 17605, 17606 | 32474327 | 42 | 7.00E-47 | Rhodopirellula baltica SH 1 | ribulose-phosphate 3-epimerase [Campylobacter jejuni RM1221] gb AAW35088.1 ribulose-phosphate 3-epimerase [Campylobacter jejuni RM1221] | | | | 5.1.3.3 |
| 17607, 17608 | 57237505 | 29 | 1.00E-13 | Campylobacter jejuni RM1221 | Sigma factor sigB regulation protein rsbU [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] protein rsbU [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] adenylosuccinate synthetase [Porphyromonas gingivalis W83] ref NP_904762.1 adenylosuccinate synthetase [Porphyromonas gingivalis W83] sp Q7MWW8 PURA_PORGI Adenylosuccinate synthetase (IMP-aspartate ligase) (AdSS) (AMPSase) | | | | 5.1.3.1 |
| 17609, 17610 | 19704426 | 29 | 1.00E-23 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | DNA polymerase I [Rhodopirellula baltica SH 1] emb CAD77785.1 DNA polymerase I [Pirellula sp.] | | | | 3.1.3.16 |
| 1761, 1762 | 34396595 | 63 | 3.00E-39 | Porphyromonas gingivalis W83 | polysaccharide deacetylase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94407.1 polysaccharide deacetylase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | 6.3.4.4 |
| 17617, 17618 | 32477714 | 52 | 7.00E-70 | Rhodopirellula baltica SH 1 | putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD47859.1 , putative glycosyltransferase [Bacteroides fragilis YCH46] | | | | 2.7.7.7 |
| 17619, 17620 | 46562204 | 32 | 1.00E-11 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449] ref NP_860449.1 hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449] | | | | 3.5.1.- |
| 17623, 17624 | 53712401 | 42 | 1.00E-18 | Bacteroides fragilis YCH46 | | | | | |
| 17625, 17626 | 32262467 | 41 | 3.00E-17 | Helicobacter hepaticus ATCC 51449 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|----------|
| 17627, 17628 | 47776153 | 42 | 3.00E-22 | Bacillus anthracis str. 'Ames Ancestor' | abc transporter, atp-binding protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_029415.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. Sterne] ref NP_845690.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. Ames] gb AAP27176.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. Ames] gb AAT35373.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT55468.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. Sterne] EXTRACELLULAR SOLUTE-BINDING PROTEIN, PUTATIVE [Wollinella succinogenes DSM 1740] emb CAE09521.1 EXTRACELLULAR SOLUTE-BINDING PROTEIN, PUTATIVE [Wollinella succinogenes] | | | | 1.8.-.- |
| 17629, 17630 | 34556806 | 53 | 2.00E-89 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0023 [Wollinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wollinella succinogenes] | | | | |
| 17631, 17632 | 34556481 | 33 | 9.00E-48 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0023 [Wollinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wollinella succinogenes] | | | | |
| 17633, 17634 | 34556481 | 51 | 1.00E-34 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0023 [Wollinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wollinella succinogenes] | | | | 2.7.3.- |
| 17635, 17636 | 57242456 | 39 | 4.00E-10 | Campylobacter upsaliensis RM3195 | probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195] gb EAL53524.1 probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195] | | | | |
| 17637, 17638 | 32473273 | 58 | 7.00E-65 | Rhodopirella baltica SH 1 | hypothetical protein RB4721 [Rhodopirella baltica SH 1] emb CAD73953.1 conserved hypothetical protein [Pirella sp.] | | | | |
| 17639, 17640 | 51892500 | 33 | 1.00E-09 | Symbiobacterium thermophilum IAM 14863 | glycosyl transferase [Symbiobacterium thermophilum IAM 14863] dbj BAD40347.1 glycosyl transferase [Symbiobacterium thermophilum IAM 14863] | | | | |
| 17645, 17646 | 46119894 | 41 | 2.00E-41 | Crocospaera watsonii WH 8501 | COG1106: Predicted ATPases [Crocospaera watsonii WH 8501] | | | | |
| 17647, 17648 | 15693610 | 25 | 9.00E-14 | Clostridium acetobutylicum ATCC 824 | Membrane permease, predicted cation efflux pumps [Clostridium acetobutylicum ATCC 824] gb AAK78299.1 Membrane permease, predicted cation efflux pumps [Clostridium acetobutylicum ATCC 824] p j H96938 membrane permease, probable cation efflux pumps [imported] - Clostridium acetobutylicum | | | | |
| 17649, 17650 | 53714613 | 35 | 3.00E-17 | Bacteroides fragilis YCH46 | hypothetical protein BF3327 [Bacteroides fragilis YCH46] dbj BAD50071.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 17651, 17652 | 42512 | 74 | 3.00E-37 | Escherichia coli | unnamed protein product [Escherichia coli] sp P17222 T1SP_ECOLI Type I restriction enzyme Ecoptri specificity protein (S protein) (S.Ecoprti) p j S09626 prB protein - Escherichia coli | | | | 3.1.21.- |
| 17653, 17654 | 18309265 | 42 | 5.00E-42 | Clostridium perfringens str. 13 | hypothetical protein CPE0283 [Clostridium perfringens str. 13] dbj BAB79989.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|--|--|----|----------|----------|
| 17655, 17656 | 52006159 | 38 | 6.00E-50 | Thiobacillus denitrificans ATCC 25259 | COG3587: Restriction endonuclease [Thiobacillus denitrificans ATCC 25259] | | | | |
| 17657, 17658 | 48844551 | 35 | 7.00E-13 | Geobacter metallireducens GS-15 | COG1061: DNA or RNA helicases of superfamily II [Geobacter metallireducens GS-15] | | | | |
| 17661, 17662 | 34556604 | 52 | 4.00E-29 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0156 [Wolinella succinogenes DSM 1740] emb CAE09319.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 17663, 17664 | 54401435 | 49 | 6.00E-73 | Salmonella enterica subsp. salamae serovar Greenside | UDP-GlcNAc 4-epimerase [Salmonella enterica subsp. salamae serovar (Greenside)] | | | | 5.1.3.2 |
| 17665, 17666 | 34558271 | 67 | 1.00E-111 | Wolinella succinogenes DSM 1740 | DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10986.1 DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 95 | 2.00E-07 | 2.7.7.7 |
| 17667, 17668 | 51248483 | 50 | 1.00E-31 | Desulfotalea psychrophila LSV54 | probable peptide synthase [Desulfotalea psychrophila LSV54] emb CAG37360.1 probable peptide synthase [Desulfotalea psychrophila LSV54] | | | | |
| 17669, 17670 | 56459317 | 31 | 8.00E-24 | Idiomarina lohiensis L2TR | Intracellular signaling protein (GAF, GGDEF, EAL domains) [Idiomarina lohiensis L2TR] gb AAV81049.1 Intracellular signaling protein (GAF, GGDEF, EAL domains) [Idiomarina lohiensis L2TR] | | | | 2.7.3.- |
| 1767, 1768 | 14591553 | 34 | 7.00E-39 | Pyrococcus horikoshii OT3 | chromosome assembly protein [Pyrococcus horikoshii OT3] dbj BAA30917.1 1179aa long hypothetical chromosome assembly protein [Pyrococcus horikoshii OT3] pir F71190 probable chromosome assembly protein - Pyrococcus horikoshii | | | | 3.1.3.3 |
| 17671, 17672 | 29349780 | 48 | 5.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT4372 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79477.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 17673, 17674 | 48854899 | 60 | 3.00E-56 | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | | 2.1.1.- |
| 17675, 17676 | 34557975 | 71 | 1.00E-122 | Wolinella succinogenes DSM 1740 | AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes] | Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome | 93 | 2.00E-13 | 3.4.24.- |
| 17677, 17678 | 32262066 | 45 | 3.00E-46 | Helicobacter hepaticus ATCC 51449 | rib NP_860049.1 riboflavin kinase/FAD synthase RibF [Helicobacter hepaticus ATCC 51449] | | | | 2.7.1.26 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|
| 17679, 17680 | 34557551 | 30 | 5.00E-19 | Wollinella succinogenes DSM 1740 | hypothetical protein WS1181 [Wollinella succinogenes DSM 1740] emb CAE10266.1 hypothetical protein [Wollinella succinogenes] | | | |
| 17681, 17682 | 32261560 | 51 | 1.00E-25 | Helicobacter hepaticus ATCC 51449 | glucose inhibited division protein A [Helicobacter hepaticus ATCC 51449] ref NP_859544.1 glucose inhibited division protein A [Helicobacter hepaticus ATCC 51449] | | | |
| 17683, 17684 | 57238060 | 52 | 2.00E-66 | Campylobacter jejuni RM1221 | glucose inhibited division protein A [Campylobacter jejuni RM1221] gb AAW35643.1 glucose inhibited division protein A [Campylobacter jejuni RM1221] | Mycoplasma mobile 163K complete genome | 88 | 9.00E-09 |
| 17685, 17686 | 34558795 | 43 | 2.00E-58 | Alvinella pompejana epibiont 6C6 | TonB-dependent receptor [Alvinella pompejana epibiont 6C6] S-ADENOSYLMETHIONINE-DEPENDENT METHYLTRANSFERASE | | | |
| 17687, 17688 | 34557883 | 32 | 8.00E-20 | Wollinella succinogenes DSM 1740 | [Wollinella succinogenes DSM 1740] emb CAE10598.1 S- ADENOSYLMETHIONINE-DEPENDENT METHYLTRANSFERASE [Wollinella succinogenes] | | | 2.1.1.- |
| 17689, 17690 | 17230890 | 33 | 7.00E-17 | Nostoc sp. PCC 7120 | hypothetical protein ali3398 [Nostoc sp. PCC 7120] pir JAG2230 hypothetical protein ali3398 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75097.1 ali3398 [Nostoc sp. PCC 7120] | | | |
| 1769, 1770 | 29347079 | 37 | 6.00E-16 | Bacteroides thetaiotaomicron VPI-5482 | phenylalanyl-tRNA synthetase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76776.1 phenylalanyl-tRNA synthetase alpha chain [Bacteroides thetaiotaomicron VPI-5482] sp Q8A756 SYFA_BACTN Phenylalanyl-tRNA synthetase alpha chain (Phenylalanine-tRNA ligase alpha chain) (PheRS) | | | 6.1.1.20 |
| 17691, 17692 | 14518364 | 60 | 6.00E-74 | Microscilla sp. PRE1 | putative transposase [Microscilla sp. PRE1] gb AAK62881.1 MS159, putative transposase [Microscilla sp. PRE1] | | | |
| 17693, 17694 | 48833941 | 36 | 2.00E-26 | Magnetococcus sp. MC-1 | COG5421: Transposase [Magnetococcus sp. MC-1] | | | |
| 17695, 17696 | 50084270 | 74 | 5.00E-64 | Acinetobacter sp. ADP1 | cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyrinic acid synthase | | | 3.-.-.- |
| 17697, 17698 | 50084270 | 40 | 5.00E-22 | Acinetobacter sp. ADP1 | cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyrinic acid synthase | | | |
| 17699, 17700 | 34557966 | 52 | 1.00E-49 | Wollinella succinogenes DSM 1740 | ATP-DEPENDENT HELICASE [Wollinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wollinella succinogenes] | | | 3.6.1.- |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|--|----------|
| 17701, | 34557966 | 55 | 1.00E-55 | Wolinella succinogenes DSM 1740 | ATP-DEPENDENT HELICASE [Wolinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wolinella succinogenes] | | | | 3.6.1.- |
| 17702 | AAU3601 | 40 | 2.00E-33 | | Desc:Helicobacter pylori cellular proliferation protein #326. Org:Helicobacter pylori | | | | |
| 17703, | 48837900 | 42 | 5.00E-19 | Methanosarcina barkeri str. fusaro | COG1817: Uncharacterized protein conserved in archaea [Methanosarcina barkeri str. fusaro] | | | | |
| 17709, | 48837900 | 44 | 5.00E-54 | Methanosarcina barkeri str. fusaro | COG1817: Uncharacterized protein conserved in archaea [Methanosarcina barkeri str. fusaro] | | | | |
| 17710, | 57241815 | 29 | 8.00E-22 | Campylobacter lari RM2100 | signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54233.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100] | | | | 2.7.3.- |
| 17711, | 53691904 | 32 | 2.00E-16 | Desulfovibrio desulfuricans G20 | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Desulfovibrio desulfuricans G20] | | | | |
| 17712, | 57167845 | 55 | 4.00E-94 | Campylobacter coli RM2228 | glutamyl-tRNA synthetase [Campylobacter coli RM2228] gb EAL57631.1 glutamyl-tRNA synthetase [Campylobacter coli RM2228] | | | | 6.1.1.17 |
| 17727, | 34557946 | 41 | 2.00E-23 | Wolinella succinogenes DSM 1740 | RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes DSM 1740] emb CAE10661.1 RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes] | | | | 2.7.3.- |
| 17733, | 57242733 | 41 | 1.00E-49 | Campylobacter upsaliensis RM3195 | sensor histidine kinase, putative [Campylobacter upsaliensis RM3195] gb EAL53446.1 sensor histidine kinase, putative [Campylobacter upsaliensis RM3195] | | | | 2.7.3.- |
| 17734, | 7592813 | 52 | 7.00E-68 | Actinobacillus actinomycetemcom itans | GDP-mannose pyrophosphorylase homolog [Actinobacillus actinomycetemcomitans] | | | | 2.7.7.22 |
| 17735, | 48855454 | 31 | 1.00E-34 | Cytophaga hutchinsonii | hypothetical protein Chut02001791 [Cytophaga hutchinsonii] | | | | |
| 17737, | 31194301 | 42 | 4.00E-31 | Anopheles gambiae | ENSANGP00000000011 [Anopheles gambiae] | | | | |
| 17739, | 21228716 | 30 | 1.00E-10 | Methanosarcina mazei Go1 | hypothetical protein MM2614 [Methanosarcina mazei Go1] gb AAM32310.1 hypothetical protein [Methanosarcina mazei Go1] | | | | |
| 17740, | 50591466 | 37 | 5.00E-13 | Streptococcus suis 89/1591 | COG1011: Predicted hydrolase (HAD superfamily) [Streptococcus suis 89/1591] | | | | 3.8.1.2 |
| 17741, | 34556770 | 37 | 5.00E-29 | Wolinella succinogenes DSM 1740 | Putative Dethiobiotin synthetase [Wolinella succinogenes DSM 1740] emb CAE09485.1 Putative Dethiobiotin synthetase [Wolinella succinogenes] | | | | 6.3.3.3 |
| 17742, | 34557808 | 58 | 6.00E-70 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1465 [Wolinella succinogenes DSM 1740] emb CAE10523.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|--|----------|
| 1775, | 48856903 | 39 | 1.00E-52 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | | |
| 1776 | | | | | COG3279: Response regulator of the LytR/AlgR family [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 17757, | 48854415 | 40 | 1.00E-39 | Cytophaga hutchinsonii | hypothetical protein VVA1493 [Vibrio vulnificus YJ016] dbj BA097519.1 | | | | |
| 17758 | | | | | hypothetical protein [Vibrio vulnificus YJ016] | | | | |
| 17759, | 37677153 | 33 | 2.00E-25 | Vibrio vulnificus | phosphoglycerate dehydrogenase [Campylobacter coli RM2228] | | | | |
| 17760 | | | | | phosphoglycerate dehydrogenase [Campylobacter coli RM2228] | | | | |
| 17761, | 57168512 | 60 | 3.00E-78 | Campylobacter coli RM2228 | UDP-N-acetylmuramoyl-D-glutamate-2, 6-diaminopimelate ligase [Campylobacter lari RM2100] | | | | 6.3.2.13 |
| 17762 | | | | | UDP-N-acetylmuramoyl-D-glutamate-2, 6-diaminopimelate ligase [Campylobacter lari RM2100] | | | | |
| 17763, | 57240646 | 60 | 2.00E-42 | Campylobacter lari RM2100 | APOLIPOPROTEIN N-ACYLTRANSFERASE [Wolliella succinogenes DSM 1740] emb CAE09249.1 APOLIPOPROTEIN N-ACYLTRANSFERASE [Wolliella succinogenes] sp Q7MAR3 LNT_WOLSU.Apolipoprotein N-acyltransferase (ALP N-acyltransferase) | | | | 2.3.1.- |
| 17764 | | | | | citrate lyase alpha chain [Clostridium tetani E88] gb AAO37018.1 citrate lyase alpha chain [Clostridium tetani E88] | | | | 2.8.3.10 |
| 17765, | 34556534 | 45 | 7.00E-28 | Wolliella succinogenes DSM 1740 | glycosyltransferase, putative [Deinococcus radiodurans R1] gb AAF12451.1 glycosyltransferase, putative [Deinococcus radiodurans] pir F75587 | | | | |
| 17766 | | | | | probable glycosyltransferase - Deinococcus radiodurans (strain R1) | | | | |
| 17767, | 15807989 | 39 | 3.00E-18 | Deinococcus radiodurans R1 | COG0500: SAM-dependent methyltransferases [Mesorhizobium sp. BNC1] | | | | 2.1.1.64 |
| 17768, | 28212137 | 50 | 1.00E-63 | Clostridium tetani E88 | spore coat polysaccharide biosynthesis protein; SpsA [Synecocystis sp. PCC 6803] dbj BAA18053.1 spore coat polysaccharide biosynthesis protein; SpsA [Synecocystis sp. PCC 6803] pir S75492 spore coat polysaccharide biosynthesis protein spsA - Synecocystis sp. (strain PCC 6803) | | | | |
| 17769, | 45916450 | 25 | 4.00E-10 | Mesorhizobium sp. BNC1 | COG2202: FOG: PAS/PAC domain [Pseudomonas aeruginosa UCBPP-PA14] | | | | |
| 17770 | | | | | Phospho-2-dehydro-3-deoxyheptonate aldolase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93688.1 Phospho-2-dehydro-3-deoxyheptonate aldolase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | 4.1.2.15 |
| 17771, | 16330645 | 44 | 8.00E-28 | Synechocystis sp. PCC 6803 | | | | | |
| 17772 | | | | | | | | | |
| 17773, | 53727219 | 44 | 4.00E-20 | Pseudomonas aeruginosa UCBPP-PA14 | | | | | |
| 17774 | | | | | | | | | |
| 17775, | | | | | | | | | |
| 17776 | | | | | | | | | |
| 17777, | 19704894 | 54 | 2.00E-63 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | | | | | |
| 17778 | | | | | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|----------------|---------------------------------|---|--|----|------------------|
| 17781, 17782 | 34557551 | 39 | 1.00E-33 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS1181 [Wolinella succinogenes DSM 1740] emb CAE10266.1 hypothetical protein [Wolinella succinogenes] | | | |
| 17787, 17788 | 48862510 | 47 | 4.00E-18 | degradans 2-40 | Microbulbifer | COG0778: Nitroreductase [Microbulbifer degradans 2-40] Desc: Helicobacter pylori cellular proliferation protein #241. Org: Helicobacter pylori | | | 1.-.-.- |
| 17789, 17790 | AAU3592 6 | 62 | 6.00E-46 | | | | | | 4.6.1.4 |
| 17791, 17792 | 57168806 | 70 | 9.00E-47 | RM2228 | Campylobacter coli | chorismate synthase [Campylobacter coli RM2228] gb EAL56536.1 chorismate synthase [Campylobacter coli RM2228] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 6/6 | 85 | 7.00E-08 4.6.1.4 |
| 17795, 17796 | 34557593 | 48 | 3.00E-81 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS1227 [Wolinella succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wolinella succinogenes] sp P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridylate synthase) [Uracil hydrolyase] | | | |
| 17797, 17798 | 29348698 | 45 | 2.00E-66 | VPI-5482 | Bacteroides thetaiotaomicron | hypothetical protein BT3289 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78395.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 17799, 17800 | 57167799 | 24 | 3.00E-14 | RM2228 | Campylobacter coli | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL57585.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | |
| 17801, 17802 | 34556868 | 30 | 7.00E-33 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS0441 [Wolinella succinogenes DSM 1740] emb CAE09583.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 17803, 17804 | 53715372 | 63 | 4.00E-88 | YCH46 | Bacteroides fragilis | putative GTP-binding protein [Bacteroides fragilis YCH46] db BAD50830.1 putative GTP-binding protein [Bacteroides fragilis YCH46] | | | |
| 17805, 17806 | 48854613 | 32 | 8.00E-20 | hutchinsonii | Cytophaga | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] hypothetical protein TM0744 [Thermotoga maritima MSB8] gb AAD35825.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir C72340 probable hexosyltransferase (EC 2.4.1.-) TM0744 - Thermotoga maritima (strain MSB8) | | | 2.7.3.- |
| 17807, 17808 | 15643507 | 38 | 2.00E-31 | maritima MSB8 | Thermotoga | | | | 2.4.1.- |
| 17815, 17816 | 34557673 | 29 | 4.00E-11 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS1312 [Wolinella succinogenes DSM 1740] emb CAE10388.1 hypothetical protein [Wolinella succinogenes] | | | |
| 17817, 17818 | 57505998 | 29 | 4.00E-19 | RM3195 | Campylobacter upsaliensis | partitioning protein, putative [Campylobacter upsaliensis RM3195] gb EAL52588.1 partitioning protein, putative [Campylobacter upsaliensis RM3195] | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|---|--|----|------------------|
| 17819, 17820 | 42518123 | 37 | 6.00E-11 | Lactobacillus johnsonii NCC 533 | hypothetical protein LJ0037 [Lactobacillus johnsonii NCC 533] gb AA08019.1 hypothetical protein LJ0037 [Lactobacillus johnsonii NCC 533] | | | |
| 17823, 17824 | 53715360 | 76 | 1.00E-112 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50818.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] | Coxiella burnetii strain RSA 493, section 2 of 7 of the complete genome | 95 | 1.00E-07 3.6.1.- |
| 17825, 17826 | 48854506 | 42 | 2.00E-24 | Cytophaga hutchinsonii | hypothetical protein Chut02002705 [Cytophaga hutchinsonii] hypothetical protein air4323 [Nostoc sp. PCC 7120] pir AD2346 hypothetical protein air4323 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB76022.1 air4323 [Nostoc sp. PCC 7120] | | | 3.6.1.- |
| 17827, 17828 | 17231815 | 34 | 8.00E-11 | Nostoc sp. PCC 7120 | Amylovoran biosynthesis AmsK [Bacillus cereus ATCC 14579] gb AAP12133.1 Amylovoran biosynthesis AmsK [Bacillus cereus ATCC 14579] | | | |
| 17829, 17830 | 30023301 | 29 | 5.00E-10 | Bacillus cereus ATCC 14579 | COG3569: Topoisomerase IB [Cytophaga hutchinsonii] | | | |
| 1783, 1784 | 48855551 | 55 | 6.00E-57 | Cytophaga hutchinsonii | COG0835: Chemotaxis signal transduction protein [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 17831, 17832 | 48845934 | 49 | 6.00E-32 | Geobacter metallireducens GS-15 | Histidinol-phosphatase; UDP-N-acetylmuramoylalanine-D-glutamyl-meso- diaminopimelate-D-alanine ligase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95654.1 Histidinol-phosphatase; UDP-N-acetylmuramoylalanine-D-glutamyl-meso-diaminopimelate-D-alanyl- D-alanine ligase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | 3.1.3.15 |
| 17835, 17836 | 19704793 | 35 | 2.00E-20 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | putative arginate O-acetyltransferase protein [Nitrosomonas europaea ATCC 19718] emb CAD84965.1 putative arginate O-acetyltransferase protein [Nitrosomonas europaea ATCC 19718] | | | |
| 17837, 17838 | 30249053 | 57 | 9.00E-66 | Nitrosomonas europaea ATCC 19718 | hypothetical protein WS1181 [Wolonia succinogenes DSM 1740] emb CAE10266.1 hypothetical protein [Wolonia succinogenes] | | | |
| 17839, 17840 | 34557551 | 38 | 1.00E-35 | Wolonia succinogenes DSM 1740 | nitrous oxide reductase [Wolonia succinogenes] DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45292.1 DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis] | | | 1.7.99.6 |
| 17841, 17842 | 46934822 | 70 | 1.00E-133 | Wolonia succinogenes | | | | |
| 17847, 17848 | 56707780 | 57 | 1.00E-73 | Francisella tularensis subsp. tularensis Schu 4 | | | | |

| | | | | | | | | |
|-------------------------------------|----------------------|----------|----------------------|---|--|---------|--|--|
| 17849, 17850, 17851, 17852 | 12512884 45528155 | 42 59 | 7.00E-30 9.00E-23 | Escherichia coli O157:H7 Crocosphaera watsonii WH 8501 Vibrio parahaemolyticus RIMD 2210633 | deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] ref NP_285856.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7 EDL933] ref NP_308191.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] sp Q8X8Y9 DGT_P_ECO57 Deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase) pir D85500 deoxyguanosine triphosphate triphosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain EDL933) dbj BAB33587.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] pir D90649 deoxyguanosine triphosphate triphosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) | 3.1.5.1 | | |
| 17853, 17854 | 28901031 | 57 | 4.00E-34 | hypotheical protein VPA1176 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62519.1 hypotheical protein [Vibrio parahaemolyticus] | | | | |
| 17855, 17856 | 15669145 | 31 | 2.00E-11 | Methanocaldococ- us jannaschii DSM 2661 | histidinol-phosphate aminotransferase (hisC) [Methanocaldococcus jannaschii DSM 2661] gb AAB98960.1 histidinol-phosphate aminotransferase (hisC) [Methanocaldococcus jannaschii DSM 2661] pir C64419 histidinol-phosphate transaminase (EC 2.6.1.9) - Methanococcus jannaschii sp Q58365 HIS8_METJA Histidinol-phosphate aminotransferase (imidazole acetol-phosphate transaminase) | 2.6.1.9 | | |
| 17857, 17858 | 29349895 | 51 | 9.00E-68 | Bacteroides thetaiotaomicron VPI-5482 | putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79592.1 putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482] | 3.2.1.- | | |
| 17861, 17862 | 46135621 | 37 | 3.00E-36 | Anabaena variabilis ATCC 29413 | COG1201: Lhr-like helicases [Anabaena variabilis ATCC 29413] | 3.6.1.- | | |
| 17865, 17866 | 42781306 | 54 | 1.00E-90 | Bacillus cereus ATCC 10987 | isoleucyl-tRNA synthetase [Bacillus cereus ATCC 10987] gb AAS41161.1 isoleucyl-tRNA synthetase [Bacillus cereus ATCC 10987] | 6.1.1.5 | | |
| 17867, 17868 | 28210025 | 34 | 2.00E-25 | Clostridium tetani E88 | isoleucyl-tRNA synthetase [Clostridium tetani E88] gb AAO34906.1 isoleucyl- tRNA synthetase [Clostridium tetani E88] | 6.1.1.5 | | |
| 1787, 1788 | 29349217 | 53 | 4.00E-78 | Bacteroides thetaiotaomicron VPI-5482 | ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78914.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|--|--|--|--|--|----------|
| 17871, | 11498895 | 37 | 2.00E-41 | Archaeoglobus fulgidus DSM 4304 | cell division control protein 48, AAA family (cdc48-1) [Archaeoglobus fulgidus DSM 4304] gb AAB89948.1 cell division control protein 48, AAA family (cdc48-1) [Archaeoglobus fulgidus DSM 4304] pir H69411 cell division control protein 48, AAA family (cdc48-1) homolog - Archaeoglobus fulgidus sp O28972 YC97_ARCFU Cell division cycle protein 48 homolog AF1297 | | | | 2.7.1.- |
| 17873, | 53715849 | 63 | 1.00E-106 | Bacteroides fragilis YCH46 | ribonuclease R [Bacteroides fragilis YCH46] dbj BAD51307.1 ribonuclease R [Bacteroides fragilis YCH46] | | | | 3.1.- |
| 17875, | 34557247 | 66 | 6.00E-41 | Wolnella succinogenes DSM 1740 | TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolnella succinogenes DSM 1740] emb CAE09962.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolnella succinogenes] | | | | 2.7.3.- |
| 17877, | 50302185 | 34 | 2.00E-14 | Kluyveromyces fragilis | unnamed protein product [Kluyveromyces fragilis] emb CAH02614.1 unnamed protein product [Kluyveromyces fragilis] NRRL Y-1140] | | | | 2.7.3.- |
| 17879, | 53713067 | 25 | 1.00E-10 | Bacteroides fragilis YCH46 | hypothetical protein BF1778 [Bacteroides fragilis YCH46] dbj BAD48525.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 17883, | | | | Bacteroides thetaiotaomicron | hypothetical protein BT3127 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78233.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 17884 | 29348536 | 43 | 4.00E-35 | VPI-5482 | hypothetical protein aq_321 [Aquifex aeolicus VF5] gb AAC06618.1 putative protein [Aquifex aeolicus VF5] pir F70328 hypothetical protein aq_321 - Aquifex aeolicus | | | | |
| 17885, | 15605841 | 53 | 4.00E-47 | Aquifex aeolicus VF5 | COG0840: Methyl-accepting chemotaxis protein [Desulfovibrio desulfuricans G20] | | | | |
| 17887, | 23474422 | 29 | 5.00E-17 | Desulfovibrio desulfuricans G20 | COG3124: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 17889, | 48853925 | 47 | 2.00E-45 | Cytophaga hutchinsonii | COG1793: ATP-dependent DNA ligase [Cytophaga hutchinsonii] | | | | 6.5.1.1 |
| 1789, | | | | Cytophaga hutchinsonii | glycerophosphoryl diester phosphodiesterase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94660.1 | | | | |
| 1790 | 48854052 | 57 | 4.00E-95 | hutchinsonii | glycerophosphoryl diester phosphodiesterase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | 3.1.4.46 |
| 17891, | 46578593 | 35 | 6.00E-33 | Hildenborough | ribosomal protein L22 (BL 17) [Bacillus licheniformis ATCC 14580] gb AAU21767.1 ribosomal protein L22 (BL 17) [Bacillus licheniformis ATCC 14580] ref YP_089805.1 RplV [Bacillus licheniformis ATCC 14580] gb AAU39112.1 RplV [Bacillus licheniformis DSM 13] | | | | |
| 17893, | 52078614 | 47 | 2.00E-21 | Bacillus licheniformis ATCC 14580 | mannose-1-phosphate guanylyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | 2.7.7.13 |
| 17894 | | | | | | | | | |
| 17897, | | | | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | | | | | |
| 17898 | 45658050 | 48 | 6.00E-44 | Fiocruz L1-130 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|--|--|--|----|----------|----------|
| 17901, 17902 | 21228306 | 75 | 1.00E-104 | Methanosarcina mazel Go1 | hypothetical protein MIM2204 [Methanosarcina mazel Go1] gb AAM31900.1 hypothetical protein [Methanosarcina mazel Go1] | Desc: Methanococcus jannaschii large circular extrachromosomal element. Org: Methanococcus jannaschii | 95 | 1.00E-07 | 3.1.21.3 |
| 17903, 17904 | 34557740 | 48 | 2.00E-54 | Wolinella succinogenes DSM 1740 | NIFEN2 [Wolinella succinogenes DSM 1740] emb CAE10455.1 NIFEN2 [Wolinella succinogenes] | | | | 1.18.6.1 |
| 17905, 17906 | 53730557 | 39 | 7.00E-44 | Dechloromonas aromatica RCB | COG3696: Putative silver efflux pump [Dechloromonas aromatica RCB] | | | | |
| 17907, 17908 | 51246943 | 38 | 8.00E-21 | Desulfotalea psychrophila LSV54 | hypothetical protein DP3091 [Desulfotalea psychrophila LSV54] emb CAG37820.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | | |
| 17909, 17910 | 39997909 | 26 | 9.00E-07 | Geobacter sulfurreducens PCA | sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gb AAR36210.1 sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] | | | | |
| 1791, 1792 | 15643716 | 55 | 8.00E-48 | Thermotoga maritima MSB8 | ribose ABC transporter, ATP-binding protein [Thermotoga maritima MSB8] gb AAD36035.1 ribose ABC transporter, ATP-binding protein [Thermotoga maritima MSB8] pir E72314 ribose ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8) | | | | |
| 17911, 17912 | 14602171 | 35 | 2.00E-09 | Aeropyrum permix K1 | polysulfide reductase [Aeropyrum permix K1] dbj BAA81623.1 250aa long hypothetical polysulfide reductase [Aeropyrum permix K1] pir G72495 probable polysulfide reductase APE2605 - Aeropyrum permix (strain K1) | Bacillus cereus ZK, complete genome | 97 | 1.00E-07 | 1.8.-.- |
| 17917, 17918 | 32262428 | 63 | 1.00E-44 | Helicobacter hepaticus ATCC 51449 | ATP-dependent zinc metalloproteinase [Helicobacter hepaticus ATCC 51449] ref NP_860410.1 ATP-dependent zinc metalloproteinase. [Helicobacter hepaticus ATCC 51449] | | | | 1.2.7.- |
| 17921, 17922 | 57241365 | 40 | 2.00E-51 | Campylobacter lari RM2100 | NADH-ubiquinone oxidoreductase, NQO3 subunit (NQO3) [Campylobacter lari RM2100] gb EAL54477.1 NADH-ubiquinone oxidoreductase, NQO3 subunit (NQO3) [Campylobacter lari RM2100] | | | | 3.4.24.- |
| 17923, 17924 | 29348867 | 37 | 1.00E-48 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3458 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78564.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.6.5.3 |
| 17925, 17926 | 34556460 | 45 | 3.00E-33 | Wolinella succinogenes DSM 1740 | DNA POLYMERASE III, BETA CHAIN [Wolinella succinogenes DSM 1740] emb CAE09175.1 DNA POLYMERASE III, BETA CHAIN [Wolinella succinogenes] | | | | |
| 17927, 17928 | 34556459 | 43 | 4.00E-27 | Wolinella succinogenes DSM 1740 | dnaA, probable chromosomal replication initiator protein [Wolinella succinogenes DSM 1740] emb CAE09174.1 dnaA, probable chromosomal replication initiator protein [Wolinella succinogenes] | | | | 2.7.7.7 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|--|----------|
| 1793, 1794 | 15897063 | 29 | 6.00E-18 | Sulfolobus solfataricus P2 | Esterase, tropinesterase related protein [Sulfolobus solfataricus P2] gb AAK40458.1 Esterase, tropinesterase related protein [Sulfolobus solfataricus P2] emb CAA69549.1 orf c04020 [Sulfolobus solfataricus pfl]S75387 hypothetical protein c04020 - Sulfolobus solfataricus | | | | 3.1.- |
| 17931, 17932 | 34558174 | 55 | 1.00E-70 | Wollinella succinogenes DSM 1740 | SEPTUM SITE-DETERMINING PROTEIN MIND CELL DIVISION INHIBITOR MIND [Wollinella succinogenes DSM 1740] emb CAE10889.1 SEPTUM SITE-DETERMINING PROTEIN MIND CELL DIVISION INHIBITOR MIND [Wollinella succinogenes] | | | | |
| 17933, 17934 | 53711849 | 28 | 2.00E-08 | Bacteroides fragilis YCH46 | membrane fusion efflux protein [Bacteroides fragilis YCH46] dbj BAD47307.1 membrane fusion efflux protein [Bacteroides fragilis YCH46] | | | | |
| 17935, 17936 | 34557146 | 47 | 9.00E-88 | Wollinella succinogenes DSM 1740 | A/G-SPECIFIC ADENINE GLYCOSYLASE EC 3.2.2. [Wollinella succinogenes DSM 1740] emb CAE09861.1 A/G-SPECIFIC ADENINE GLYCOSYLASE EC 3.2.2. [Wollinella succinogenes] | | | | 3.2.2.- |
| 17939, 17940 | 46580602 | 35 | 2.00E-15 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96670.1 site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | |
| 17941, 17942 | 34558334 | 48 | 2.00E-74 | Wollinella succinogenes DSM 1740 | PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wollinella succinogenes DSM 1740] emb CAE11049.1 PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wollinella succinogenes] | | | | 2.4.2.- |
| 17943, 17944 | 21227351 | 53 | 9.00E-79 | Methanosarcina mazei Go1 | Ribulose biphosphate carboxylase large chain [Methanosarcina mazei Go1] gb AAM30945.1 Ribulose biphosphate carboxylase large chain [Methanosarcina mazei Go1] sp Q8PXXG9 RBL_METMA Ribulose biphosphate carboxylase (RuBisCO) | | | | 4.1.1.39 |
| 17947, 17948 | 34558179 | 47 | 2.00E-24 | Wollinella succinogenes DSM 1740 | conserved hypothetical protein-Predicted endonuclease [Wollinella succinogenes DSM 1740] emb CAE10894.1 conserved hypothetical protein-Predicted endonuclease [Wollinella succinogenes] | | | | |
| 17951, 17952 | 48853472 | 47 | 1.00E-16 | Cytophaga hutchinsonii | hypothetical protein Chut02003804 [Cytophaga hutchinsonii] | | | | |
| 17953, 17954 | 34557966 | 59 | 4.00E-40 | Wollinella succinogenes DSM 1740 | ATP-DEPENDENT HELICASE [Wollinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wollinella succinogenes] | | | | 3.6.1.- |
| 17955, 17956 | 48856952 | 51 | 3.00E-83 | Cytophaga hutchinsonii | COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii] | | | | 4.1.3.27 |
| 17957, 17958 | 40062476 | 41 | 4.00E-54 | uncultured bacterium 105 | hypothetical protein EBAC750-01A01.2 [uncultured bacterium 105] | | | | |
| 17959, 17960 | 29348819 | 36 | 8.00E-08 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3410 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78516.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A295 Y10_BACTN Hypothetical UPF0145 protein BT3410 | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|---|--|--|--|---------|
| 17961, 17962 | 9657465 | 32 | 5.00E-08 | Vibrio cholerae O1 biovar eltor str. N16961 | GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232481.1 GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961] pir JF82502 GGDEF family protein VCA0080 [imported] - Vibrio cholerae strain N16961 serogroup O1 | | | | |
| 17963, 17964 | 45358725 | 53 | 9.00E-71 | Methanococcus maripaludis S2 | Flavodoxin:Beta-lactamase-like [Methanococcus maripaludis S2] (emb CAF30718.1 Flavodoxin:Beta-lactamase-like [Methanococcus maripaludis S2]) | | | | |
| 17967, 17968 | 48854285 | 32 | 3.00E-13 | Cytophaga hutchinsonii | COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 17969, 17970 | 54310375 | 26 | 3.00E-14 | Photobacterium profundum SS9 | putative MSHA biogenesis protein MshH [Photobacterium profundum SS9] emb CAG21593.1 putative MSHA biogenesis protein MshH [Photobacterium profundum] | | | | |
| 17971, 17972 | 20091095 | 35 | 5.00E-23 | Methanosarcina acetivorans C2A | sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AA005650.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A] | | | | 2.7.3.- |
| 17973, 17974 | AAR2046 0 | 36 | 1.00E-41 | | Desc:Glutamine 2-oxo-glutarate amino transferase. Org:Zea mays | | | | 1.4.7.1 |
| 17975, 17976 | 16125068 | 32 | 2.00E-18 | Caulobacter crescentus CB15 | TonB-dependent receptor, putative [Caulobacter crescentus CB15] gb AAK22800.1 TonB-dependent receptor, putative [Caulobacter crescentus CB15] pir D87350 TonB-dependent receptor, probable [imported] - Caulobacter crescentus | | | | |
| 17977, 17978 | 48855401 | 35 | 3.00E-12 | Cytophaga hutchinsonii | COG2332: Cytochrome c-type biogenesis protein CcmE [Cytophaga hutchinsonii] | | | | |
| 17983, 17984 | 53756233 | 36 | 2.00E-40 | Methylococcus capsulatus str. Bath | paraquat-inducible protein B [Methylococcus capsulatus str. Bath] ref YP_112894.1 paraquat-inducible protein B [Methylococcus capsulatus str. Bath] | | | | |
| 17985, 17986 | 48854120 | 53 | 1.00E-74 | Cytophaga hutchinsonii | COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] | | | | 6.2.1.3 |
| 17987, 17988 | 48854120 | 41 | 2.00E-55 | Cytophaga hutchinsonii | COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] | | | | 6.2.1.3 |
| 17991, 17992 | 52856660 | 21 | 1.00E-08 | Xylella fastidiosa Ann-1 | COG0671: Membrane-associated phospholipid phosphatase [Xylella fastidiosa Ann-1] | | | | |
| 17993, 17994 | 9657891 | 34 | 7.00E-24 | Vibrio cholerae O1 biovar eltor str. N16961 | conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232879.1 hypothetical protein VCA0487 [Vibrio cholerae O1 biovar eltor str. N16961] pir D82453 conserved hypothetical protein VCA0487 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 17997, 17998 | 51246705 | 44 | 3.00E-53 | Desulfotalea psychrophila Lsv54 | hypothetical protein DP2853 [Desulfotalea psychrophila Lsv54] emb CAG37582.1 hypothetical protein [Desulfotalea psychrophila Lsv54] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|---------------|
| 17999, 18000 | 5531408 | 51 | 1.00E-49 | Pseudomonas putida | aldehyde dehydrogenase [Pseudomonas putida] | | | | 1.2.1.3 |
| 18003, 18004 | 39996595 | 55 | 4.00E-39 | Geobacter sulfurreducens PCA | sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA] gb AAR34869.1 sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA] | | | | 2.7.3.- |
| 18005, 18006 | 29348659 | 42 | 2.00E-43 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3250 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78356.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 18007, 18008 | 48854999 | 49 | 6.00E-24 | Cytophaga hutchinsonii | COG1832: Predicted CoA-binding protein [Cytophaga hutchinsonii] | | | | |
| 18009, 18010 | 29349404 | 47 | 1.00E-56 | Bacteroides thetaiotaomicron VPI-5482 | putative peptidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79101.1 putative peptidase [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.5.1.- |
| 18011, 18012 | 48853377 | 62 | 5.00E-48 | Cytophaga hutchinsonii | COG3832: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 18015, 18016 | 34556560 | 34 | 4.00E-18 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | 2.7.3.- |
| 18017, 18018 | 48853783 | 51 | 8.00E-43 | Cytophaga hutchinsonii | COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] | | | | 2.7.7.7 |
| 18023, 18024 | 48853984 | 37 | 5.00E-31 | Cytophaga hutchinsonii | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | | |
| 18025, 18026 | 29346467 | 25 | 1.00E-15 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1057 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76164.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 18029, 18030 | 51595992 | 54 | 5.00E-78 | Yersinia pseudotuberculosis IP 32953 | oligopeptidase B [Yersinia pseudotuberculosis IP 32953] ref NP_992969.1 oligopeptidase B [Yersinia pestis biovar Medievalis str. 91001] ref NP_405347.1 oligopeptidase B [Yersinia pestis CO92] gb AAS61846.1 oligopeptidase B [Yersinia pestis biovar Medievalis str. 91001] emb CAC90598.1 oligopeptidase B [Yersinia pestis CO92] emb CAH20895.1 oligopeptidase B [Yersinia pseudotuberculosis IP 32953] pir AB0217 oligopeptidase B (EC 3.4.21.83) [imported] - Yersinia pestis (strain CO92) | | | | 3.4.21.8 3 |
| 1803, 1804 | 46135321 | 51 | 1.00E-81 | Anabaena variabilis ATCC 29413 | hypothetical protein Avar03000604 [Anabaena variabilis ATCC 29413] | | | | |
| 18037, 18038 | 48854617 | 53 | 2.00E-40 | Cytophaga hutchinsonii | COG1576: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 18039, 18040 | 53714521 | 35 | 7.00E-19 | Bacteroides fragilis YCH46 | hypothetical protein BF3234 [Bacteroides fragilis YCH46] db BAD49979.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|--|--|--|----|----------|----------|
| 18043, | 9857170 | 24 | 1.00E-11 | Streptomyces coelicolor A3(2) | hypothetical protein [Streptomyces coelicolor A3(2)] ref NP_628388.1 | | | | |
| 18044 | | | | coelicolor A3(2) | hypothetical protein SCO4213 [Streptomyces coelicolor A3(2)] | | | | |
| 18047, | 48855172 | 31 | 2.00E-14 | Cytophaga hutchinsonii | COG2812: DNA polymerase III, gamma/tau subunits [Cytophaga hutchinsonii] | | | | 2.7.7.7 |
| 18048 | | | | Thiobacillus denitrificans ATCC 25259 | COG0225: Peptide methionine sulfoxide reductase [Thiobacillus denitrificans ATCC 25259] | | | | 1.8.4.6 |
| 18049, | 52006378 | 54 | 1.00E-35 | Methanosarcina mazei Go1 | Inorganic pyrophosphatase [Methanosarcina mazei Go1] gb AAAM31137.1 | | | | 3.6.1.1 |
| 18050 | 21227543 | 48 | 2.00E-17 | Campylobacter coli RM2228 | Inorganic pyrophosphatase [Methanosarcina mazei Go1] conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 18053, | 57169084 | 37 | 3.00E-13 | Psychrobacter sp. 273-4 | hypothetical protein Psyc03002392 [Psychrobacter sp. 273-4] | | | | |
| 18054 | 46141189 | 43 | 9.00E-39 | Haemophilus ducreyi 35000HP | type III restriction enzyme [Haemophilus ducreyi 35000HP] ref NP_874067.1 | | | | 3.1.21.5 |
| 18057, | 33148938 | 33 | 3.00E-23 | Haemophilus influenzae R2846 | type III restriction enzyme [Haemophilus ducreyi 35000HP] COG0259: Pyridoxamine-phosphate oxidase [Haemophilus influenzae R2846] | | | | 1.4.3.5 |
| 18058 | 46129161 | 54 | 1.00E-60 | Haemophilus influenzae 86-028NP | COG1393: Arsenate reductase and related proteins, glutaredoxin family [Haemophilus influenzae 86-028NP] | | | | 1.--- |
| 18059, | 48868784 | 40 | 1.00E-18 | Pseudomonas aeruginosa PAO1 | hypothetical protein PA0043 [Pseudomonas aeruginosa PAO1] pir F83639 | | | | |
| 18060 | 9945865 | 39 | 2.00E-25 | Clostridium thermocellum | hypothetical protein PA0043 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_248733.1 hypothetical protein PA0043 [Pseudomonas aeruginosa PAO1] | | | | |
| 18063, | 48859484 | 42 | 1.00E-17 | Streptococcus thermophilus CNRZ1066 | COG1015: Phosphopentomutase [Clostridium thermocellum ATCC 27405] | | | | 5.4.2.1 |
| 18064 | 55823155 | 31 | 4.00E-31 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | coproporphyrinogen III oxidase [Streptococcus thermophilus CNRZ1066] gb AAV62781.1 coproporphyrinogen III oxidase [Streptococcus thermophilus CNRZ1066] | | | | 1.--- |
| 18065, | 45656817 | 91 | 1.00E-103 | Cytophaga hutchinsonii | type I restriction enzyme [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS69540.1 type I restriction enzyme [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | Legionella pneumophila str. Lens complete genome | 81 | 2.00E-77 | 3.1.21.3 |
| 18066 | 48856925 | 33 | 8.00E-23 | | COG1309: Transcriptional regulator [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | |
|----------------------------------|----------|----|----------|---|--|--|----|----------|
| 18099, 18100 | 29347468 | 47 | 7.00E-58 | Bacteroides thetaiotaomicron VPI-5482 | putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77165.1 putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.5.1.1 |
| 18101, 18102 | 20093291 | 28 | 5.00E-19 | Methanosarcina acetivorans C2A | Na-K-Cl cotransporter [Methanosarcina acetivorans C2A] gb AAM07846.1 Na-K-Cl cotransporter [Methanosarcina acetivorans str. C2A] | | | |
| 18103, 18104 | 53756837 | 34 | 1.00E-20 | Methylococcus capsulatus str. Bath | nitrogen regulation protein NtrY, putative [Methylococcus capsulatus str. Bath] ref YP_115241.1 nitrogen regulation protein NtrY, putative [Methylococcus capsulatus str. Bath] | | | 2.7.3.- |
| 18105, 18106 1811, 1812 | 48854978 | 45 | 6.00E-60 | Cytophaga hutchinsonii | COG1410: Methionine synthase I, cobalamin-binding domain [Cytophaga hutchinsonii] | Vibrio fischeri gene for cobalamin- dependent methionine synthase, Na+/H+ antiporter and aspartokinase III, partial and complete cds | 93 | 9.00E-09 |
| 18111, 18112 | 48854664 | 37 | 1.00E-42 | Cytophaga hutchinsonii | COG2217: Cation transport ATPase [Cytophaga hutchinsonii] | | | 3.6.1.- |
| 18113, 18114 | 51246929 | 50 | 1.00E-65 | Desulfotalea psychrophila LSV54 | probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] emb CAG37806.1 probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] | | | 3.4.21.- |
| 18117, 18118 | 32475768 | 43 | 6.00E-47 | Rhodopirellula baltica SH 1 | conserved hypothetical protein-putative secreted protein [Rhodopirellula baltica SH 1] emb CAD76137.1 conserved hypothetical protein-putative secreted protein [Pirellula sp.] | | | |
| 18119, 18120 | 56962313 | 38 | 1.00E-26 | Bacillus clausii KSM-K16 | hypothetical protein ABC0537 [Bacillus clausii KSM-K16] dbj BAD63077.1 conserved hypothetical protein [Bacillus clausii KSM-K16] | | | |
| 18121, 18122 | 54309817 | 71 | 1.00E-63 | Photobacterium profundum SS9 | putative UDP-glucose dehydrogenase [Photobacterium profundum SS9] emb CAG21035.1 putative UDP-glucose dehydrogenase [Photobacterium profundum] | | | 1.1.1.22 |
| 18123, 18124 | 48854132 | 41 | 3.00E-19 | Cytophaga hutchinsonii | COG0367: Asparagine synthase (glutamine-hydrolyzing) [Cytophaga hutchinsonii] | | | 6.3.5.4 |
| | 49236610 | 35 | 2.00E-31 | Moorella thermoacetica | COG0247: Fe-S oxidoreductase [Moorella thermoacetica ATCC 39073] | | | 1.1.99.5 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|--|----------|
| 18129, 18130 | 21229550 | 55 | 5.00E-18 | Xanthomonas campestris pv: campestris str. ATCC 33913 | hypothetical protein XCC0072 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39391.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | | |
| 1813, 1814 | 28901110 | 27 | 3.00E-13 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA1255 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62598.1 hypothetical protein [Vibrio parahaemolyticus] | | | | |
| 18133, 18134 | 29346307 | 50 | 2.00E-56 | Bacteroides thetaiotaomicron VPI-5482 | chaperone protein htpG (heat shock protein htpG) [Bacteroides thetaiotaomicron VPI-5482] gb AAO76004.1 chaperone protein htpG (heat shock protein htpG) [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 18135, 18136 | 34397856 | 45 | 4.00E-18 | Porphyromonas gingivalis W83 | ribosomal protein L23 [Porphyromonas gingivalis W83] ref NP_906018.1 ribosomal protein L23 [Porphyromonas gingivalis W83] | | | | |
| 18137, 18138 | 24373378 | 43 | 8.00E-14 | Shewanella oneidensis MR-1 | DNA-binding protein, putative [Shewanella oneidensis MR-1] gb AAN54865.1 DNA-binding protein, putative [Shewanella oneidensis MR-1] | | | | |
| 18139, 18140 | 56675038 | 33 | 7.00E-17 | uncultured bacterium | cellulase [uncultured bacterium] | | | | |
| 18141, 18142 | 20809032 | 36 | 4.00E-39 | Thermoanaerobact er tengcongensis MB4 | Sensory transduction histidine kinases [Thermoanaerobacter tengcongensis MB4] gb AAM25807.1 Sensory transduction histidine kinases [Thermoanaerobacter tengcongensis MB4] | | | | 2.7.3.- |
| 18145, 18146 | 53713022 | 44 | 1.00E-42 | Bacteroides fragilis YCH46 | beta-mannosidase [Bacteroides fragilis YCH46] dbj BAC56899.2 beta-mannosidase [Bacteroides fragilis YCH46] dbj BAD48480.1 beta-mannosidase [Bacteroides fragilis YCH46] | | | | 3.2.1.25 |
| 18149, 18150 | 48855136 | 60 | 3.00E-43 | Cytophaga hutchinsonii | COG0118: Glutamine amidotransferase [Cytophaga hutchinsonii] | | | | 2.4.2.- |
| 1815, 1816 | 17547338 | 38 | 3.00E-12 | Ralstonia solanacearum GMI1000 | hypothetical protein RS00923 [Ralstonia solanacearum GMI1000] emb CAD16326.1 CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] | | | | |
| 18151, 18152 | 48853807 | 33 | 6.00E-23 | Cytophaga hutchinsonii | COG0793: Periplasmic protease [Cytophaga hutchinsonii] | | | | |
| 18153, 18154 | 48854129 | 42 | 5.00E-24 | Cytophaga hutchinsonii | COG0172: Seryl-tRNA synthetase [Cytophaga hutchinsonii] | | | | 6.1.1.11 |
| 18155, 18156 | 34557419 | 39 | 2.00E-21 | Wollinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes] | | | | 2.7.3.- |
| 18157, 18158 | 45250013 | 69 | 4.00E-58 | Aneurinibacillus thermoaerophilus | dTDP-glucose 4,6-dehydratase [Aneurinibacillus thermoaerophilus] | | | | 4.2.1.46 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 18159, 18160 | 9632024 | 42 | 6.00E-12 | Paramedium bursaria Chlorella virus 1 | contains ATP/GTP-binding site motif A [Paramedium bursaria Chlorella virus 1] pif1 17959 hypothetical protein A456L - Chlorella virus PBCV-1 | | | | |
| 18161, 18162 | 24214410 | 50 | 9.00E-61 | Leptospira interrogans serovar Lai str. 56601 | Sensory transduction histidine kinase [Leptospira interrogans serovar Lai str. 56601] | | | | 2.7.3.- |
| 18163, 18164 | 53712683 | 45 | 9.00E-45 | Bacteroides fragilis YCH46 | tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | | |
| 18165, 18166 | 48854288 | 39 | 2.00E-34 | Cytophaga hutchinsonii | COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii] | | | | |
| 18167, 18168 | 7445809 | 47 | 6.00E-39 | Thermoanaerobact erium thermosulfurigenes | hypothetical ABC exporter component A - Thermoanaerobacterium thermosulfurigenes gb AAB0804.1 AbcA [Thermoanaerobacterium thermosulfurigenes] | | | | 3.4.21.- |
| 18169, 18170 | 53712391 | 65 | 1.00E-45 | Bacteroides fragilis YCH46 | UDP-ManNAc dehydrogenase [Bacteroides fragilis YCH46] dbj BAD47849.1 | | | | 1.1.1.- |
| 1817, 1818 | 34104413 | 49 | 1.00E-43 | Chromobacterium violaceum ATCC 12472 | probable Bifunctional: UDP-N-acetylglucosamineglucose-1-phosphate thymidyltransferase; Glucosamine-1-phosphate [Chromobacterium violaceum ATCC 12472] ref NP_902773.1 probable Bifunctional: UDP-N-acetylglucosamineglucose-1-phosphate thymidyltransferase; Glucosamine-1-phosphate [Chromobacterium violaceum ATCC 12472] | | | | 2.7.7.24 |
| 18173, 18174 | 48854571 | 54 | 8.00E-49 | Cytophaga hutchinsonii | COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Cytophaga hutchinsonii] | | | | 2.4.1.- |
| 18175, 18176 | 22960110 | 39 | 4.00E-10 | Rhodobacter sphaeroides 2.4.1 | COG2808: Transcriptional regulator [Rhodobacter sphaeroides 2.4.1] | | | | |
| 18179, 18180 | 20807925 | 38 | 1.00E-11 | Thermoanaerobact er tengcongensis MB4 | Acetate kinase [Thermoanaerobacter tengcongensis MB4] sp Q8R9V4 ACKA_THETN Acetate kinase (Acetokinase) | | | | 2.7.2.1 |
| 18183, 18184 | 24372586 | 25 | 7.00E-07 | Shewanella oneidensis MR-1 | rhomboid family protein [Shewanella oneidensis MR-1] | | | | |
| 18185, 18186 | 18309557 | 30 | 5.00E-10 | Clostridium perfringens str. 13 | two-component response regulator [Clostridium perfringens str. 13] dbj BAB80281.1 two-component response regulator [Clostridium perfringens str. 13] | | | | |
| 18191, 18192 | 32470867 | 34 | 5.00E-18 | Rhodopirellula baltica SH 1 | hypothetical protein RB360 [Rhodopirellula baltica SH 1] emb CAD71533.1 hypothetical protein [Pirellula sp.] | | | | |

| | | | | | | |
|-----------------|--------------|----|----------|---|--|----------|
| 18193, 18194 | 47527329 | 44 | 4.00E-35 | Bacillus anthracis str. 'Ames Ancestor' | methylated-dna--protein-cysteine s-methyltransferase [Bacillus anthracis str. 'Ames Ancestor'] ref YP_028156.1 methylated-DNA--protein-cysteine S- methyltransferase [Bacillus anthracis str. Sterne] ref NP_844441.1 methylated-DNA--protein-cysteine S-methyltransferase [Bacillus anthracis str. Ames] gb AAP25927.1 methylated-DNA--protein-cysteine S- methyltransferase [Bacillus anthracis str. Ames] gb AAT31153.1 methylated- DNA--protein-cysteine S-methyltransferase [Bacillus anthracis str. 'Ames Ancestor'] gb AAT54207.1 methylated-DNA--protein-cysteine S- methyltransferase [Bacillus anthracis str. Sterne] | 2.1.1.63 |
| 18195, 18196 | 24372116 | 53 | 2.00E-32 | Shewanella oneidensis MR-1 | large conductance mechanosensitive channel protein [Shewanella oneidensis MR-1] gb AAN53603.1 large conductance mechanosensitive channel protein [Shewanella oneidensis MR-1] | |
| 18197, 18198 | 21242288 | 35 | 1.00E-30 | Xanthomonas axonopodis pv. citri str. 306 | hypothetical protein XAC1537 [Xanthomonas axonopodis pv. citri str. 306] gb AAM36406.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] | |
| 18203, 18204 | 27367689 | 57 | 4.00E-73 | Vibrio vulnificus CMCP6 | Pseudouridylylase synthase, 23S RNA-specific [Vibrio vulnificus CMCP6] gb AAO08206.1 Pseudouridylylase synthase, 23S RNA-specific [Vibrio vulnificus CMCP6] | 4.2.1.70 |
| 18205, 18206 | 29349619 | 69 | 1.00E-70 | Bacteroides thetaiotaomicron VPI-5482 | putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79316.1 putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides thetaiotaomicron VPI-5482] | 6.3.3.1 |
| 18207, 18208 | AAW7163 9 | 25 | 8.00E-18 | | Desc:Omega-cyclohexane fatty acid biosynthesis enzyme #2 ORF1. Org:Alcyclobacillus acidocaldarius | |
| 18209, 18210 | 53713904 | 69 | 1.00E-93 | Bacteroides fragilis YCH46 | exonuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46] | 1.8.-.- |
| 1821, 1822 | 14520906 | 39 | 2.00E-48 | Pyrococcus abyssal GE5 | hypothetical protein PAB1903 [Pyrococcus abyssi GE5] emb CAB49612.1 Hypothetical protein [Pyrococcus abyssi] pir C75112 hypothetical protein PAB1903 - Pyrococcus abyssi (strain Orsay) | |
| 18213, 18214 | 29350165 | 29 | 2.00E-08 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT4757 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79862.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482] | |
| 18215, 18216 | 49653726 | 28 | 1.00E-08 | Debaryomyces hansenii CBS767 | unnamed protein product [Debaryomyces hansenii CBS767] ref XP_458060.1 unnamed protein product [Debaryomyces hansenii] | |
| 18219, 18220 | 32471625 | 48 | 9.00E-51 | Rhodopirellula baltica SH 1 | hypothetical protein RB1854 [Rhodopirellula baltica SH 1] emb CAD72299.1 conserved hypothetical protein [Pirellula sp.] | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|----------|----------|
| 18221, 18222 | 48856921 | 58 | 4.00E-49 | Cytophaga hutchinsonii | COG0388: Predicted amidohydrolase [Cytophaga hutchinsonii] | Wollnella succinogenes, complete genome; segment 5/7 | 93 | 2.00E-08 | 6.3.2.1 |
| 18231, 18232 | 48854699 | 70 | 5.00E-30 | Cytophaga hutchinsonii | COG3324: Predicted enzyme related to lactoylglutathione lyase [Cytophaga hutchinsonii] | | | | |
| 18235, 18236 | 27366639 | 42 | 4.00E-27 | Vibrio vulnificus CMCP6 | Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] gb AAO07156.1] | | | | |
| 18239, 18240 | 53715841 | 51 | 6.00E-46 | Bacteroides fragilis YCH46 | Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] Smf protein DNA processing chain A [Bacteroides fragilis YCH46] | | | | 3.5.4.12 |
| 18241, 18242 | 53712946 | 59 | 7.00E-42 | Bacteroides fragilis YCH46 | mannose-6-phosphate isomerase [Bacteroides fragilis YCH46] dbj BAD48404.1] mannose-6-phosphate isomerase [Bacteroides fragilis YCH46] | | | | 5.3.1.8 |
| 18243, 18244 | 56461099 | 57 | 6.00E-99 | Idiomarina loihensis L2TR | Carboxynorspermidine dehydrogenase [Idiomarina loihensis L2TR] gb AAV82831.1] Carboxynorspermidine dehydrogenase [Idiomarina loihensis L2TR] | Geobacter sulfurreducens PCA, complete genome | 83 | 5.00E-17 | 1.1.1.- |
| 18249, 18250 | 48854777 | 45 | 6.00E-42 | Cytophaga hutchinsonii | COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii] | | | | |
| 1825, 1826 | 23127068 | 64 | 3.00E-91 | Nostoc punctiforme PCC 73102 | COG1002: Type II restriction enzyme, methylase subunits [Nostoc punctiforme PCC 73102] | | | | |
| 18253, 18254 | 52080825 | 31 | 5.00E-13 | Bacillus licheniformis ATCC 14580 | two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] gb AAU23978.1] two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] ref YP_092025.1] ResE1 [Bacillus licheniformis ATCC 14580] gb AAU41332.1] ResE1 [Bacillus licheniformis DSM 13] | | | | 2.7.3.- |
| 18255, 18256 | 56677219 | 24 | 3.00E-11 | Silicibacter pomeroi DSS-3 | conserved hypothetical protein [Silicibacter pomeroi DSS-3] ref YP_165830.1] hypothetical protein SPO0570 [Silicibacter pomeroi DSS-3] | | | | |
| 18257, 18258 | 21242288 | 40 | 9.00E-29 | Xanthomonas axonopodis pv. citri str. 306 | hypothetical protein XAC1537 [Xanthomonas axonopodis pv. citri str. 306] gb AAM36406.1] conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 18259, 18260 | 45547643 | 33 | 7.00E-10 | Rubrobacter xylanophilus DSM 9941 | COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Rubrobacter xylanophilus DSM 9941] | | | | |
| 18261, 18262 | 48855790 | 32 | 9.00E-15 | Cytophaga hutchinsonii | COG5343: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |

| | | | | | | |
|-------------------------------------|----------------------|----------|----------------------|--|---|--|
| 18263, 18264, 18265, 18266 | 39997854 48853741 | 44 41 | 9.00E-53 2.00E-10 | Geobacter sulfurreducens PCA Cytophaga hutchinsonii | FAD-dependent glycerol-3-phosphate dehydrogenase subunit [Geobacter sulfurreducens PCA] gb AA036155.1 FAD-dependent glycerol-3-phosphate dehydrogenase subunit [Geobacter sulfurreducens PCA] | 1.1.99.5 2.7.3.- |
| 18267, 18268 | 48853741 34556853 | 41 53 | 2.00E-10 2.00E-65 | Wolinella succinogenes DSM 1740 | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] TRIOSEPHOSPHATE ISOMERASE TIM [Wolinella succinogenes DSM 1740] emb CAE09568.1 TRIOSEPHOSPHATE ISOMERASE TIM [Wolinella succinogenes] sp Q7MA77 TPIS_WOLSU Triosephosphate isomerase (TIM) (Triose-phosphate isomerase) | 5.3.1.1 |
| 18271, 18272 | 53735964 | 32 | 6.00E-07 | Crocospaera watsonii WH 8501 | hypothetical protein Cwat03001091 [Crocospaera watsonii WH 8501] | |
| 18275, 18276 | 52011137 | 85 | 1.00E-105 | Silicibacter sp. TM1040 | COG0086: DNA-directed RNA polymerase, beta' subunit/160 kD subunit [Silicibacter sp. TM1040] | Brucella suis 1330 chromosome I, complete sequence 85 1.00E-22 2.7.7.6 |
| 18279, 18280 | 29350007 | 35 | 2.00E-31 | Bacteroides thetataoimicron VPI-5482 | putative transcriptional regulator [Bacteroides thetataoimicron VPI-5482] gb AA079704.1 putative transcriptional regulator [Bacteroides thetataoimicron VPI-5482] | |
| 18283, 18284 | 48855914 | 30 | 4.00E-28 | Cytophaga hutchinsonii | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii] | |
| 18285, 18286 | 46580986 | 36 | 2.00E-09 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | transcriptional regulator, TetR family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97054.1 transcriptional regulator, TetR family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | |
| 1829, 1830 | 48853635 | 48 | 4.00E-42 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | 2.7.3.- |
| 18291, 18292 | 34398079 | 38 | 1.00E-13 | Porphyromonas gingivalis W83 | ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65301.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_906240.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904402.1 ISPg4, transposase [Porphyromonas gingivalis W83] | |
| 18295, 18296 | 34102201 | 33 | 3.00E-11 | Chromobacterium violaceum ATCC 12472 | probable 5-carboxymethyl-2-hydroxymuconate D-isomerase [Chromobacterium violaceum ATCC 12472] ref NP_900563.1 probable 5- carboxymethyl-2-hydroxymuconate D-isomerase [Chromobacterium violaceum ATCC 12472] | 5.3.3.10 |
| 18297, 18298 | 56708912 | 35 | 9.00E-18 | Silicibacter pomeroi DSS-3 | hypothetical protein SPOA0125 [Silicibacter pomeroi DSS-3] gb AAV97262.1 hypothetical protein SPOA0125 [Silicibacter pomeroi DSS- 3] | |
| 18299, 18300 | 23128981 | 39 | 3.00E-27 | Nostoc punctiforme PCC 73102 | COG2319: FOG: WD40 repeat [Nostoc punctiforme PCC 73102] | 2.7.1.37 |

| | | | | | | | | | |
|--------------|----------|----|-----------|--------------------------------------|---|--|--|----|------------------|
| 183, 184 | 20808046 | 41 | 1.00E-52 | Thermoanaerobacter tengcongensis MB4 | predicted GTPases [Thermoanaerobacter tengcongensis MB4] gblAAM24821.1 predicted GTPases [Thermoanaerobacter tengcongensis MB4] sp Q8R9J1 ENGA_THETN GTP-binding protein engA | | | | |
| 18301, 18302 | 34557235 | 45 | 3.00E-29 | Wolinella succinogenes DSM 1740 | PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes DSM 1740] emb CAE0950.1 PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes] | | | | |
| 18305, 18306 | 53711360 | 46 | 5.00E-50 | Bacteroides fragilis YCH46 | putative Tricom-like protease [Bacteroides fragilis YCH46] dbj BAD46818.1 putative Tricom-like protease [Bacteroides fragilis YCH46] | | | | 3.4.21.- |
| 18307, 18308 | 34396235 | 42 | 1.00E-33 | Porphyromonas gingivalis W83 | sensor histidine kinase [Porphyromonas gingivalis W83] ref NP_904403.1 sensor histidine kinase [Porphyromonas gingivalis W83] | | | | 2.7.3.- |
| 1831, 1832 | ABU5672 | 4 | 4.00E-13 | | Desc:Lung cancer-associated polypeptide #317. Org:Unidentified | | | | 2.7.1.- |
| 18311, 18312 | 48855398 | 29 | 6.00E-29 | Cytophaga hutchinsonii | COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii] type I restriction-modification system methyltransferase subunit [Vibrio vulnificus YJ016] dbj BAC93580.1 type I restriction-modification system methyltransferase subunit [Vibrio vulnificus YJ016] | | | | 3.4.- |
| 18313, 18314 | 37679000 | 70 | 1.00E-102 | Vibrio vulnificus YJ016 | | | | | 2.1.1.72 |
| 18315, 18316 | 31196343 | 55 | 1.00E-20 | Anopheles gambiae | ENSANGP0000001688 [Anopheles gambiae] | | | | 3.1.21.3 |
| 18321, 18322 | 48853833 | 56 | 2.00E-38 | Cytophaga hutchinsonii | COG0576: Molecular chaperone GrpE (heat shock protein) [Cytophaga hutchinsonii] | | | | |
| 18333, 18334 | 48853635 | 46 | 5.00E-36 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | |
| 18337, 18338 | 48831369 | 40 | 1.00E-45 | Magnetococcus sp. MC-1 | COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Magnetococcus sp. MC-1] | | | 87 | 2.00E-09/2.7.3.- |
| 18343, 18344 | 15837098 | 29 | 3.00E-13 | Xylella fastidiosa 9a5c | hypothetical protein XF0496 [Xylella fastidiosa 9a5c] gb AAF83306.1 conserved hypothetical protein [Xylella fastidiosa 9a5c] pir A82801 conserved hypothetical protein XF0496 [imported] - Xylella fastidiosa (strain 9a5c) | | | | 1.2.7.- |
| 18345, 18346 | 48859741 | 49 | 8.00E-51 | Clostridium thermocellum ATCC 27405 | COG2360: Leu/Phe-tRNA-protein transferase [Clostridium thermocellum ATCC 27405] | | | | 2.3.2.6 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|---------|
| 18347, 18348 | 29608580 | 31 | 3.00E-18 | Streptomyces avermittilis MA-4680 | hypothetical protein [Streptomyces avermittilis MA-4680] ref NP_826099.1 hypothetical protein SAV4922 [Streptomyces avermittilis MA-4680] | | | | |
| 1835, 1836 | 46202632 | 51 | 1.00E-25 | Magnetospirillum magnetotacticum MS-1 | COG2202: FOG: PAS/PAC domain [Magnetospirillum magnetotacticum MS-1] | | | | |
| 18353, 18354 | 49485641 | 32 | 4.00E-27 | Staphylococcus aureus subsp. aureus MSSA476 | hypothetical protein SAS0734 [Staphylococcus aureus subsp. aureus MSSA476] ref NP_645548.1 hypothetical protein MW0731 [Staphylococcus aureus subsp. aureus MW2] emb CAG42510.1 conserved hypothetical protein [Staphylococcus aureus subsp. aureus MSSA476] db BAB94596.1 MW0731 [Staphylococcus aureus subsp. aureus MW2] | | | | |
| 18357, 18358 | 48853890 | 67 | 2.00E-49 | Cytophaga hutchinsonii | COG0210: Superfamily I DNA and RNA helicases [Cytophaga hutchinsonii] | | | | 3.6.1.- |
| 18359, 18360 | 48856934 | 47 | 4.00E-48 | Cytophaga hutchinsonii | COG1058: Predicted nucleotide-utilizing enzyme related to molybdopterinosynthesis enzyme MoeA [Cytophaga hutchinsonii] | | | | |
| 18361, 18362 | 48854804 | 60 | 8.00E-24 | Cytophaga hutchinsonii | COG0661: Predicted unusual protein kinase [Cytophaga hutchinsonii] | | | | |
| 18365, 18366 | AB8477 | 49 | 6.00E-31 | | Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org: Cytophaga hutchinsonii | | | | |
| 18367, 18368 | 48836151 | 41 | 4.00E-33 | Thermobifida fusca | COG0210: Superfamily I DNA and RNA helicases [Thermobifida fusca] | | | | 3.6.1.- |
| 18369, 18370 | 23128175 | 46 | 2.00E-13 | Nostoc punctiforme PCC 73102 | COG0463: Glycosyltransferases Involved in cell wall biogenesis [Nostoc punctiforme PCC 73102] | | | | 2.4.1.- |
| 18371, 18372 | 48895505 | 46 | 1.00E-18 | Trichodesmium erythraeum IMS101 | COG3222: Uncharacterized protein conserved in bacteria [Trichodesmium erythraeum IMS101] | | | | |
| 18373, 18374 | 48825855 | 29 | 6.00E-09 | Enterococcus faecium | hypothetical protein Efae03000852 [Enterococcus faecium] | | | | |
| 18375, 18376 | 48854895 | 54 | 1.00E-55 | Cytophaga hutchinsonii | COG0491: Zn-dependent hydrolases, including glyoxylases [Cytophaga hutchinsonii] | | | | |
| 18377, 18378 | 48854970 | 30 | 1.00E-11 | Cytophaga hutchinsonii | COG0308: Aminopeptidase N [Cytophaga hutchinsonii] | | | | |
| 18383, 18384 | 53712046 | 63 | 5.00E-32 | Bacteroides fragilis YCH46 | putative alpha-1,2-mannosidase [Bacteroides fragilis YCH46] db BAD47504.1 putative alpha-1,2-mannosidase [Bacteroides fragilis YCH46] | | | | |
| 18389, 18390 | 15606814 | 41 | 6.00E-29 | Aquifex aeolicus VF5 | beta 1,4 glucosyltransferase [Aquifex aeolicus VF5] gb AAC07593.1 beta 1,4 glucosyltransferase [Aquifex aeolicus VF5] pir B70450 beta 1,4 glucosyltransferase - Aquifex aeolicus | | | | 2.4.-.- |

| | | | | | | |
|-----------------|----------|----|----------|--|---|----------|
| 18391, 18392 | 15895588 | 32 | 7.00E-27 | Clostridium acetobutylicum ATCC 824 | Predicted glycosyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK80277.1 Predicted glycosyltransferase [Clostridium acetobutylicum ATCC 824] pir B97186 probable glycosyltransferase CAC2321 [imported] - Clostridium acetobutylicum | 2.4.1.- |
| 18393, 18394 | 48856925 | 30 | 2.00E-10 | Cytophaga hutchinsonii | COG1309: Transcriptional regulator [Cytophaga hutchinsonii] | |
| 18395, 18396 | 48856042 | 45 | 6.00E-20 | Cytophaga hutchinsonii | COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii] Probable sigma(54) modulation protein; SSU ribosomal protein S30P, putative [Campylobacter lari RM2100] gb EAL55561.1 Probable sigma(54) modulation protein; SSU ribosomal protein S30P, putative [Campylobacter lari RM2100] | 3.4.24.- |
| 18399, 18400 | 57240447 | 47 | 4.00E-38 | Campylobacter lari RM2100 | COG0793: Periplasmic protease [Cytophaga hutchinsonii] hypothetical protein BT3977 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79082.1 conserved hypothetical protein [Bacteroides thetaitotaomicron VPI-5482] | 3.4.21.- |
| 18401, 18402 | 48853807 | 38 | 7.00E-45 | Cytophaga hutchinsonii | Branched-chain amino acid aminotransferase [Methanopyrus kandleri AV19] gb AAM02840.1 Branched-chain amino acid aminotransferase [Methanopyrus kandleri AV19] | 2.6.1.42 |
| 18403, 18404 | 29349385 | 32 | 8.00E-10 | Bacteroides thetaitotaomicron VPI-5482 | ORF5 [Moritella marina] | 3.4.21.- |
| 18405, 18406 | 20095063 | 30 | 8.00E-13 | Methanopyrus kandleri AV19 | putative phenylacetic acid degradation NADH oxidoreductase [Corynebacterium efficiens YS-314] dbj BAC17481.1 putative phenylacetic acid degradation NADH oxidoreductase [Corynebacterium efficiens YS-314] ribonuclease HII [Porphyromonas gingivalis W83] ref NP_905006.1 ribonuclease HII [Porphyromonas gingivalis W83] sp Q51832 RNH2_PORGI Ribonuclease HII (RNase HII) COG1381: Recombinational DNA repair protein (RecF pathway) [Cytophaga hutchinsonii] | 1.6.99.7 |
| 18407, 18408 | 6691651 | 35 | 7.00E-24 | Moritella marina | GldB [Flavobacterium johnsoniae] | 3.1.26.4 |
| 18409, 18410 | 25027227 | 39 | 3.00E-27 | Corynebacterium efficiens YS-314 | GldB [Flavobacterium johnsoniae] | |
| 1841, 1842 | 34396840 | 57 | 8.00E-39 | Porphyromonas gingivalis W83 | GldB [Flavobacterium johnsoniae] | |
| 18413, 18414 | 48856963 | 43 | 3.00E-19 | Cytophaga hutchinsonii | GldB [Flavobacterium johnsoniae] | |
| 18415, 18416 | 5360168 | 38 | 6.00E-19 | Flavobacterium johnsoniae | GldB [Flavobacterium johnsoniae] | |
| 18417, 18418 | 5360168 | 38 | 2.00E-18 | Flavobacterium johnsoniae | GldB [Flavobacterium johnsoniae] | |
| 18421, 18422 | 29346727 | 61 | 4.00E-52 | Bacteroides thetaitotaomicron VPI-5482 | riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76424.1 riboflavin synthase alpha chain [Bacteroides thetaitotaomicron VPI-5482] | 2.5.1.9 |
| 18423, 18424 | 46446120 | 54 | 2.00E-25 | Parachlamydia sp. UWE25 | hypothetical protein pc0486 [Parachlamydia sp. UWE25] emb CAF23210.1 hypothetical protein [Parachlamydia sp. UWE25] | |

| | | | | | | | | | |
|--------|----------|----|----------|-----------------------------------|--|--|--|--|----------|
| 18425, | 32404060 | 26 | 1.00E-07 | Neurospora crassa | predicted protein [Neurospora crassa] emb CAD70330.1 putative protein [Neurospora crassa] gb EAA27596.1 predicted protein [Neurospora crassa] | | | | |
| 18426 | AAU7962 | 24 | 3.00E-07 | | Desc:Corynebacterium glutamicum transcription regulator, mkeE17. | | | | |
| 18427, | | | | | Org:Corynebacterium glutamicum | | | | |
| 18428 | 2 | | | | | | | | |
| 1843, | 55376565 | 37 | 6.00E-18 | Haloarcula marismortui ATCC 43049 | DNA polymerase B2 exonuclease domain [Haloarcula marismortui ATCC 43049] gb AAV44711.1 DNA polymerase B2 exonuclease domain | | | | 2.7.7.7 |
| 1844 | | | | | [Haloarcula marismortui ATCC 43049] | | | | |
| 18431, | 24373054 | 31 | 4.00E-18 | Shewanella oneidensis MR-1 | GGDEF family protein [Shewanella oneidensis MR-1] gb AAN54541.1 | | | | |
| 18432 | | | | | GGDEF family protein [Shewanella oneidensis MR-1] | | | | |
| 18433, | 48854489 | 52 | 9.00E-26 | Cytophaga hutchinsonii | hypothetical protein Chut02002688 [Cytophaga hutchinsonii] | | | | |
| 18434 | | | | | | | | | |
| 18443, | | | | | UDP-glucose-6 dehydrogenase, putative [Porphyromonas gingivalis W83] | | | | |
| 18444 | 34397294 | 55 | 1.00E-28 | Porphyromonas gingivalis W83 | ref NP_905458.1 UDP-glucose-6 dehydrogenase, putative [Porphyromonas gingivalis W83] | | | | 1.1.1.- |
| 18445, | | | | | | | | | |
| 18446 | 48854228 | 39 | 1.00E-48 | Cytophaga hutchinsonii | COG1819: Glycosyl transferases, related to UDP-glucuronosyltransferase [Cytophaga hutchinsonii] | | | | |
| 18447, | | | | | hypothetical protein PP4510 [Pseudomonas putida KT2440] | | | | |
| 18448 | 26991195 | 45 | 6.00E-34 | Pseudomonas putida KT2440 | gb AAN70084.1 conserved hypothetical protein [Pseudomonas putida KT2440] | | | | |
| 18449, | | | | | 2-isopropylmalate synthase LeuA [Bacteroides fragilis YCH46] | | | | 4.1.3.12 |
| 18450 | 53714730 | 63 | 2.00E-83 | Bacteroides fragilis YCH46 | dbj BAD50188.1 2-isopropylmalate synthase LeuA [Bacteroides fragilis YCH46] | | | | |
| 18451, | | | | | | | | | |
| 18452 | 48856112 | 40 | 2.00E-53 | Cytophaga hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 18453, | | | | | hypothetical protein OB0915 [Oceanobacillus ihayensis HTE831] | | | | |
| 18454 | 23098370 | 53 | 1.00E-41 | Oceanobacillus ihayensis HTE831 | dbj BAC12871.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831] | | | | |
| 18457, | | | | | riboflavin biosynthesis protein RibD [Bacteroides fragilis YCH46] | | | | 1.1.1.19 |
| 18458 | 53711798 | 58 | 6.00E-67 | Bacteroides fragilis YCH46 | dbj BAD47256.1 riboflavin biosynthesis protein RibD [Bacteroides fragilis YCH46] | | | | 3 |
| 18459, | | | | | DNA-3-methyladenine glycosidase I [Coxiella burnetii RSA 493] | | | | |
| 18460 | 29653730 | 55 | 7.00E-59 | Coxiella burnetii RSA 493 | gb AAO89936.1 DNA-3-methyladenine glycosidase I [Coxiella burnetii RSA 493] | | | | 3.2.2.20 |
| 18463, | | | | | ORF_10; similar to Zinc-binding dehydrogenases [Pseudomonas aeruginosa] gb AAM27562.1 ORF_10; similar to Zinc-binding dehydrogenases [Pseudomonas aeruginosa] | | | | 1.1.1.- |
| 18464 | 20559950 | 44 | 3.00E-17 | Pseudomonas aeruginosa | | | | | |
| 18465, | | | | | | | | | |
| 18466 | 48860575 | 31 | 1.00E-12 | Microbulifer degradans 2-40 | hypothetical protein Mdeg02004210 [Microbulifer degradans 2-40] | | | | |

| | | | | | | | | |
|-------------------------------------|----------|----|----------|---|---|--|----|------------------|
| 18467, 18468, 18469, 18470 | 29655030 | 50 | 2.00E-22 | Coxiella burnetii RSA 493 | conserved hypothetical protein TIGR00252 [Coxiella burnetii RSA 493] gb AAO91236.1 conserved hypothetical protein TIGR00252 [Coxiella burnetii RSA 493] sp Q83AY5 YH42_COXBU Hypothetical UPF0102 protein CBU1742 | | | 3.1.-.- |
| 18470 | 58003149 | 58 | 3.00E-33 | Gluconobacter oxydans 621H | Serine hydroxymethyl transferase [Gluconobacter oxydans 621H] putative NADH dehydrogenase [Bacteroides fragilis YCH46] dbj BAD48348.1 putative NADH dehydrogenase [Bacteroides fragilis YCH46] | | | 2.1.2.1 |
| 1847, 1848 | 53712890 | 48 | 1.00E-57 | Bacteroides fragilis YCH46 | | | | 1.6.99.3 |
| 18471, 18472 | 55769919 | 52 | 2.00E-66 | Oryza sativa (japonica cultivar- group) | putative leucyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)] dbj BAD52586.1 putative leucyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)] | Desc:Staphylococcus aureus DNA for cellular proliferation protein #863. Org:Staphylococcus aureus | 91 | 1.00E-07 6.1.1.4 |
| 18475, 18476 | 47459121 | 27 | 4.00E-08 | Mycoplasma mobile 163K | type I restriction enzyme m protein [Mycoplasma mobile 163K] gb AAT27772.1 type I restriction enzyme m protein [Mycoplasma mobile 163K] | | | |
| 18477, 18478 | 48854976 | 45 | 4.00E-42 | Cytophaga hutchinsonii | COG0119: Isopropylmalate/homocitrate/citramalate synthases [Cytophaga hutchinsonii] | | | 4.1.3.4 |
| 18479, 18480 | 48854542 | 40 | 2.00E-39 | Cytophaga hutchinsonii | COG1748: Saccharopine dehydrogenase and related proteins [Cytophaga hutchinsonii] | | | 1.5.1.7 |
| 18481, 18482 | 29346142 | 38 | 1.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO75839.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.3.- |
| 18483, 18484 | 28897283 | 24 | 3.00E-11 | Vibrio parahaemolyticus RIMD 2210633 | integrase/recombinase XerD [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58772.1 integrase/recombinase XerD [Vibrio parahaemolyticus] | | | |
| 18485, 18486 | 48855767 | 43 | 4.00E-21 | Cytophaga hutchinsonii | COG0123: Deacetylases, including yeast histone deacetylase and acetoin utilization protein [Cytophaga hutchinsonii] | | | |
| 18487, 18488 | 47529986 | 54 | 9.00E-21 | Bacillus anthracis str. 'Ames Ancestor' | septom formation protein maf [Bacillus anthracis str. 'Ames Ancestor'] ref YP_030599.1 septum formation protein Maf [Bacillus anthracis str. Ames] ref NP_846900.1 septum formation protein Maf [Bacillus anthracis str. Ames] ref NP_658486.1 Maf, Maf-like protein [Bacillus anthracis str. A2012] gb AAP28386.1 septum formation protein Maf [Bacillus anthracis str. Ames] gb AAT33810.1 septum formation protein Maf [Bacillus anthracis str. Ames Ancestor] gb AAT56650.1 septum formation protein Maf [Bacillus anthracis str. Sterne] sp Q81LD6 MAF_BACAN Septum formation protein Maf | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|----------|
| 18489, 18490 | 21241606 | 45 | 1.00E-07 | Xanthomonas axonopodis pv. citri str. 306 | hypothetical protein XAC0836 [Xanthomonas axonopodis pv. citri str. 306] gb AAAM35724.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 1849, 1850 | 45510657 | 55 | 2.00E-63 | Anabaena variabilis ATCC 29413 | COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Anabaena variabilis ATCC 29413] | | | | 3.1.21.3 |
| 18491, 18492 | 37520843 | 51 | 5.00E-24 | Gloeobacter violaceus PCC 7421 | hypothetical protein glr1374 [Gloeobacter violaceus PCC 7421] dbj BAC89315.1 glr1374 [Gloeobacter violaceus PCC 7421] | | | | |
| 18493, 18494 | 29349247 | 54 | 7.00E-56 | Bacteroides thetaiotaomicron VPI-5482 | ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78944.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.8.-.- |
| 18495, 18496 | 8886019 | 50 | 2.00E-41 | Chryseobacterium meningosepticum | PI-irrepressible alkaline phosphatase PafA [Chryseobacterium meningosepticum] | | | | |
| 18497, 18498 | 53715368 | 36 | 1.00E-07 | Bacteroides fragilis YCH46 | hypothetical protein BF4084 [Bacteroides fragilis YCH46] dbj BAD50826.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | - |
| 18501, 18502 | 48839680 | 27 | 5.00E-08 | Methanoscirina barkeri str. fusaro | COG1668: ABC-type Na ⁺ efflux pump, permease component [Methanoscirina barkeri str. fusaro] | | | | |
| 18503, 18504 | 48856549 | 58 | 6.00E-32 | Cytophaga hutchinsonii | COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Cytophaga hutchinsonii] | | | | 2.7.-.- |
| 18505, 18506 | 9655931 | 56 | 3.00E-48 | Vibrio cholerae O1 biovar eltor str. N16961 | conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231075.1 hypothetical protein VC1432 [Vibrio cholerae O1 biovar eltor str. N16961] p D82199 conserved hypothetical protein VC1432 [Imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 18507, 18508 | 48856923 | 32 | 1.00E-28 | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | | |
| 18509, 18510 | 53758661 | 52 | 2.00E-43 | Methylococcus capsulatus str. Bath | pyruvate ferredoxin/flavodoxin oxidoreductase family protein [Methylococcus capsulatus str. Bath] ref YP_113272.1 pyruvate ferredoxin/flavodoxin oxidoreductase family protein [Methylococcus capsulatus str. Bath] | | | | 1.2.7.1 |
| 1851, 1852 | 48856045 | 24 | 9.00E-11 | Cytophaga hutchinsonii | hypothetical protein Chut02001277 [Cytophaga hutchinsonii] | | | | |
| 18511, 18512 | 28199976 | 28 | 2.00E-13 | Xylella fastidiosa Temecula1 | hypothetical protein PD2120 [Xylella fastidiosa Temecula1] gb AAO29939.1 conserved hypothetical protein [Xylella fastidiosa Temecula1] | | | | |
| 18513, 18514 | 52425551 | 37 | 1.00E-25 | Mannheimia succiniciproducens MBEL55E | RfaG protein [Mannheimia succiniciproducens MBEL55E] gb AAU38103.1 RfaG protein [Mannheimia succiniciproducens MBEL55E] | | | | 2.4.1.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|------------------|
| 18517, 18518 | 29347648 | 39 | 3.00E-22 | Bacteroides thetaiotaomicron VPI-5482 | putative biotin--(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77345.1 putative biotin--(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | 6.3.4.15 |
| 18533, 18534 | 56708241 | 50 | 1.00E-41 | Francisella tularensis subsp. tularensis Schu 4 | DNA-methyltransferase, type I restriction-modification enzyme subunit M [Francisella tularensis subsp. tularensis Schu 4] emb CAG45804.1 DNA- methyltransferase, type I restriction-modification enzyme subunit M [Francisella tularensis subsp. tularensis] | | | |
| 18535, 18536 | 58000733 | 33 | 1.00E-08 | Gluconobacter oxydans 621H | Type I restriction-modification enzyme S subunit [Gluconobacter oxydans 621H] | | | 3.1.21.3 |
| 18537, 18538 | ABB4904 | 41 | 3.00E-37 | | Desc:Listeria monocytogenes protein #1747. Org:Listeria monocytogenes | | | 6.2.1.26 |
| 18539, 18540 | 46202152 | 36 | 4.00E-33 | Magnetospirillum magnetotacticum MS-1 | COG0582: Integrase [Magnetospirillum magnetotacticum MS-1] | | | |
| 18541, 18542 | 23004335 | 33 | 2.00E-10 | Magnetospirillum magnetotacticum MS-1 | COG1974: SOS-response transcriptional repressors (RecA-mediated autopeptidases) [Magnetospirillum magnetotacticum MS-1] | | | 3.4.21.8 8 |
| 18545, 18546 | 21243533 | 30 | 3.00E-24 | Xanthomonas axonopodis pv. citri str. 306 | beta-lactamase [Xanthomonas axonopodis pv. citri str. 306] gb AAM37651.1 beta-lactamase [Xanthomonas axonopodis pv. citri str. 306] | | | |
| 18547, 18548 | 34397294 | 38 | 2.00E-12 | Porphyrromonas gingivalis W83 | UDP-glucose-6 dehydrogenase, putative [Porphyrromonas gingivalis W83] ref NP_905458.1 UDP-glucose-6 dehydrogenase, putative [Porphyrromonas gingivalis W83] | | | 1.1.1.- |
| 18549, 18550 | 48854895 | 57 | 5.00E-53 | Cytophaga hutchinsonii | COG0491: Zn-dependent hydrolases, including glyoxylases [Cytophaga hutchinsonii] | | | |
| 18551, 18552 | 56678640 | 78 | 7.00E-46 | Silicibacter pomeroiy DSS-3 | RecA [Silicibacter pomeroiy DSS-3] ref YP_167265.1 RecA [Silicibacter pomeroiy DSS-3] | Agrobacterium tumefaciens str. C58 circular chromosome, section 167 of 256 of the complete sequence | 89 | 5.00E-12 3.1.-.- |
| 18555, 18556 | 39996620 | 44 | 6.00E-09 | Geobacter sulfurreducens PCA | phenylalanyl-tRNA synthetase, beta subunit [Geobacter sulfurreducens PCA] gb AAR34894.1 phenylalanyl-tRNA synthetase, beta subunit [Geobacter sulfurreducens PCA] | | | 6.1.1.20 |
| 18557, 18558 | 53714985 | 30 | 3.00E-14 | Bacteroides fragilis YCH46 | putative membrane peptidase [Bacteroides fragilis YCH46] db BAD50443.1 putative membrane peptidase [Bacteroides fragilis YCH46] | | | |
| 18559, 18560 | 48856025 | 29 | 8.00E-18 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------|---|---|----|----------|----------|
| 18561, | 29027481 | 58 | 5.00E-57 | Aster yellows phytoplasma | threonine dehydratase [Aster yellows phytoplasma] | Streptococcus mutans UA159 section 21 of 185 of the complete genome | 93 | 2.00E-08 | 4.2.1.16 |
| 18562 | | | | | ABC transporter ATP-binding protein [Clostridium tetani E88] | | | | |
| 18563, | 28210316 | 69 | 5.00E-24 | Clostridium tetani E88 | gb AAO35197.1 ABC transporter ATP-binding protein [Clostridium tetani E88] | | | | |
| 18564 | | | | | | | | | |
| 18565, | 56962820 | 37 | 1.00E-33 | Bacillus clausii KSM-K16 | multidrug ABC transporter ATP-binding protein [Bacillus clausii KSM-K16] | | | | 1.8.-.- |
| 18566 | | | | | dbj BAD63585.1 multidrug ABC transporter ATP-binding protein [Bacillus clausii KSM-K16] | | | | |
| 18571, | 48854785 | 37 | 1.00E-18 | Cytophaga hutchinsonii | COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii] | | | | 2.7.7.- |
| 18572 | | | | | | | | | |
| 18575, | 48856042 | 52 | 3.00E-26 | Cytophaga hutchinsonii | COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii] | | | | 3.4.24.- |
| 18576 | | | | | | | | | |
| 18577, | 48854859 | 39 | 2.00E-22 | Cytophaga hutchinsonii | COG0108: 3,4-dihydroxy-2-butanone 4-phosphate synthase [Cytophaga hutchinsonii] | | | | 3.5.4.25 |
| 18578 | | | | | | | | | |
| 18579, | 48853829 | 57 | 2.00E-58 | Cytophaga hutchinsonii | COG0498: Threonine synthase [Cytophaga hutchinsonii] | | | | 4.2.99.2 |
| 18580 | | | | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] | | | | |
| 18581, | 34557291 | 40 | 3.00E-33 | Cytophaga hutchinsonii | emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | 2.4.1.18 |
| 18582 | | | | | | | | | 2 |
| 18585, | 48855019 | 50 | 2.00E-62 | Cytophaga hutchinsonii | COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii] | | | | |
| 18586 | | | | | | | | | |
| 18587, | 48853588 | 26 | 7.00E-12 | Cytophaga hutchinsonii | COG1388: FOG: LysM repeat [Cytophaga hutchinsonii] | | | | |
| 18588 | | | | | | | | | |
| 18589, | 48856321 | 57 | 6.00E-43 | Cytophaga hutchinsonii | COG4430: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 18590 | | | | | | | | | |
| 18591, | | | | | probable DNA polymerase III epsilon chain [Clostridium perfringens str. 13] | | | | |
| 18592 | 18310383 | 39 | 4.00E-45 | Clostridium perfringens str. 13 | dbj BAB81107.1 probable DNA polymerase III epsilon chain [Clostridium perfringens str. 13] | | | | 2.7.7.7 |
| 18595, | | | | Geobacter metallireducens GS | COG4191: Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Geobacter metallireducens GS-15] | | | | |
| 18596 | 48846657 | 40 | 1.00E-37 | Geobacter violaceus PCC 7421 | two-component hybrid sensor and regulator [Geobacter violaceus PCC 7421] dbj BAC38659.1 two-component hybrid sensor and regulator [Geobacter violaceus PCC 7421] | | | | 2.7.3.- |
| 18597, | | | | | | | | | |
| 18598 | 37520287 | 46 | 2.00E-47 | Geobacter violaceus PCC 7421 | | | | | 2.7.3.- |
| 18599, | | | | Pyrococcus horikoshii OT3 | hypothetical protein PH0398 [Pyrococcus horikoshii OT3] dbj BAA29473.1 334aa long hypothetical protein [Pyrococcus horikoshii OT3] pir D71148 | | | | |
| 18600 | 14590306 | 31 | 6.00E-10 | Pyrococcus horikoshii OT3 | hypothetical protein PH0398 - Pyrococcus horikoshii | | | | |

| | | | | | | | | |
|-----------------|--------------|----|----------|---|--|--|--|----------|
| 18601, 18602 | 54295894 | 42 | 3.00E-56 | Legionella pneumophila str. Paris | hypothetical protein plpp0051 [Legionella pneumophila str. Paris] emb CAH17228.1 hypothetical protein [Legionella pneumophila str. Paris] | | | |
| 18603, 18604 | 54295894 | 61 | 2.00E-81 | Legionella pneumophila str. Paris | hypothetical protein plpp0051 [Legionella pneumophila str. Paris] emb CAH17228.1 hypothetical protein [Legionella pneumophila str. Paris] | | | |
| 18605, 18606 | 42523942 | 49 | 3.00E-25 | Bdellovibrio bacteriovorus HD100 | SEC-independent protein translocase protein TATC [Bdellovibrio bacteriovorus HD100] emb CAE80315.1 SEC-independent protein translocase protein TATC [Bdellovibrio bacteriovorus HD100] | | | |
| 18609, 18610 | AAB1851 5 | 44 | 1.00E-33 | | Desc:Amino acid sequence of prolyl-tripeptidyl peptidase DPP. Org:Porphyromonas gingivalis | | | 3.4.14.- |
| 18611, 18612 | 48855584 | 31 | 1.00E-40 | Cytophaga hutchinsonii | COG0010: Arginase/agmatinase/formimionoglutamate hydrolase, arginase family [Cytophaga hutchinsonii] | | | 3.5.3.1 |
| 18615, 18616 | 48856329 | 60 | 1.00E-82 | Cytophaga hutchinsonii | COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | 1.8.- |
| 18619, 18620 | 21675046 | 45 | 4.00E-15 | Chlorobium tepidum TLS | hypothetical protein CT2237 [Chlorobium tepidum TLS] gb AAM73453.1 hypothetical protein [Chlorobium tepidum TLS] | | | |
| 18623, 18624 | 29347938 | 42 | 2.00E-17 | Bacteroides thetaiotaomicron VPI-5482 | putative Na+-dependent phosphate transporter [Bacteroides thetaiotaomicron VPI-5482] gb AAO77635.1 putative Na+-dependent phosphate transporter [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 18625, 18626 | 57158781 | 44 | 2.00E-17 | Thermococcus kodakaraensis | carbohydrate esterase, family 1 [Thermococcus kodakaraensis] ref YP_182935.1 carbohydrate esterase, family 1 [Thermococcus kodakaraensis] | | | 3.2.1.41 |
| 1863, 1864 | 48855446 | 32 | 3.00E-32 | Cytophaga hutchinsonii | COG1173: ABC-type dipeptide/oligopeptide/nickel transport systems, permease components [Cytophaga hutchinsonii] | | | |
| 18631, 18632 | 34398049 | 55 | 8.00E-40 | Porphyromonas gingivalis W83 | conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_906210.1 hypothetical protein PG2158 [Porphyromonas gingivalis W83] | | | |
| 18633, 18634 | 55246965 | 69 | 1.00E-36 | Anopheles gambiae str. PEST | ENSANGP00000000220 [Anopheles gambiae str. PEST] ref XP_561052.1 ENSANGP00000000220 [Anopheles gambiae str. PEST] | | | 2.3.1.30 |
| 18635, 18636 | 48850961 | 69 | 1.00E-40 | Novosphingobium aromaticivorans DSM 12444 | COG0250: Transcription antiterminator [Novosphingobium aromaticivorans DSM 12444] | | | |
| 18637, 18638 | 27366639 | 50 | 1.00E-22 | Vibrio vulnificus CMCP6 | Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] gb AAO07156.1 Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] | | | |
| 18639, 18640 | 21702210 | 34 | 9.00E-18 | Flavobacterium sp. 92 | cyclomaltodextrinase [Flavobacterium sp. 92] | | | |
| 18643, 18644 | 28974569 | 28 | 1.00E-11 | Pseudomonas sp. Y2 | putative ring-oxydation complex protein 5 [Pseudomonas sp. Y2] | | | 1.18.1.2 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|
| 18647, 18648 | 29348988 | 50 | 2.00E-71 | Bacteroides thetaiotaomicron VPI-5482 | topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] gb AAO78885.1 topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | 5.99.1.- |
| 18651, 18652 | 48855884 | 46 | 5.00E-21 | Cytophaga hutchinsonii | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | |
| 18653, 18654 | 15643161 | 33 | 5.00E-25 | Thermotoga maritima MSB8 | NADH oxidase, putative [Thermotoga maritima MSB8] gb AAD35480.1 NADH oxidase, putative [Thermotoga maritima MSB8] pir J72382 hypothetical protein TM0395 - Thermotoga maritima (strain MSB8) | | | 1.6.- |
| 18655, 18656 | 48853860 | 65 | 1.00E-40 | Cytophaga hutchinsonii | hypothetical protein Chut02003506 [Cytophaga hutchinsonii] | Desulfotalea psychrophila LSv54 chromosome | 81 | 5.00E-12 |
| 18657, 18658 | 21674610 | 55 | 1.00E-10 | Chlorobium tepidum TLS | hypothetical protein CT1796 [Chlorobium tepidum TLS] gb AAM73017.1 hypothetical protein [Chlorobium tepidum TLS] | | | |
| 18659, 18660 | 53691661 | 55 | 3.00E-43 | Desulfovibrio desulfuricans G20 | COG3039: Transposase and inactivated derivatives, IS5 family [Desulfovibrio desulfuricans G20] | | | |
| 18661, 18662 | 29349972 | 62 | 1.00E-79 | Bacteroides thetaiotaomicron VPI-5482 | putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.4.1.83 |
| 18663, 18664 | 29349649 | 44 | 9.00E-74 | Bacteroides thetaiotaomicron VPI-5482 | beta-galactosidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79346.1 beta-galactosidase [Bacteroides thetaiotaomicron VPI- 5482] | | | 3.2.1.23 |
| 18669, 18670 | 45658173 | 27 | 8.00E-10 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | hypothetical protein LIC12325 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_711602.1 hypothetical protein LA1421 [Leptospira interrogans serovar Lai str. 56601] gb AAN48620.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS70896.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | |
| 18671, 18672 | 48837936 | 44 | 2.00E-43 | Methanosarcina barkeri str. fusaro | COG1162: Predicted GTPases [Methanosarcina barkeri str. fusaro] | | | 3.6.1.- |
| 18677, 18678 | 39997048 | 43 | 2.00E-30 | Geobacter sulfurreducens PCA | capK related-protein [Geobacter sulfurreducens PCA] gb AAR35326.1 capK related-protein [Geobacter sulfurreducens PCA] | | | |
| 18679, 18680 | 48854755 | 54 | 8.00E-71 | Cytophaga hutchinsonii | COG0774: UDP-3-O-acetyl-N-acetylglucosamine deacetylase [Cytophaga hutchinsonii] | | | 4.2.1.- |
| 18681, 18682 | 34397292 | 52 | 2.00E-24 | Porphyromonas gingivalis W83 | translation elongation factor P [Porphyromonas gingivalis W83] ref NP_905456.1 translation elongation factor P [Porphyromonas gingivalis W83] sp Q7MV32 EFP2_PORGI Elongation factor P 2 (EF-P 2) | Orion yellows phytoplasma OY-M DNA, complete genome | 92 | 2.00E-11 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|---|----|----------|----------|
| 18683, 18684 | 29345629 | 43 | 5.00E-17 | Bacteroides thetaiotaomicron VPI-5482 | thioredoxin C-2 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75326.1] thioredoxin C-2 [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.6.4.5 |
| 18685, 18686 | 15614651 | 68 | 3.00E-45 | Bacillus halodurans C-125 | hypothetical protein BH2088 [Bacillus halodurans C-125] dbj BAB05807.1] BH2088 [Bacillus halodurans C-125] pir H83910 hypothetical protein BH2088 [imported] - Bacillus halodurans (strain C-125) dbj BAA75367.1] Ydel [Bacillus halodurans] | | | | |
| 18687, 18688 | 53712279 | 24 | 3.00E-16 | Bacteroides fragilis YCH46 | outer membrane assembly protein [Bacteroides fragilis YCH46] dbj BAD47737.1] outer membrane assembly protein [Bacteroides fragilis YCH46] | | | | |
| 18689, 18690 | 48854415 | 42 | 1.00E-44 | Cytophaga hutchinsonii | COG3279: Response regulator of the LysR/AigR family [Cytophaga hutchinsonii] | | | | |
| 18691, 18692 | 48860518 | 52 | 6.00E-21 | Clostridium thermocellum ATCC 27405 | COG0261: Ribosomal protein L21 [Clostridium thermocellum ATCC 27405] | | | | |
| 18693, 18694 | 48856677 | 37 | 6.00E-44 | Cytophaga hutchinsonii | COG0232: dGTP triphosphohydrolase [Cytophaga hutchinsonii] | | | | 3.1.5.1 |
| 18695, 18696 | 48856576 | 46 | 7.00E-45 | Cytophaga hutchinsonii | COG1071: Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit [Cytophaga hutchinsonii] | | | | 1.2.4.1 |
| 18697, 18698 | 46202152 | 37 | 3.00E-40 | Magnetospirillum magnetotacticum MS-1 | COG0582: Integrase [Magnetospirillum magnetotacticum MS-1] | | | | |
| 18701, 18702 | 31195865 | 75 | 3.00E-46 | Anopheles gambiae | ENSANGP00000000381 [Anopheles gambiae] | Anopheles gambiae ENSANGP00000000 0381 (ENSANGG00000000 00361) mRNA, partial cds | 87 | 3.00E-10 | 4.4.1.11 |
| 18703, 18704 | 29345661 | 69 | 5.00E-88 | Bacteroides thetaiotaomicron VPI-5482 | dolichol-phosphate mannosyltransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO75358.1] dolichol-phosphate mannosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.4.1.83 |
| 18709, 18710 | 48856872 | 57 | 7.00E-70 | Cytophaga hutchinsonii | COG1533: DNA repair photolyase [Cytophaga hutchinsonii] | | | | |
| 18711, 18712 | 21229991 | 39 | 1.00E-16 | Xanthomonas campestris pv. campestris str. ATCC 33913 | hypothetical protein XCC0516 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39832.1] conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|-------|
| 18713, 18714 | 56460818 | 32 | 5.00E-19 | Idiomarina loihensis L2TR | Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihensis L2TR] | | | | |
| 18715, 18716 | 48859742 | 30 | 1.00E-31 | Clostridium thermocellum ATCC 27405 | hypothetical protein Chte02000885 [Clostridium thermocellum ATCC 27405] | | | | |
| 18717, 18718 | 37522197 | 25 | 5.00E-13 | Gloeobacter violaceus PCC 7421 | hypothetical protein gli2628 [Gloeobacter violaceus PCC 7421] dbj BAC90569.1 gli2628 [Gloeobacter violaceus PCC 7421] | | | | |
| 18719, 18720 | 32474463 | 47 | 3.00E-15 | Rhodopirellula baltica SH 1 | choline sulfatase [Rhodopirellula baltica SH 1] emb CAD75003.1 choline sulfatase [Pirellula sp.] | | | | |
| 18723, 18724 | 29347646 | 45 | 3.00E-20 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2236 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77343.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A5K3 YM36_BACTN Hypothetical UPF0102 protein BT2236 | | | | 3.1-- |
| 18725, 18726 | 48853984 | 42 | 1.00E-30 | Cytophaga hutchinsonii | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | | |
| 1873, 1874 | 48858374 | 35 | 1.00E-19 | Clostridium thermocellum ATCC 27405 | COG2908: Uncharacterized protein conserved in bacteria [Clostridium thermocellum ATCC 27405] | | | | |
| 18731, 18732 | 45659049 | 26 | 1.00E-14 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC13227 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714224.1 hypothetical protein LA4044 [Leptospira interrogans serovar Lai str. 56601] gb AAN51242.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS71772.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 18733, 18734 | 53734828 | 31 | 3.00E-08 | Crocospaera watsonii WH 8501 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Crocospaera watsonii WH 8501] | | | | |
| 18735, 18736 | 53729796 | 64 | 5.00E-69 | Dechloromonas aromatica RCB | COG0178: Excinuclease ATPase subunit [Dechloromonas aromatica RCB] | | | | |
| 18739, 18740 | 48853553 | 37 | 2.00E-19 | Cytophaga hutchinsonii | COG0715: ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components [Cytophaga hutchinsonii] | | | | |
| 18741, 18742 | 48855418 | 66 | 2.00E-79 | Cytophaga hutchinsonii | COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii] | | | | |
| 18743, 18744 | 28212164 | 56 | 3.00E-52 | Clostridium tetani E88 | LSU ribosomal protein L6P [Clostridium tetani E88] gb AAO37045.1 LSU ribosomal protein L6P [Clostridium tetani E88] | | | | |
| 18745, 18746 | 29606128 | 37 | 2.00E-14 | Streptomyces avermitilis MA-4680 | hypothetical protein [Streptomyces avermitilis MA-4680] ref NP_823656.1 hypothetical protein SAV2480 [Streptomyces avermitilis MA-4680] | | | | |

| | | | | | | | | | |
|------------------------------------|----------------------|----------|----------------------|--|---|--|----|----------|----------|
| 18747, 18748 | 46119348 | 43 | 5.00E-08 | Crocospaera watsonii WH 8501 | COG0607: Rhodanese-related sulfotransferase [Crocospaera watsonii WH 8501] | | | | |
| 18749, 18750 | 29348486 | 60 | 1.00E-65 | Bacteroides thetaiotaomicron VPI-5482 | ribonuclease R [Bacteroides thetaiotaomicron VPI-5482] gb AAO78183.1 ribonuclease R [Bacteroides thetaiotaomicron VPI-5482] | Apis mellifera similar to SD10981p (LOC413944), mRNA | 91 | 5.00E-10 | 3.1.- |
| 18751, 18752 18753, 18754 | 56459804 19068097 | 29 57 | 4.00E-20 3.00E-26 | Idiomarina lohiensis L2TR Bacteroides fragilis | Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina lohiensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina lohiensis L2TR] unknown [Bacteroides fragilis] | | | | |
| 18755, 18756 | 48853695 | 46 | 2.00E-52 | Cytophaga hutchinsonii | hypothetical protein Chut02003551 [Cytophaga hutchinsonii] | Treponema denticola ATCC 35405, section 3 of 10 of the complete genome | 95 | 1.00E-07 | |
| 18757, 18758 | 29349192 | 60 | 5.00E-83 | Bacteroides thetaiotaomicron VPI-5482 | putative alpha-1,2-mannosidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78889.1 putative alpha-1,2-mannosidase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 18761, 18762 | 48856934 | 36 | 7.00E-49 | Cytophaga hutchinsonii | COG1058: Predicted nucleotide-utilizing enzyme related to molybdopterh- biosynthesis enzyme MoeA [Cytophaga hutchinsonii] | | | | |
| 18763, 18764 | 49482329 | 59 | 7.00E-43 | Staphylococcus aureus subsp. aureus MRSA252 | putative restriction enzyme [Staphylococcus aureus subsp. aureus MRSA252] emb CAG39114.1 putative restriction enzyme [Staphylococcus aureus subsp. aureus MRSA252] | | | | 3.1.21.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|----------|
| 18765, 18766 | 57285120 | 36 | 4.00E-14 | Staphylococcus aureus subsp. aureus COL | transcriptional regulatory protein DegU, putative [Staphylococcus aureus subsp. aureus COL] ref YP_044394.1 putative response regulator [Staphylococcus aureus subsp. aureus MSSA476] ref NP_647130.1 hypothetical protein MW2313 [Staphylococcus aureus subsp. aureus MW2] ref NP_375502.1 hypothetical protein SA2179 [Staphylococcus aureus subsp. aureus N315] emb CAG44095.1 putative response regulator [Staphylococcus aureus subsp. aureus MSSA476] db BAB58553.1 response regulators of two-component regulatory [Staphylococcus aureus subsp. aureus Mu50] db BAB96178.1 MW2313 [Staphylococcus aureus subsp. aureus MW2] db BAB43481.1 SA2179 [Staphylococcus aureus subsp. aureus N315] pir H90039 hypothetical protein SA2179 [imported] - Staphylococcus aureus (strain N315) ref NP_372915.1 response regulators of two-component regulatory [Staphylococcus aureus subsp. aureus Mu50] ref YP_187192.1 transcriptional regulatory protein DegU, putative [Staphylococcus aureus subsp. aureus COL] | | | | |
| 18767, 18768 | 39995500 | 43 | 1.00E-08 | Geobacter sulfurreducens PCA | efflux transporter, RND family, MFP subunit [Geobacter sulfurreducens PCA] gb AAR33724.1 efflux transporter, RND family, MFP subunit [Geobacter sulfurreducens PCA] | | | | |
| 18769, 18770 | 48847126 | 48 | 2.00E-64 | Geobacter metallireducens GS | COG0841: Cation/multidrug efflux pump [Geobacter metallireducens GS-15] | | | | |
| 18773, 18774 | 24214680 | 36 | 5.00E-28 | Leptospira interrogans serovar Lai str. 56601 | hypothetical protein LA1980 [Leptospira interrogans serovar Lai str. 56601] gb AAN49179.1 hypothetical protein [Leptospira interrogans serovar lai str. 56601] | | | | |
| 18779, 18780 | 17232048 | 61 | 6.00E-20 | Nostoc sp. PCC 7120 | hypothetical protein al4556 [Nostoc sp. PCC 7120] db BAB76255.1 al4556 [Nostoc sp. PCC 7120] pir AD2375 hypothetical protein al4556 [imported] - Nostoc sp. (strain PCC 7120) | | | | |
| 18781, 18782 | 48853836 | 59 | 2.00E-85 | Cytophaga hutchinsonii | COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii] | | | 3.2.1.4 | |
| 18783, 18784 | 48861416 | 75 | 2.00E-50 | Microbulifer degradans 2-40 | COG0177: Predicted EndoIII-related endonuclease [Microbulifer degradans 2-40] | | | 4.2.99.1 | |
| 18787, 18788 | 29346789 | 62 | 2.00E-55 | Bacteroides thetaiotaomicron VPI-5482 | phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76486.1 phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A7Z5 HIS4_BACTN 1-(5-phosphoribosyl)-5-(5-phosphoribosylamino)methylideneamino) imidazole-4-carboxamide isomerase (Phosphoribosylformimino-5-aminimidazole carboxamide ribotide isomerase) | | | 8 | 5.3.1.16 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|--|----------|
| 1879, 1880 | 29608208 | 42 | 1.00E-23 | Streptomyces avermitilis MA-4680 | putative aminotransferase [Streptomyces avermitilis MA-4680] ref NP_825728.1 putative aminotransferase [Streptomyces avermitilis MA-4680] | | | | 2.6.1.- |
| 18791, 18792 | 12518097 | 52 | 2.00E-79 | Escherichia coli O157:H7 | gamma-glutamyltranspeptidase [Escherichia coli O157:H7] ref NP_289992.1 gamma-glutamyltranspeptidase [Escherichia coli O157:H7 EDL933] ref NP_312320.1 gamma-glutamyltranspeptidase [Escherichia coli O157:H7] dbj BAB37716.1 gamma-glutamyltranspeptidase [Escherichia coli O157:H7] pir E86011 gamma-glutamyltranspeptidase [imported] - Escherichia coli (strain O157:H7, substrain EDL933) pir E91165 gamma- glutamyltranspeptidase [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952) | | | | 2.3.2.2 |
| 18797, 18798 | 21674986 | 60 | 3.00E-52 | Chlorobium tepidum TLS | ribosomal protein L5 [Chlorobium tepidum TLS] gb AAM73393.1 ribosomal protein L5 [Chlorobium tepidum TLS] sp Q8KA4 RL5_ CHL TE 50S ribosomal protein L5 | | | | |
| 18799, 18800 | 47568001 | 38 | 3.00E-22 | Bacillus cereus G9241 | phospholipid N-methyltransferase, putative [Bacillus cereus G9241] gb EAL13649.1 phospholipid N-methyltransferase, putative [Bacillus cereus G9241] | | | | 2.1.1.17 |
| 18801, 18802 | 56750401 | 31 | 1.00E-18 | Synechococcus elongatus PCC 6301 | hypothetical protein syc0392_d [Synechococcus elongatus PCC 6301] dbj BAD78582.1 hypothetical protein [Synechococcus elongatus PCC 6301] hypothetical protein OB0730 [Oceanobacillus thelyensis HTE831] dbj BAC12686.1 hypothetical conserved protein [Oceanobacillus thelyensis HTE831] | | | | 2.7.3.- |
| 18803, 18804 | 23098185 | 28 | 4.00E-09 | Oceanobacillus thehelyensis HTE831 | hypothetical protein sil1188 [Synechocystis sp. PCC 6803] dbj BAA16860.1 sil1188 [Synechocystis sp. PCC 6803] pir S74709 hypothetical protein sil1188 - Synechocystis sp. (strain PCC 6803) | | | | |
| 18809, 18810 | 16329452 | 51 | 3.00E-42 | Synechocystis sp. PCC 6803 | signal recognition particle-docking protein FtsY [Porphyromonas gingivalis W83] ref NP_904493.1 signal recognition particle-docking protein FtsY [Porphyromonas gingivalis W83] COG2723: Beta-glucosidase/6-phospho-beta-glucosidase/beta- galactosidase [Cytophaga hutchinsonii] | | | | 3.2.1.21 |
| 18811, 18812 | 34396325 | 55 | 2.00E-30 | Porphyromonas gingivalis W83 | putative restriction modification enzyme S subunit [Escherichia coli] | | | | 3.1.21.3 |
| 18813, 18814 | 48854229 | 54 | 8.00E-74 | Cytophaga hutchinsonii | putative glycosyltransferase [Thermosynechococcus elongatus BP-1] dbj BAC07799.1 tr0246 [Thermosynechococcus elongatus BP-1] | | | | 2.4.1.- |
| 18815, 18816 | 52420939 | 44 | 2.00E-57 | Escherichia coli | hypothetical protein ip1865 [Legionella pneumophila str. Lens] emb CAH16104.1 hypothetical protein [Legionella pneumophila str. Lens] | | | | |
| 18817, 18818 | 22297790 | 33 | 2.00E-37 | Thermosynechococcus elongatus BP-1 | | | | | |
| 18821, 18822 | 54294788 | 30 | 2.00E-21 | Legionella pneumophila str. Lens | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|---|----|----------|----------|
| 18827, 18828 | 17229587 | 41 | 3.00E-35 | Nostoc sp. PCC 7120 | two-component sensor histidine kinase [Nostoc sp. PCC 7120] pirJ A2067 two-component sensor histidine kinase all2095 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73794.1 two-component sensor histidine kinase [Nostoc sp. PCC 7120] | | | | 2.7.3.- |
| 1883, 1884 | 23128083 | 44 | 9.00E-60 | Nostoc punctiforme PCC 73102 | COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 18831, 18832 | 46117862 | 33 | 2.00E-20 | Crocospaera watsonii WH 8501 | COG0500: SAM-dependent methyltransferases [Crocospaera watsonii WH 8501] | | | | 2.1.1.64 |
| 18839, 18840 | 48868784 | 40 | 1.00E-18 | Haemophilus influenzae 86- 028NP | COG1393: Arsenate reductase and related proteins, glutaredoxin family [Haemophilus influenzae 86-028NP] | | | | 1.-.-.- |
| 18843, 18844 | 48853747 | 64 | 2.00E-73 | Cytophaga hutchinsonii | COG0441: Threonyl-tRNA synthetase [Cytophaga hutchinsonii] | | | | 6.1.1.3 |
| 18845, 18846 | 53715747 | 76 | 7.00E-76 | Bacteroides fragilis YCH46 | adenosylhomocysteinase [Bacteroides fragilis YCH46] dbj BAD51205.1 adenosylhomocysteinase [Bacteroides fragilis YCH46] | Bdellovibrio bacteriovorus complete genome, strain HD 100; segment 4/11 | 89 | 4.00E-13 | 3.3.1.1 |
| 1885, 1888 | 28211485 | 34 | 1.00E-19 | Clostridium tetani E88 | two-component sensor kinase yesM [Clostridium tetani E88] | | | | 2.7.3.- |
| 18853, 18854 | 46202304 | 25 | 7.00E-16 | Magnetospirillum magnetotacticum MS-1 | COG2931: RTX toxins and related Ca ²⁺ -binding proteins [Magnetospirillum magnetotacticum MS-1] | | | | |
| 18863, 18864 | 23452763 | 35 | 7.00E-10 | Campylobacter jejuni | RloA [Campylobacter jejuni] | | | | |
| 18867, 18868 | 48863689 | 45 | 2.00E-19 | Microbulbifer degradans 2-40 | COG0346: Lactoylglutathione lyase and related lyases [Microbulbifer degradans 2-40] | | | | |
| 1887, 1888 | 34397532 | 69 | 2.00E-63 | Porphyromonas gingivalis W83 | dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis W83] ref NP_905695.1 dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis W83] dbj BAD18851.1 dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis] | | | | 4.2.1.46 |
| 18873, 18874 | 23002261 | 30 | 2.00E-17 | Lactobacillus gasseri | COG1074: ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains) [Lactobacillus gasseri] | | | | 3.6.1.- |

| | | | | | | | | | | | |
|--------|----------|----|----------|--|--|---|--|--|--|-------------|----------|
| 18875, | | | | | | oligoendopeptidase f [Bacillus anthracis str. 'Ames Ancestor'] ref NP_027386.1 oligoendopeptidase F [Bacillus anthracis str. Sterne] | | | | | |
| 18876 | 47526469 | 40 | 2.00E-18 | | Bacillus anthracis str. 'Ames Ancestor' | | | | | | 3.4.24.- |
| 18879, | | | | | | | | | | | |
| 18880 | 22726420 | 45 | 6.00E-53 | | Ruegeria sp. PR1b | RC142 [Ruegeria sp. PR1b] ref NP_788129.1 putative pirin-like protein | | | | | |
| 18881, | | | | | | | | | | | |
| 18882 | 48855993 | 54 | 5.00E-83 | | Cytophaga hutchinsonii | COG1233: Phytoene dehydrogenase and related proteins [Cytophaga hutchinsonii] | | | | | |
| 1889, | | | | | | | | | | | |
| 1890 | 34397532 | 69 | 2.00E-63 | | Porphyromonas gingivalis W83 | dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis W83] ref NP_905695.1 dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis W83] db BAD18851.1 dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis] | | | | 4.2.1.46 | |
| 18891, | | | | | | | | | | | |
| 18892 | 31195605 | 73 | 5.00E-93 | | Anopheles gambiae | ENSANGP0000013686 [Anopheles gambiae] | | | | | |
| 18893, | | | | | | | | | | | |
| 18894 | 48855393 | 30 | 5.00E-33 | | Cytophaga hutchinsonii | COG0665: Glycine/D-amino acid oxidases (deaminating) [Cytophaga hutchinsonii] | | | | 88 2.00E-25 | |
| 18895, | | | | | | | | | | | |
| 18896 | 42525629 | 32 | 1.00E-25 | | Treponema denticola ATCC 35405 | M23/M37 peptidase domain protein [Treponema denticola ATCC 35405] gb AAS10608.1 M23/M37 peptidase domain protein [Treponema denticola ATCC 35405] | | | | | 3.5.1.- |
| 189, | | | | | | | | | | | |
| 190 | 56675038 | 38 | 4.00E-14 | | uncultured bacterium | cellulase [uncultured bacterium] | | | | | |
| 18901, | | | | | | | | | | | |
| 18902 | 48854129 | 49 | 2.00E-41 | | Cytophaga hutchinsonii | COG0172: Seryl-tRNA synthetase [Cytophaga hutchinsonii] | | | | | 6.1.1.11 |
| 18903, | | | | | | | | | | | |
| 18904 | 45658998 | 58 | 6.00E-80 | | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | Tas [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714153.1 Aldo/keto reductase family protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51171.1 Aldo/keto reductase family protein [Leptospira interrogans serovar Lai str. 56601] gb AAS71721.1 Tas [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | | 1.1.1.- |
| 18905, | | | | | | | | | | | |
| 18906 | 53759004 | 54 | 9.00E-45 | | Methylococcus capsulatus str. Bath | peptidyl-prolyl cis-trans isomerase B [Methylococcus capsulatus str. Bath] ref YP_113035.1 peptidyl-prolyl cis-trans isomerase B [Methylococcus capsulatus str. Bath] | | | | | 5.2.1.8 |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|--|----------|
| 18909, | 27366639 | 38 | 9.00E-07 | <i>Vibrio vulnificus</i> CMCP6 | Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] gb AAO07156.1] | | | | |
| 18910 | | | | CMCP6 | Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] | | | | |
| 1891, | 53795040 | 38 | 3.00E-21 | <i>Chloroflexus aurantiacus</i> | COG2172: Anti-sigma regulatory factor (Ser/Thr protein kinase) [Chloroflexus aurantiacus] | | | | |
| 18911, | 48856125 | 44 | 5.00E-16 | <i>Cytophaga hutchinsonii</i> | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] | | | | |
| 18912 | | | | | conserved hypothetical protein [Bacillus cereus G9241] | | | | |
| 18913, | 47566234 | 29 | 2.00E-10 | <i>Bacillus cereus</i> G9241 | gb EAL15118.1] conserved hypothetical protein [Bacillus cereus G9241] | | | | |
| 18914 | | | | <i>Wolinella succinogenes</i> DSM 1740 | hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] | | | | |
| 18915, | 34557509 | 54 | 1.00E-73 | | emb CAE10224.1] hypothetical protein [Wolinella succinogenes] | | | | |
| 18916 | | | | <i>Chlorobium tepidum</i> TLS | FtsQ protein, putative [Chlorobium tepidum TLS] gb AAM71280.1] FtsQ protein, putative [Chlorobium tepidum TLS] | | | | |
| 18917, | 21672873 | 24 | 1.00E-09 | | | | | | |
| 18918 | | | | <i>Leptospira interrogans</i> serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN4862.1] Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] | | | | |
| 18923, | 24214122 | 31 | 6.00E-31 | Includes: Adenine-specific methyltransferase activity | Restriction enzyme Bgl alpha subunit [Includes: Adenine-specific methyltransferase activity] pir J53125 restriction enzyme Bgl alpha chain - | | | | 2.1.1.72 |
| 18931, | 586070 | 40 | 1.00E-35 | | Bacillus coagulans gb AAA16626.1] restriction endonuclease alpha subunit | | | | |
| 18932 | | | | <i>Cytophaga hutchinsonii</i> | COG3279: Response regulator of the LytR/AlgR family [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 18933, | 48855702 | 34 | 7.00E-35 | | COG0501: Zn-dependent protease with chaperone function [Cytophaga hutchinsonii] | | | | 3.4.24.- |
| 18934 | | | | <i>Cytophaga hutchinsonii</i> | | | | | 2.7.7.- |
| 18935, | 48855017 | 42 | 2.00E-53 | | COG0358: DNA primase (bacterial type) [Cytophaga hutchinsonii] | | | | |
| 18936 | | | | <i>Methanosarcina mazei</i> Go1 | (S)-2-hydroxy-acid dehydrogenase [Methanosarcina mazei Go1] gb AAM30987.1] (S)-2-hydroxy-acid dehydrogenase [Methanosarcina mazei Go1] | | | | 1.1.3.15 |
| 18937, | 48854863 | 58 | 2.00E-97 | | COG2017: Galactose mutarotase and related enzymes [Oenococcus oeni PSU-1] | | | | |
| 18938 | | | | <i>Oenococcus oeni</i> PSU-1 | | | | | |
| 18939, | 21227393 | 42 | 4.00E-32 | | COG0262: Dihydrofolate reductase [Cytophaga hutchinsonii] | | | | 3.4.24.- |
| 18940 | | | | <i>Cytophaga hutchinsonii</i> | | | | | |
| 18945, | 48855028 | 42 | 6.00E-26 | | long-chain-fatty-acid--CoA ligase [Erwinia carotovora subsp. atroseptica SCR11043] emb CAG75275.1] long-chain-fatty-acid--CoA ligase [Erwinia carotovora subsp. atroseptica SCR11043] | | | | 6.2.1.3 |
| 18946 | | | | <i>Erwinia carotovora</i> subsp. atroseptica SCR11043 | | | | | |
| 18947, | 48855111 | 71 | 3.00E-65 | | | | | | |
| 18948 | | | | | | | | | |
| 18949, | 50121300 | 58 | 2.00E-70 | | | | | | |
| 18950 | | | | | | | | | |

| | | | | | | | | | | | | |
|-----------------|--|--|--|--|--|--|--|--|--|----|----------|----------|
| 1895, 1896 | | | | | | | | | Desc:Drosophila melanogaster expressed polynucleotide SEQ ID NO 38933. Org:Drosophila melanogaster | 97 | 2.00E-07 | |
| 18951, 18952 | | | | | | | | | hypothetical protein BT3847 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78952.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 18953, 18954 | | | | | | | | | putative YnfP protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62133.1 putative YnfP protein [Vibrio parahaemolyticus] | | | |
| 18955, 18956 | | | | | | | | | site-specific recombinase, resolvase family [Silicibacter pomeroyi DSS-3] ref YP_166469.1 site-specific recombinase, resolvase family [Silicibacter pomeroyi DSS-3] | | | |
| 18957, 18958 | | | | | | | | | COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii] | | | |
| 18959, 18960 | | | | | | | | | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 18961, 18962 | | | | | | | | | Vibrio vulnificus CMCP6 chromosome 1 section 7 of 11 of the complete sequence | ## | 5.00E-07 | 2.5.1.31 |
| 18963, 18964 | | | | | | | | | COG0020: Undecaprenyl pyrophosphate synthase [Cytophaga hutchinsonii] ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] ref NP_904660.1 ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] | | | 3.6.1.- |
| 18967, 18968 | | | | | | | | | PilL protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM37943.1 PilL protein [Xanthomonas axonopodis pv. citri str. 306] | | | |
| 1897, 1898 | | | | | | | | | hypothetical protein H11590 [Haemophilus influenzae Rd KW20] gb AAC23238.1 conserved hypothetical protein [Haemophilus influenzae Rd KW20] pir F64172 hypothetical protein H11590 - Haemophilus influenzae (strain Rd KW20) sp P45262 YCAJ_HAEIN Hypothetical protein H11590 | | | 2.7.7.7 |
| 18971, 18972 | | | | | | | | | conserved hypothetical protein [uncultured archaeon GZfos34H9] | | | |

| 18977, 18978 | AAV3437 2 | 28 | 2.00E-08 | | Desc:Porphorymonas gingivalis protein PG39. Org:Porphorymonas gingivalis | | | | |
|-----------------|--------------|----|----------|--|---|---|----|----------|----------|
| 18981, 18982 | 13123737 | 70 | 3.00E-54 | Campylobacter jejuni | putative acetyltransferase [Campylobacter jejuni] phosphoribosylamine-glycine ligase [Campylobacter lari RM2100] phosphoribosylamine-glycine ligase [Campylobacter lari RM2100] | Campylobacter jejuni strain TGH 9011 contig147 Tgh114, Tgh020, Tgh021, Tgh022, Tgh160, Tgh011, Tgh42, Tgh043, Tgh004, Tgh001, Tgh002, and Tgh003s genes, complete cds | 79 | 4.00E-10 | 2.3.1.- |
| 18983, 18984 | 57241824 | 46 | 1.00E-58 | Campylobacter lari RM2100 | hypothetical protein MA2730 [Methanosarcina acetivorans C2A] gb AAM06109.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | | 6.3.4.13 |
| 18985, 18986 | 20091554 | 36 | 8.00E-08 | Methanosarcina acetivorans C2A | COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii] COG3324: Predicted enzyme related to lactoylglutathione lyase [Burkholderia fungorum LB400] | | | | 2.1.1.- |
| 18987, 18988 | 48854785 | 36 | 1.00E-29 | Cytophaga hutchinsonii | putative nitrogen utilization substance protein [Bacteroides fragilis YCH46] dbj BAD47949.1 putative nitrogen utilization substance protein [Bacteroides fragilis YCH46] | | | | 2.7.7.- |
| 18989, 18990 | 48786618 | 42 | 6.00E-19 | Burkholderia fungorum LB400 | RIBONUCLEASE [Wolinella succinogenes DSM 1740] emb CAE10885.1 RIBONUCLEASE [Wolinella succinogenes] | | | | |
| 18991, 18992 | 53712491 | 29 | 5.00E-32 | Bacteroides fragilis YCH46 | hypothetical protein BF2432 [Bacteroides fragilis YCH46] dbj BAD49181.1 conserved hypothetical protein [Bacteroides fragilis YCH46] putative protease [Bacteroides fragilis YCH46] dbj BAD49186.1 putative protease [Bacteroides fragilis YCH46] | | | | 3.4.21.- |
| 18993, 18994 | 34558170 | 29 | 1.00E-10 | Wolinella succinogenes DSM 1740 | Diguanylate cyclase/phosphodiesterase domain 2 (EAL) [Nitrosomonas europaea ATCC 19718] emb CAD85611.1 Diguanylate cyclase/phosphodiesterase domain 2 (EAL) [Nitrosomonas europaea ATCC 19718] | | | | |
| 18997, 18998 | 53713723 | 31 | 4.00E-30 | Bacteroides fragilis YCH46 | sensory box protein [Pseudomonas putida KT2440] gb AAN67598.1 sensory box protein [Pseudomonas putida KT2440] | | | | 2.7.3.- |
| 18999, 19000 | 53713728 | 36 | 1.00E-37 | Bacteroides fragilis YCH46 | | | | | |
| 19001, 19002 | 30249662 | 45 | 2.00E-42 | Nitrosomonas europaea ATCC 19718 | | | | | |
| | 26988709 | 32 | 1.00E-22 | Pseudomonas putida KT2440 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|--|----------|
| 19005, 19006 | 38233405 | 42 | 3.00E-38 | Corynebacterium diphtheriae NCTC 13129 | hypothetical protein DIP0806 [Corynebacterium diphtheriae NCTC 13129] emb CAE49324.1 Putative phage protein [Corynebacterium diphtheriae] | | | | |
| 19007, 19008 | 53712411 | 55 | 1.00E-38 | Bacteroides fragilis YCH46 | putative hypoxanthine guanine phosphoribosyltransferase [Bacteroides fragilis YCH46] gb AAD40728.1 putative hypoxanthine guanine phosphoribosyltransferase [Bacteroides fragilis] db BAD47869.1 putative hypoxanthine guanine phosphoribosyltransferase [Bacteroides fragilis YCH46] | | | | 2.4.2.8 |
| 19009, 19010 | 48853835 | 59 | 1.00E-24 | Cytophaga hutchinsonii | COG0563: Adenylate kinase and related kinases [Cytophaga hutchinsonii] transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_812706.1 transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_811980.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] ref NP_810669.1 transposase, invertase [Bacteroides thetaiotaomicron VPI- 5482] ref NP_810516.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] ref NP_809398.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO79845.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78900.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78174.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76863.1 transposase, invertase [Bacteroides thetaitotaomicron VPI-5482] gb AAO76710.1 transposase [Bacteroides thetaitotaomicron VPI-5482] gb AAO75592.1 transposase [Bacteroides thetaitotaomicron VPI-5482] | | | | 2.7.4.3 |
| 1901, 1902 | 29350148 | 51 | 1.00E-31 | Bacteroides thetaitotaomicron VPI-5482 | hypothetical protein Bd2807 [Bdellovibrio bacteriovorus HD100] emb CAE80590.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100] | | | | |
| 19011, 19012 | 42524217 | 28 | 4.00E-07 | Bdellovibrio bacteriovorus HD100 | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | | |
| 19015, 19016 | 48855561 | 55 | 1.00E-42 | Cytophaga hutchinsonii | COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii] | | | | 3.4.-.- |
| 19017, 19018 | 48855398 | 27 | 4.00E-22 | Cytophaga hutchinsonii | hypothetical protein W50260 [Wolinetella succinogenes DSM 1740] emb CAE09415.1 conserved hypothetical protein [Wolinetella succinogenes] | | | | |
| 19021, 19022 | 34556700 | 45 | 4.00E-27 | Wolinetella succinogenes DSM 1740 | COG5544: Predicted periplasmic lipoprotein [Cytophaga hutchinsonii] | | | | |
| 19023, 19024 | 48856547 | 44 | 3.00E-49 | Cytophaga hutchinsonii | MGC82638 protein [Xenopus laevis] | | | | |
| 19025, 19026 | 49256557 | 54 | 1.00E-60 | Xenopus laevis | COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Cytophaga hutchinsonii] | | | | 4.2.1.17 |
| 19027, 19028 | 48855770 | 42 | 6.00E-17 | Cytophaga hutchinsonii | | | | | 2.5.1.- |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|--|--|--|--|---------------|
| 19029, 19030 | 42524558 | 42 | 1.00E-53 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd3175 [Bdellovibrio bacteriovorus HD100] emb CAE80931.1 ptrB [Bdellovibrio bacteriovorus HD100] | | | | 3.4.21.8 3 |
| 1903, 1904 | 48854665 | 44 | 1.00E-39 | Cytophaga hutchinsonii | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | | |
| 19031, 19032 | AA13439 9 | 39 | 2.00E-23 | | Desc.Porphorymonas gingivalis protein PG63. Org: Porphorymonas gingivalis | | | | |
| 19033, 19034 | 46446972 | 70 | 1.00E-70 | Parachlamydia sp. UWE25 | probable 3-methyladenine-DNA glycosylase I [Parachlamydia sp. UWE25] emb CAF24062.1 probable 3-methyladenine-DNA glycosylase I [Parachlamydia sp. UWE25] | | | | 3.2.2.20 |
| 19035, 19036 | 48831629 | 42 | 2.00E-31 | Magnetococcus sp. MC-1 | COG0248: Exopolyphosphatase [Magnetococcus sp. MC-1] | | | | 3.6.1.11 |
| 19037, 19038 | 21242876 | 39 | 7.00E-36 | Xanthomonas axonopodis pv. citri str. 306 | two-component system regulatory protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM36994.1 two-component system regulatory protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 19039, 19040 | 48856046 | 38 | 1.00E-40 | Cytophaga hutchinsonii | COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii] | | | | |
| 19045, 19046 | 52080825 | 33 | 3.00E-33 | Bacillus licheniformis ATCC 14580 | two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] gb AAU23978.1 two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] ref YP_092025.1 ResE1 [Bacillus licheniformis ATCC 14580] gb AAU41332.1 ResE1 [Bacillus licheniformis DSM 13] | | | | 2.7.3.- |
| 19049, 19050 | 53711887 | 48 | 2.00E-34 | Bacteroides fragilis YCH46 | putative alpha-rhamnosidase [Bacteroides fragilis YCH46] db BAD47345.1 putative alpha-rhamnosidase [Bacteroides fragilis YCH46] | | | | |
| 1905, 1906 | 54294440 | 43 | 5.00E-39 | Legionella pneumophila str. Lens | Legionella secretion system protein D [Legionella pneumophila str. Lens] emb CAH15749.1 Legionella secretion system protein D [Legionella pneumophila str. Lens] | | | | |
| 19057, 19058 | 48856412 | 57 | 5.00E-50 | Cytophaga hutchinsonii | COG3604: Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains [Cytophaga hutchinsonii] | | | | |
| 19061, 19062 | 29346818 | 43 | 3.00E-42 | Bacteroides thetaiotaomicron VPI-5482 | putative Tricorn-like protease [Bacteroides thetaiotaomicron VPI-5482] gb AAO76515.1 putative Tricorn-like protease [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.4.21.- |
| 19063, 19064 | 15603199 | 42 | 6.00E-42 | Pasteurella multocida subsp. multocida str. Pm70 | ApbE [Pasteurella multocida subsp. multocida str. Pm70] gb AAK03418.1 ApbE [Pasteurella multocida subsp. multocida str. Pm70] | | | | |

| | | | | | | | | | | | |
|---|----------------|----------|----------|---|---|---|----|----------|---------|---------|--|
| 19065, 19066 | 29350005 | 57 | 3.00E-68 | Bacteroides thetaitaomicron VPI-5482 | endopeptidase Clp ATP-binding chain B [Bacteroides thetaitaomicron VPI-5482] sp Q89Y3 CLPB_BACTN Chaperone clpB gb AAO79702.1 endopeptidase Clp ATP-binding chain B [Bacteroides thetaitaomicron VPI-5482] | Desc:Genomic fragment #36. Org:Moraxella catarrhalis | 82 | 5.00E-10 | | | |
| 19067, 19068 19069, 19070 | 15894574 44 | 9.00E-16 | ATCC 824 | Clostridium acetobutylicum ATCC 824 | Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [Clostridium acetobutylicum ATCC 824] gb AAK79263.1 Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [Clostridium acetobutylicum ATCC 824] pir D97059 membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [imported] - Clostridium acetobutylicum | | | | | | |
| 19071, 19072 | 48858243 46 | 3.00E-28 | | Cytophaga hutchinsonii | COG1284: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | | | |
| 19073, 19074 | 21674236 40 | 2.00E-34 | | Chlorobium tepidum TLS | hypothetical protein CT1415 [Chlorobium tepidum TLS] gb AAM72643.1 conserved hypothetical protein [Chlorobium tepidum TLS] | | | | | | |
| 19075, 19076 | 52425551 39 | 4.00E-22 | | Mannheimia succiniciproducens MBEL55E | RfaG protein [Mannheimia succiniciproducens MBEL55E] gb AAU38103.1 RfaG protein [Mannheimia succiniciproducens MBEL55E] probable methyltransferase [Chromobacterium violaceum ATCC 12472] ref NP_901781.1 probable methyltransferase [Chromobacterium violaceum ATCC 12472] | | | | 2.4.1.- | | |
| 19077, 19078 19079, 19080 | 34103421 49 | 5.00E-30 | 12472 | Chromobacterium violaceum ATCC | hypothetical protein BL00270 [Bacillus licheniformis ATCC 14580] gb AAU25728.1 hypothetical protein BL00270 [Bacillus licheniformis ATCC 14580] ref YP_093799.1 hypothetical protein BLI04293 [Bacillus licheniformis ATCC 14580] gb AAU43106.1 hypothetical protein BLI04293 [Bacillus licheniformis DSM 13] | | | | | | |
| 19081, 19082 19083, 19084 | 52082575 33 | 1.00E-15 | | Bacillus licheniformis ATCC | hypothetical protein Chut02002840 [Cytophaga hutchinsonii] | | | | | | |
| 19085, 19086 19087, 19088 | 48854173 29 | 5.00E-11 | | Cytophaga hutchinsonii | putative peptidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78570.1 putative peptidase [Bacteroides thetaiotaomicron VPI-5482] | | | | | | |
| 19089, 19090 | 29348873 31 | 1.00E-35 | | Bacteroides thetaitaomicron VPI-5482 | COG0582: Integrase [Microbulbifer degradans 2-40] hypothetical protein [Streptomyces coelicolor A3(2)] ref NP_628388.1 hypothetical protein SCO4213 [Streptomyces coelicolor A3(2)] | | | | | | |
| 19083, 19084 19085, 19086 19087, 19088 | 48864132 30 | 8.00E-12 | | Microbulbifer degradans 2-40 | COG1109: Phosphomannomultase [Cytophaga hutchinsonii] | | | | | 5.4.2.8 | |
| 19089, 19090 | 9857170 24 | 9.00E-25 | | Streptomyces coelicolor A3(2) | Penicillin-binding protein [Bacillus cereus ATCC 14579] gb AAP07521.1 Penicillin-binding protein [Bacillus cereus ATCC 14579] | | | | | 3.5.2.6 | |
| 19087, 19088 | 48854793 58 | 2.00E-91 | | Cytophaga hutchinsonii | | | | | | | |
| 19089, 19090 | 30018689 36 | 5.00E-22 | | Bacillus cereus ATCC 14579 | | | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|--|----------|
| 1909, 1910 | 42630962 | 30 | 3.00E-25 | Haemophilus Influenzae R2866 | COG3587: Restriction endonuclease [Haemophilus influenzae R2866] | | | | 3.1.21.5 |
| 19091, 19092 | | | | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0582 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75689.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| | 29345992 | 59 | 3.00E-30 | | two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 19095, 19096 | | | | Bacteroides thetaiotaomicron VPI-5482 | gb AAO79216.1 two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |
| 19097, 19098 | 29349519 | 30 | 2.00E-30 | Azotobacter vinelandii | hypothetical protein Avin02000281 [Azotobacter vinelandii] | | | | |
| | 53613162 | 29 | 2.00E-08 | | hypothetical SAM-dependent methyltransferase [Photobacterium profundum SS9] emb CAG22764.1 hypothetical SAM-dependent methyltransferase [Photobacterium profundum] | | | | |
| 19099, 19100 | | | | Photobacterium profundum SS9 | COG2114: Adenylate cyclase, family 3 (some proteins contain HAM/P domain) [Magnetococcus sp. MC-1] | | | | |
| 19101, 19102 | 54302571 | 49 | 4.00E-34 | Magnetococcus sp. MC-1 | COG0363: 6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase [Cytophaga hutchinsonii] | | | | 3.5.99.6 |
| 19103, 19104 | 48833211 | 35 | 2.00E-12 | Cytophaga hutchinsonii | transcriptional repressor of sporulation and degradative enzymes production [Geobacillus kaustophilus HTA426] dbj BAD75999.1 transcriptional repressor of sporulation and degradative enzymes production [Geobacillus kaustophilus HTA426] | | | | |
| 19105, 19106 | 48853763 | 48 | 1.00E-36 | Geobacillus kaustophilus HTA426 | COG0302: GTP cyclohydrolase I [Cytophaga hutchinsonii] | | | | 3.5.4.16 |
| 19107, 19108 | 56420249 | 39 | 4.00E-35 | Cytophaga hutchinsonii | type III restriction-modification system Styl.TI enzyme mod [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV78249.1 type III restriction-modification system Styl.TI enzyme mod [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] | | | | 2.1.1.72 |
| | 48854835 | 77 | 3.00E-45 | Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150 | RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI- 5482] gb AAO77599.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 1911, 1912 | 56414486 | 33 | 6.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | SEC-independent protein translocase protein TATC [Bdellovibrio bacteriovorus HD100] emb CAE80315.1 SEC-independent protein translocase protein TATC [Bdellovibrio bacteriovorus HD100] | | | | |
| 19113, 19114 | 29347902 | 30 | 2.00E-17 | Bdellovibrio bacteriovorus HD100 | COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Rubrobacter xylanophilus DSM 9941] Desc: Putative glycosyltransferase, involved in cell wall biogenesis #1. Org: Pyrococcus abyssi | | | | 2.4.-:- |
| 19115, 19116 | 42523942 | 28 | 5.00E-11 | Rubrobacter xylanophilus DSM 9941 | | | | | |
| 19119, 19120 | 45547643 | 32 | 5.00E-34 | | | | | | |
| 19121, 19122 | AAB9631 | 41 | 3.00E-40 | | | | | | |

| | | | | | | | | |
|---------------------------|----------|----|----------|---|---|--|-------------|----------|
| 19123, 19124 | 23117013 | 54 | 2.00E-51 | Desulfotobacterium hafnense DCB-2 | COG0266: Formamidopyrimidine-DNA glycosylase [Desulfotobacterium hafnense DCB-2] | | | 3.2.2.23 |
| 1913, 1914 | | | | Nostoc punctiforme | | | | |
| 19131, 19132 | 23127436 | 31 | 1.00E-17 | PCC 73102 | COG0465: ATP-dependent Zn proteases [Nostoc punctiforme PCC 73102] | | | 2.7.1.- |
| 19132, 19133, 19134 | 48861674 | 51 | 2.00E-35 | Microbulbifer degradans 2-40 | COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Microbulbifer degradans 2-40] | | | |
| | 58459705 | 37 | 2.00E-18 | Idiomarina | Cation transport ATPase [Idiomarina loihiensis L2TR] gb AAV81437.1] | | | |
| | | | | loihiensis L2TR | Cation transport ATPase [Idiomarina loihiensis L2TR] | | | 3.6.3.4 |
| 19139, 19140 | 21674082 | 67 | 6.00E-73 | Chlorobium tepidum TLS | PhoH family protein [Chlorobium tepidum TLS] gb AAM72489.1] PhoH family protein [Chlorobium tepidum TLS] | | 88 5.00E-10 | |
| 19141, 19142 | 42522964 | 43 | 8.00E-15 | Bdellovibrio bacteriovorus HD100 | transcriptional regulator, MarR family [Bdellovibrio bacteriovorus HD100] emb CAE79337.1] transcriptional regulator, MarR family [Bdellovibrio bacteriovorus HD100] | | | |
| 19145, 19146 | 29346568 | 44 | 5.00E-23 | Bacteroides thetaiotaomicron VPI-5482 | Na ⁺ -translocating NADH-quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO76265.1] Na ⁺ -translocating NADH- quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482] | | | 1.6.5.- |
| 19147, 19148 | 26989029 | 46 | 3.00E-23 | Pseudomonas putida KT2440 | hypothetical protein PP2305 [Pseudomonas putida KT2440] gb AAN67918.1] conserved hypothetical protein [Pseudomonas putida KT2440] | | | 3.4.21.- |
| 19149, 19150 | 23013248 | 33 | 3.00E-26 | Magnetospirillum magnetotacticum MS-1 | COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1] | | | 2.7.3.- |
| 1915, 1916 | 48854041 | 35 | 2.00E-28 | Cytophaga hutchinsonii | COG2808: Transcriptional regulator [Cytophaga hutchinsonii] | | | |
| 19151, 19152 | 54401435 | 41 | 7.00E-29 | Salmonella enterica subsp. salamae serovar Greenside | UDP-GlcNAc 4-epimerase [Salmonella enterica subsp. salamae serovar Greenside] | | | 4.2.1.46 |
| 19155, 19156 | 48863906 | 46 | 1.00E-52 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02000268 [Microbulbifer degradans 2-40] | | | |
| 19157, 19158 | 48853745 | 27 | 5.00E-17 | Cytophaga hutchinsonii | hypothetical protein Chut02003380 [Cytophaga hutchinsonii] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 19159, 19160 | 28899839 | 48 | 3.00E-43 | Vibrio parahaemolyticus RIMD 2210633 | putative cyclohexadienyl dehydratase precursor signal peptide protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61328.1 putative cyclohexadienyl dehydratase precursor signal peptide protein [Vibrio parahaemolyticus] | | | | 4.2.-.- |
| 19161, 19162 | 56677705 | 35 | 4.00E-17 | Silicibacter pomeroiyi DSS-3 | glutamine amidotransferase, class-I [Silicibacter pomeroiyi DSS-3] ref YP_166322.1 glutamine amidotransferase, class-I [Silicibacter pomeroiyi DSS-3] | | | | |
| 19165, 19166 | 34397542 | 32 | 1.00E-32 | Porphyrromonas gingivalis W83 | transcriptional regulator, Crp family [Porphyrromonas gingivalis W83] ref NP_905705.1 transcriptional regulator, Crp family [Porphyrromonas gingivalis W83] | | | | |
| 19169, 19170 | 48855281 | 42 | 4.00E-28 | Cytophaga hutchinsonii | COG0484: DnaJ-class molecular chaperone with C-terminal Zn finger domain [Cytophaga hutchinsonii] | | | | |
| 1917, 1918 | 48855210 | 49 | 3.00E-96 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | | |
| 19173, 19174 | 57236797 | 39 | 1.00E-48 | Flavobacterium johnsoniae | SprA [Flavobacterium johnsoniae] | | | | |
| 19175, 19176 | 48830838 | 73 | 6.00E-74 | Magnetococcus sp. MC-1 | COG1961: Site-specific recombinases, DNA invertase Pin homologs [Magnetococcus sp. MC-1] | | | | |
| 19177, 19178 | 40063063 | 27 | 1.00E-15 | uncultured bacterium 560 | transcriptional activator, putative, Baf family [uncultured bacterium 560] conserved hypothetical protein [Streptomyces coelicolor A3(2)] | | | | 6.3.4.15 |
| 19179, 19180 | 24418969 | 30 | 5.00E-18 | Streptomyces coelicolor A3(2) | ref NP_733735.1 hypothetical protein SCO7509 [Streptomyces coelicolor A3(2)] | | | | |
| 19181, 19182 | 53712337 | 43 | 6.00E-25 | Bacteroides fragilis YCH46 | RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD47795.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] | | | | |
| 19183, 19184 | 48853549 | 40 | 7.00E-48 | Cytophaga hutchinsonii | COG0277: FAD/FMN-containing dehydrogenases [Cytophaga hutchinsonii] | | | | 1.1.99.5 |
| 19185, 19186 | 53712491 | 33 | 3.00E-23 | Bacteroides fragilis YCH46 | putative nitrogen utilization substance protein [Bacteroides fragilis YCH46] dbj BAD47949.1 putative nitrogen utilization substance protein [Bacteroides fragilis YCH46] | | | | |
| 19189, 19190 | 27382463 | 36 | 9.00E-13 | Bradyrhizobium japonicum USDA 110 | hypothetical protein bll7352 [Bradyrhizobium japonicum USDA 110] dbj BAC52617.1 bll7352 [Bradyrhizobium japonicum USDA 110] | | | | |
| 19191, 19192 | 15678468 | 43 | 2.00E-22 | Methanothermobac ter thermautotrophicus str. Delta H | sensory transduction regulatory protein [Methanothermobacter thermautotrophicus str. Delta H] gb AAB84946.1 sensory transduction regulatory protein [Methanothermobacter thermotrophicus str. Delta H] pir E69157 sensory transduction regulatory protein - Methanobacterium thermautotrophicum (strain Delta H) | | | | 2.7.3.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|----------|----------|
| 19193, 19194 | 16802462 | 42 | 8.00E-07 | EGD-e | Listeria monocytogenes | hypothetical protein lmo0418 [Listeria monocytogenes EGD-e] ref YP_013044.1 hypothetical protein LMO72365_0437 [Listeria monocytogenes str. 4b F2365] ref ZP_00234032.1 conserved hypothetical protein [Listeria monocytogenes str. 1/2a F6854] ref ZP_00230268.1 conserved hypothetical protein [Listeria monocytogenes str. 4b H7858] gb EAL09815.1 conserved hypothetical protein [Listeria monocytogenes str. 4b H7858] gb EAL06100.1 conserved hypothetical protein [Listeria monocytogenes str. 1/2a F6854] emb CAC98497.1 lmo0418 [Listeria monocytogenes] gb AAT03221.1 conserved hypothetical protein [Listeria monocytogenes str. 4b F2365] pir AC1127 hypothetical protein lmo0418 [Imported] - Listeria monocytogenes (strain EGD-e) | | | |
| 19195, 19196 | 52142333 | 28 | 2.00E-13 | Bacillus cereus ZK | possible DNA helicase [Bacillus cereus ZK] helicase [Bacillus cereus ZK] | possible DNA helicase [Bacillus cereus ZK] | | | 3.6.1.- |
| 19197, 19198 | 29654094 | 28 | 8.00E-16 | RSA 493 | Coxiella burnetii RSA 493 | hypothetical protein CBU0762 [Coxiella burnetii RSA 493] gb AAO90300.1 hypothetical protein [Coxiella burnetii RSA 493] | | | |
| 19199, 19200 | 56316003 | 40 | 2.00E-47 | Azoarcus sp. Ebn1 | DNA repair protein [Azoarcus sp. Ebn1] | DNA repair protein [Azoarcus sp. Ebn1] | | | 3.4.21.- |
| 19201, 19202 | 50935741 | 27 | 1.00E-27 | Oryza sativa (japonica cultivar- group) | late embryogenesis abundant proteins-like [Oryza sativa (japonica cultivar- group)] dbj BAC83841.1 late embryogenesis abundant proteins-like [Oryza sativa (japonica cultivar-group)] | late embryogenesis abundant proteins-like [Oryza sativa (japonica cultivar- group)] dbj BAC83841.1 late embryogenesis abundant proteins-like [Oryza sativa (japonica cultivar-group)] | | | |
| 19203, 19204 | 2281663 | 62 | 7.00E-36 | Flavobacterium johnsoniae | gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [Imported] - Flavobacterium johnsoniae | gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [Imported] - Flavobacterium johnsoniae | | | |
| 19205, 19206 | 23014263 | 47 | 7.00E-25 | Magnetospirillum magnetotacticum MS-1 | COG0458: Carbamoylphosphate synthase large subunit (split gene in MJ) [Magnetospirillum magnetotacticum MS-1] | COG0458: Carbamoylphosphate synthase large subunit (split gene in MJ) [Magnetospirillum magnetotacticum MS-1] | | | |
| 19207, 19208 | 23014263 | 42 | 4.00E-32 | MS-1 | COG0458: Carbamoylphosphate synthase large subunit (split gene in MJ) [Magnetospirillum magnetotacticum MS-1] | COG0458: Carbamoylphosphate synthase large subunit (split gene in MJ) [Magnetospirillum magnetotacticum MS-1] | | | |
| 19209, 19210 | 51246929 | 48 | 5.00E-64 | Desulfotalea psychrophila LSV54 | probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] emb CAG37806.1 probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] | probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] emb CAG37806.1 probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] | | | 3.4.21.- |
| 1921, 1922 | 48838416 | 36 | 6.00E-35 | Methanosarcina barkeri str. fusaro | COG1413: FOG: HEAT repeat [Methanosarcina barkeri str. fusaro] | Methanosarcina acetivorans str. C2A, section 409 of 534 of the complete genome | 83 | 3.00E-24 | |
| 19211, 19212 | 48892140 | 27 | 6.00E-11 | Trichodesmium erythraeum IMS101 | COG2866: Predicted carboxypeptidase [Trichodesmium erythraeum IMS101] | COG2866: Predicted carboxypeptidase [Trichodesmium erythraeum IMS101] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|----------|----------|
| 19213, 19214 | 16078046 | 49 | 2.00E-47 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU09810 [Bacillus subtilis subsp. subtilis str. 168] emb CAA74443.1 hypothetical protein [Bacillus subtilis] emb CAB12820.1 yhaZ [Bacillus subtilis subsp. subtilis str. 168] pir D69820 hypothetical protein yhaZ - Bacillus subtilis | | | | |
| 19215, 19216 | 29346307 | 59 | 1.00E-73 | Bacteroides thetaiotaomicron VPI-5482 | chaperone protein htpG (heat shock protein htpG) [Bacteroides thetaiotaomicron VPI-5482] gb AAO76004.1 chaperone protein htpG (heat shock protein htpG) [Bacteroides thetaiotaomicron VPI-5482] | Bacteroides thetaiotaomicron VPI-5482, section 4 of 21 of the complete genome | 88 | 4.00E-08 | |
| 19217, 19218 | 46135592 | 43 | 5.00E-24 | Anabaena variabilis ATCC 29413 | hypothetical protein Avar03001063 [Anabaena variabilis ATCC 29413] hypothetical protein LJ0432 [Lactobacillus johnsonii NCC 533] | | | | |
| 19221, 19222 | 42518527 | 36 | 2.00E-12 | Lactobacillus johnsonii NCC 533 | gb AAS08423.1 hypothetical protein LJ0432 [Lactobacillus johnsonii NCC 533] | | | | |
| 19225, 19226 | 52082597 | 41 | 3.00E-13 | Bacillus licheniformis ATCC 14580 | putative Type I restriction-modification system M subunit [Bacillus licheniformis ATCC 14580] gb AAU25750.1 putative Type I restriction- modification system M subunit [Bacillus licheniformis ATCC 14580] ref YP_093823.1 hypothetical protein BLI04318 [Bacillus licheniformis ATCC 14580] gb AAU43130.1 putative protein [Bacillus licheniformis DSM 13] | | | | 2.1.1.72 |
| 19227, 19228 | 23002416 | 64 | 1.00E-64 | Lactobacillus gasseri | COG0286: Type I restriction-modification system methyltransferase subunit [Lactobacillus gasser] | | | | 2.1.1.72 |
| 19229, 19230 | 46120266 | 36 | 2.00E-24 | Crocospaera watsonii WH 8501 | COG1051: ADP-ribose pyrophosphatase [Crocospaera watsonii WH 8501] | | | | |
| 1923, 1924 | 48855461 | 36 | 4.00E-37 | Cytophaga hutchinsonii | COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 19235, 19236 | 53712881 | 27 | 7.00E-17 | Bacteroides fragilis YCH46 | hypothetical protein BF1590 [Bacteroides fragilis YCH46] dbj BAD48339.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 19237, 19238 | 29346555 | 59 | 5.00E-64 | Bacteroides thetaiotaomicron VPI-5482 | glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76252.1 glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A8M2 GIDB_BACTN Methyltransferase gidB (Glucose inhibited division protein B) | | | | |
| 19241, 19242 | 47566169 | 47 | 8.00E-31 | Bacillus cereus G9241 | aldohyde dehydrogenase [Bacillus cereus G9241] gb EAL15053.1 aldehyde dehydrogenase [Bacillus cereus G9241] | | | | 1.2.1.3 |
| 19243, 19244 | 34556493 | 72 | 9.00E-69 | Wolinella succinogenes DSM 1740 | PUTATIVE SUGAR EPIMERASE/DEHYDRATASE [Wolinella succinogenes DSM 1740] emb CAE09208.1 PUTATIVE SUGAR EPIMERASE/DEHYDRATASE [Wolinella succinogenes] | | | | 4.2.1.- |

| | | | | | | | | | |
|--------------------------|----------|----|----------|---|---|--|----|----------|----------|
| 19245, 19246 | 59460623 | 44 | 4.00E-31 | Idiomarina | ABC-type transport system, involved in lipoprotein release, ATPase component [Idiomarina loihiensis L2TR] gb AAV82355.1 ABC-type transport system, involved in lipoprotein release, ATPase component [Idiomarina loihiensis L2TR] | Bartonella quintana str. Toulouse, complete genome | 88 | 1.00E-06 | 1.8.-.- |
| 1925, 19251, 19252 | 48855461 | 23 | 7.00E-10 | Cytophaga hutchinsonii | COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Cytophaga hutchinsonii] | | | | |
| 19252 | 48854759 | 61 | 4.00E-38 | Cytophaga hutchinsonii | COG0604: NADPH:quinone reductase and related Zn-dependent oxidoreductases [Cytophaga hutchinsonii] | | | | |
| 19253, 19254 | 29347521 | 57 | 8.00E-50 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2111 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77218.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 19255, 19256 | 27464468 | 60 | 6.00E-38 | Enterobacter sp. RFL1396 | DNA methyltransferase [Enterobacter sp. RFL1396] ref NP_862209.1 DNA methyltransferase [Enterobacter sp. RFL1396] | | | | 2.1.1.72 |
| 19257, 19258 | 37520798 | 49 | 2.00E-21 | Gloeobacter violaceus PCC 7421 | hypothetical protein glr1229 [Gloeobacter violaceus PCC 7421] dbj BAC89170.1 glr1229 [Gloeobacter violaceus PCC 7421] | | | | |
| 19259, 19260 | 33862068 | 44 | 2.00E-71 | Prochlorococcus marinus subsp. pastoris str. CCMP1986 | Ferredoxin-dependent glutamate synthase, Fd-GOGAT [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19971.1 Ferredoxin-dependent glutamate synthase, Fd-GOGAT [Prochlorococcus marinus subsp. pastoris str. CCMP1986] | | | | 1.4.7.1 |
| 19261, 19262 | 48847259 | 29 | 7.00E-11 | Geobacter metallireducens GS-15 | hypothetical protein Gmet02000333 [Geobacter metallireducens GS-15] | | | | |
| 19265, 19266 | 29349385 | 29 | 9.00E-11 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3977 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79082.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 19267, 19268 | 48853686 | 38 | 3.00E-23 | Cytophaga hutchinsonii | COG1186: Protein chain release factor B [Cytophaga hutchinsonii] | | | | |
| 19275, 19276 | 53711522 | 54 | 1.00E-60 | Bacteroides fragilis YCH46 | ribonuclease H-related protein [Bacteroides fragilis YCH46] dbj BAD46980.1 ribonuclease H-related protein [Bacteroides fragilis YCH46] | | | | 3.1.26.4 |
| 19283, 19284 | 53714264 | 44 | 2.00E-72 | Bacteroides fragilis YCH46 | folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46] | | | | 6.3.2.17 |
| 19285, 19286 | 53714264 | 34 | 6.00E-38 | Bacteroides fragilis YCH46 | folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46] | | | | 6.3.2.17 |
| 19289, 19290 | 48856755 | 66 | 5.00E-68 | Cytophaga hutchinsonii | COG0139: Phosphoribosyl-AMP cyclohydrolase [Cytophaga hutchinsonii] | | | | 3.5.4.19 |
| 1929, 1930 | 48855800 | 60 | 3.00E-50 | Cytophaga hutchinsonii | COG0688: Phosphatidylserine decarboxylase [Cytophaga hutchinsonii] | | | | 4.1.1.65 |

| | | | | | | | | | | | |
|-----------------|----------|----|-----------|----------|---|--|--|--|--|----------|---------------|
| 19295, 19296 | 42528141 | 48 | 3.00E-33 | 35405 | Treponema denticola ATCC | Fic family protein [Treponema denticola ATCC 35405] gb AAS13158.1 Fic family protein [Treponema denticola ATCC 35405] | | | | | |
| 19297, 19298 | 32262994 | 41 | 4.00E-15 | 51449 | Helicobacter hepaticus ATCC | putative endonuclease [Helicobacter hepaticus ATCC 51449] ref NP_860974.1 putative endonuclease [Helicobacter hepaticus ATCC 51449] | | | | 3.1.21.- | |
| 19299, 19300 | 1695686 | 53 | 8.00E-62 | | Geobacillus stearothermophilus | pyruvate carboxylase [Geobacillus stearothermophilus] | | | | 6.4.1.1 | |
| 193, 194 | 32414055 | 29 | 1.00E-11 | | Neurospora crassa | hypothetical protein [Neurospora crassa] gb EAA28210.1 hypothetical protein [Neurospora crassa] | | | | | |
| | | | | | | atp-dependent ctp protease, atp-binding subunit ctpx [Bacillus anthracis str. 'Ames Ancestor'] ref YP_085795.1 ATP-dependent Ctp protease, ATP- binding subunit [Bacillus cereus ZK] gb AAU16053.1 ATP-dependent Ctp protease, ATP-binding subunit [Bacillus cereus ZK] ref YP_038522.1 ATP- dependent Ctp protease, ATP-binding subunit [Bacillus thuringiensis serovar konkukian str. 97-27] ref YP_030616.1 ATP-dependent Ctp protease, ATP- binding subunit CtpX [Bacillus anthracis str. Sterne] ref NP_980856.1 ATP- dependent Ctp protease, ATP-binding subunit CtpX [Bacillus cereus ATCC 10987] ref NP_846917.1 ATP-dependent Ctp protease, ATP-binding subunit CtpX [Bacillus anthracis str. Ames] ref NP_658503.1 AAA, ATPase family associated with various cellular activities (AAA) [Bacillus anthracis str. A2012] gb AAP28403.1 ATP-dependent Ctp protease, ATP-binding subunit CtpX [Bacillus anthracis str. Ames] gb AAT63717.1 ATP-dependent Ctp protease, ATP-binding subunit [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT33827.1 ATP-dependent Ctp protease, ATP-binding subunit CtpX [Bacillus anthracis str. 'Ames Ancestor'] gb AAT56667.1 ATP-dependent | | | | 81 | 1.00E-11 |
| 19301, 19302 | 47530003 | 65 | 1.00E-107 | | Bacillus anthracis str. 'Ames Ancestor' | Oceanobacillus lheyensis HTE831 genomic DNA, section 8/13 | | | | | |
| | | | | | Fusobacterium nucleatum subsp. vincentii ATCC | Desc:Listeria innocua DNA sequence #684. Org:Listeria innocua | | | | | |
| 19303, 19304 | 34762740 | 37 | 1.00E-56 | 49256 | Pasteurella multocida | VaiY-tRNA synthetase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24670.1 VaiY-tRNA synthetase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | | 95 | 4.00E-08 |
| 19305, 19306 | 40067365 | 58 | 3.00E-43 | | Microbulifer degradans 2-40 | Bacteriophage EJ-1 proviral DNA, complete genome | | | | 91 | 4.00E-07 |
| 1931, 1932 | 48864299 | 35 | 2.00E-14 | | Bacteroides thetaiotaomicron | COG0784: FOG: CheY-like receiver [Microbulifer degradans 2-40] | | | | | 2.7.3.- |
| 19311, 19312 | 29349412 | 55 | 1.00E-43 | VPI-5482 | | lipid-A-disaccharide synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79109.1 lipid-A-disaccharide synthase [Bacteroides thetaiotaomicron VPI-5482] | | | | | 2.4.1.18 2 |

| | | | | | | | | | | |
|--------|----------|----|----------|---------------------------|---|--|--|--|----|------------------|
| 19319, | 56675038 | 39 | 2.00E-13 | uncultured bacterium | cellulase [uncultured bacterium] | | | | | |
| 19320 | | | | bacterium | | | | | | |
| 19321, | | | | Psychrobacter sp. | | | | | | |
| 19322 | 52853726 | 32 | 4.00E-26 | 273-4 | COG1479: Uncharacterized conserved protein [Psychrobacter sp. 273-4] | | | | | |
| 19325, | | | | Bacteroides | BatD, conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76011.1 BatD, conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | | |
| 19326 | 29346314 | 32 | 2.00E-30 | thetaiotaomicron VPI-5482 | | | | | | |
| 19327, | | | | Photobacterium | hypothetical protein PBRB0725 [Photobacterium profundum SS9] | | | | | |
| 19328 | 54302404 | 41 | 2.00E-15 | profundum SS9 | emb CAG22597.1 hypothetical protein [Photobacterium profundum] | | | | | |
| | | | | | lipoprotein releasing system ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78745.1 lipoprotein releasing system ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1M1 IOLD_BACTN Lipoprotein releasing system ATP-binding protein IOLD | | | | | |
| 1933, | 29349048 | 60 | 5.00E-27 | VPI-5482 | | | | | | 1.8.-.- |
| 19331, | | | | Methanosarcina | ATPase involved in DNA repair [Methanosarcina mazei Go1] | | | | | |
| 19332 | 21227768 | 34 | 9.00E-21 | mazei Go1 | gb AAM31362.1 ATPase involved in DNA repair [Methanosarcina mazei Goe1] | | | | | |
| 19333, | | | | Methanosarcina | magnesium Mg(2+)/cobalt Co(2+) transport protein [Methanosarcina acetivorans C2A] gb AAM05128.1 magnesium Mg(2+)/cobalt Co(2+) transport protein [Methanosarcina acetivorans str. C2A] | | | | | |
| 19334 | 20090573 | 39 | 1.00E-30 | acetivorans C2A | | | | | | |
| | | | | | | | | | | |
| 19335, | | | | Cytophaga | COG1134: ABC-type polysaccharide/polyol phosphate transport system, ATPase component [Cytophaga hutchinsonii] | | | | | |
| 19336 | 48856262 | 70 | 2.00E-94 | hutchinsonii | | | | | | |
| 19337, | | | | Cytophaga | COG1682: ABC-type polysaccharide/polyol phosphate export systems, permease component [Cytophaga hutchinsonii] | | | | | |
| 19338 | 48856261 | 38 | 1.00E-10 | hutchinsonii | | | | | 91 | 6.00E-07 1.8.-.- |
| | | | | Ralstonia | | | | | | |
| 19339, | | | | metallidurans | COG1510: Predicted transcriptional regulators [Ralstonia metallidurans CH34] | | | | | |
| 19340 | 48769421 | 35 | 4.00E-26 | CH34 | | | | | | |
| | | | | | type I restriction-modification system specificity subunit [Methanosarcina mazei Go1] gb AAM31363.1 type I restriction-modification system specificity subunit [Methanosarcina mazei Goe1] | | | | | 3.1.21.3 |
| 19341, | | | | Methanosarcina | | | | | | |
| 19342 | 21227769 | 31 | 6.00E-26 | mazei Go1 | | | | | | |
| 19345, | | | | Cytophaga | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | | | |
| 19346 | 48853597 | 69 | 1.00E-91 | hutchinsonii | | | | | | 2.4.1.83 |
| | | | | Geobacter | PPIC-type PPIASE domain protein [Geobacter sulfurreducens PCA] gb AAR33351.1 PPIC-type PPIASE domain protein [Geobacter sulfurreducens PCA] | | | | | 5.2.1.8 |
| 19349, | | | | sulfurreducens | | | | | | |
| 19350 | 39995127 | 31 | 4.00E-09 | PCA | | | | | | |

| | | | | | | |
|-----------------|----------|----|----------|---|---|---------|
| 1935, 1936 | 53712402 | 62 | 3.00E-64 | Bacteroides fragilis YCH46 | putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis YCH46] gb AAD58746.1 putative undecaprenyl- phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis] dbj BAD47860.1 putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis YCH46] | 2.4.- |
| 19351, 19352 | 33599115 | 39 | 2.00E-24 | Bordetella bronchiseptica RB50 | putative asparagine synthetase [Bordetella bronchiseptica RB50] emb CAE30624.1 putative asparagine synthetase [Bordetella bronchiseptica RB50] | 6.3.5.4 |
| 19353, 19354 | 29654159 | 50 | 1.00E-45 | Coxiella burnetii RSA 493 | asparagine synthetase B, glutamine-hydrolyzing [Coxiella burnetii RSA 493] gb AAO90365.1 asparagine synthetase B, glutamine-hydrolyzing [Coxiella burnetii RSA 493] | 6.3.5.4 |
| 19355, 19356 | 31195869 | 42 | 6.00E-35 | Anopheles gambiae | ENSANGP0000000393 [Anopheles gambiae] | |
| 19357, 19358 | 48854542 | 41 | 3.00E-44 | Cytophaga hutchinsonii | COG1748: Saccharopine dehydrogenase and related proteins [Cytophaga hutchinsonii] | 1.5.1.7 |
| 19361, 19362 | 53711775 | 46 | 6.00E-58 | Bacteroides fragilis YCH46 | glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD47233.1 glycosyltransferase [Bacteroides fragilis YCH46] | |
| 19365, 19366 | 53686749 | 35 | 7.00E-11 | Nostoc punctiforme PCC 73102 | COG0187: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit [Nostoc punctiforme PCC 73102] | |
| 19367, 19368 | 56543835 | 33 | 4.00E-23 | Zymomonas mobilis subsp. mobilis ZM4 | conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_163100.1 hypothetical protein ZMO1365 [Zymomonas mobilis subsp. mobilis ZM4] | 2.7.3.- |
| 19369, 19370 | 45658787 | 24 | 6.00E-13 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_710808.1 Putative glycosyl transferase [Leptospira interrogans serovar Lai str. 56601] gb AAN47826.1 Putative glycosyl transferase [Leptospira interrogans serovar lai str. 56601] gb AAS71510.1 glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | |
| 19371, 19372 | 29349086 | 24 | 1.00E-19 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] gb AAO78783.1 two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] | 2.7.3.- |
| 19373, 19374 | 34397026 | 49 | 3.00E-52 | Porphyrionomas gingivalis W83 | conserved hypothetical protein [Porphyrionomas gingivalis W83] ref NP_905191.1 hypothetical protein PG0960 [Porphyrionomas gingivalis W83] sp Q7MVS9 TRMB_PORGI tRNA (guanine-N(7))-methyltransferase (tRNA(m7G46)-methyltransferase) | 2.1.1.- |

| | | | | | | | | |
|---|--|----------------------------|--|---|--|--|--|--|
| 19375, 19376, 19377, 19378, 19383, 19384, 19385, 19386 | 16078053 48855712 53714123 48854490 | 46 43 74 29 | 2.00E-61 1.00E-45 2.00E-59 2.00E-08 | Bacillus subtilis subsp. subtilis str. 168 Cytophaga hutchinsonii Bacteroides fragilis YCH46 Cytophaga hutchinsonii | hypothetical protein BSU09890 [Bacillus subtilis subsp. subtilis str. 168] emb CAA74424.1 Hypothetical protein [Bacillus subtilis] emb CAB12829.1 yhaQ [Bacillus subtilis subsp. subtilis str. 168] pir C69819 ABC transporter (ATP-binding protein) homolog yhaQ - Bacillus subtilis | | | 3.6.3.33 |
| 1939, 1940, 19391, 19392, 19393, 19394, 19395, 19396, 19397, 19398 | 21673557 52853852 42524139 56675038 48856840 | 44 36 41 44 44 | 1.00E-46 6.00E-31 1.00E-15 2.00E-17 4.00E-18 | Chlorobium tepidum TLS Psychrobacter sp. 273-4 Bdellovibrio bacteriovorus HD100 uncultured bacterium Cytophaga hutchinsonii | hypothetical protein Chut02000916 [Cytophaga hutchinsonii] hypothetical protein BF2831 [Bacteroides fragilis YCH46] dbj BAD49581.1 hypothetical protein [Bacteroides fragilis YCH46] hypothetical protein Chut02002689 [Cytophaga hutchinsonii] glucose-1-phosphate thymidyltransferase, putative [Chlorobium tepidum TLS] gb AAM71964.1 glucose-1-phosphate thymidyltransferase, putative [Chlorobium tepidum TLS] COG0442: Prcyl-tRNA synthetase [Psychrobacter sp. 273-4] probable HspC2 heat shock protein [Bdellovibrio bacteriovorus HD100] emb CAE80512.1 probable HspC2 heat shock protein [Bdellovibrio bacteriovorus HD100] cellulase [uncultured bacterium] COG1396: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | 2.7.7.24 |
| 19399, 19400, 19401, 19402, 19403, 19404, 19405, 19406, 19407, 19408 | 48859701 AAB9608 8 48833211 29345965 48855017 | 44 42 39 56 51 | 5.00E-17 3.00E-51 8.00E-36 3.00E-84 1.00E-63 | Clostridium thermocellum ATCC 27405 Magnetococcus sp. MC-1 Bacteroides thetaiotaomicron VPI-5482 Cytophaga hutchinsonii | COG1162: Predicted GTPases [Clostridium thermocellum ATCC 27405] Desc: Putative P. abyssi alpha-amylase. Org: Pyrococcus abyssi COG2114: Adenylate cyclase, family 3 (some proteins contain HAMP domain) [Magnetococcus sp. MC-1] amidophosphoribosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75662.1 amidophosphoribosyltransferase [Bacteroides thetaiotaomicron VPI-5482] COG0501: Zn-dependent protease with chaperone function [Cytophaga hutchinsonii] putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76816.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | 3.6.1.- 3.2.1.1 4.6.1.1 2.4.2.14 3.4.-.- |
| 19409, 19410, 19411, 19412 | 29347119 31194819 | 36 52 | 7.00E-45 5.00E-74 | Bacteroides thetaiotaomicron VPI-5482 Anopheles gambiae | ENSANGP00000002020 [Anopheles gambiae] | | | 2.4.1.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|------------------|
| 19413, 19414 | 48854902 | 30 | 6.00E-28 | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | |
| 19415, 19416 | 30249805 | 28 | 2.00E-10 | Nitrosomonas europaea ATCC 19718 | hypothetical protein NE1853 [Nitrosomonas europaea ATCC 19718] emb CAD85764.1 hypothetical protein [Nitrosomonas europaea ATCC 19718] | | | |
| 19417, 19418 | 29347660 | 58 | 2.00E-38 | Bacteroides thetaiotaomicron VPI-5482 | putative GTPase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77357.1 putative GTPase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A5I9 EGC1_BACTN Probable GTPase engC protein 1 type I restriction enzyme m protein [Mycoplasma mobile 163K] gb AAAT27772.1 type I restriction enzyme m protein [Mycoplasma mobile 163K] | Oceanobacillus theysensis HTE831 genomic DNA, section 6/13 | 91 | 1.00E-06 3.6.1.- |
| 19419, 19420 | 47459121 | 27 | 4.00E-08 | Mycoplasma mobile 163K | | | | |
| 19423, 19424 | 48854772 | 33 | 2.00E-23 | Cytophaga hutchinsonii | COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii] | | | 3.4.17.2 1 |
| 19425, 19426 | 24373489 | 39 | 5.00E-24 | Shewanella oneidensis MR-1 | HlyD family secretion protein [Shewanella oneidensis MR-1] gb AAN54976.1 HlyD family secretion protein [Shewanella oneidensis MR-1] N-acetylornithine aminotransferase [Synecococcus elongatus PCC 6301] dbj BAD79656.1 N-acetylornithine aminotransferase [Synecococcus elongatus PCC 6301] ref ZP_00351244.1 COG0161: Adenosylmethionine-8-amino-7-oxonanoate aminotransferase [Synecococcus elongatus PCC 6301] 7942] | | | 2.6.1.62 |
| 19427, 19428 | 56751475 | 47 | 1.00E-38 | Geobacter metallireducens GS-15 | COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Geobacter metallireducens GS-15] hypothetical protein, probably cold-shock inducible [Desulfotalea psychrophila LSV54] emb CAG37151.1 hypothetical protein, probably cold-shock inducible [Desulfotalea psychrophila LSV54] type I restriction-modification system, S subunit [Pseudomonas putida KT2440] gb AAN70314.1 type I restriction-modification system, S subunit [Pseudomonas putida KT2440] | | | 3.2.1.8 |
| 19433, 19434 | 26991425 | 33 | 4.00E-29 | Pseudomonas putida KT2440 | putative aldose reductase [Rhodopseudomonas palustris CGA009] emb CAE29738.1 putative aldose reductase [Rhodopseudomonas palustris CGA009] | | | 3.1.21.3 |
| 19435, 19436 | 39937357 | 49 | 2.00E-54 | Rhodopseudomonas palustris CGA009 | FOG: CheY-like receiver [Vibrio vulnificus CMCP6] gb AAO07892.1 FOG: CheY-like receiver [Vibrio vulnificus CMCP6] | | | 1.-.-.- |
| 19439, 19440 | 27367375 | 53 | 3.00E-62 | Vibrio vulnificus CMCP6 | | | | 2.7.3.- |
| 19441, 19442 | 45655974 | 41 | 4.00E-19 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | hypothetical protein LIC10060 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS68697.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | 2.7.3.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---------------------------------------|---|--|--|-----------|--|
| 19443, 19444 | 20808554 | 31 | 2.00E-29 | Thermoanaerobacter tengcongensis MB4 | predicted sugar kinase [Thermoanaerobacter tengcongensis MB4] | | | | |
| 19445, 19446 | 31195869 | 41 | 1.00E-19 | Anopheles gambiae | ENSANGP00000000393 [Anopheles gambiae] | | | | |
| 19447, 19448 | 53713710 | 53 | 5.00E-37 | Bacteroides fragilis YCH46 | conserved hypothetical protein Bata [Bacteroides fragilis YCH46] gb AAD30858.1 Bata [Bacteroides fragilis] db BAD49168.1 conserved hypothetical protein Bata [Bacteroides fragilis YCH46] | | | | |
| 1945, 1946 | 42527338 | 50 | 3.00E-55 | Treponema denticola ATCC 35405 | hypothetical protein TDE1832 [Treponema denticola ATCC 35405] ref NP_972400.1 hypothetical protein TDE1796 [Treponema denticola ATCC 35405] gb AAS12347.1 conserved hypothetical protein [Treponema denticola ATCC 35405] gb AAS12311.1 conserved hypothetical protein [Treponema denticola ATCC 35405] | | | | |
| 19457, 19458 | 15893072 | 58 | 9.00E-36 | EC:4.2.99.18 | endonuclease III [EC:4.2.99.18] [Rickettsia conorii str. Malish 7] gb AAL03687.1 endonuclease III [EC:4.2.99.18] [Rickettsia conorii str. Malish 7] pir E97843 DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - Rickettsia conorii (strain Malish 7) | | | 4.2.99.18 | |
| 19461, 19462 | 56750775 | 34 | 1.00E-12 | Synechococcus elongatus PCC 6301 | hypothetical protein syc0766_c [Synechococcus elongatus PCC 6301] db BAD78956.1 hypothetical protein [Synechococcus elongatus PCC 6301] | | | 3.1.3.5 | |
| 19469, 19470 | 47228040 | 28 | 7.00E-19 | Tetraodon nigroviridis | unnamed protein product [Tetraodon nigroviridis] | | | 5.1.1.- | |
| 19471, 19472 | 28274156 | 62 | 1.00E-42 | Tannerella forsythensis | GlyA [Tannerella forsythensis] | | | 2.1.2.1 | |
| 19473, 19474 | 34397184 | 36 | 4.00E-36 | Porphyromonas gingivalis W83 | glycosyl transferase, group 2 family protein [Porphyromonas gingivalis W83] ref NP_905348.1 glycosyl transferase, group 2 family protein [Porphyromonas gingivalis W83] | | | 2.4.- | |
| 19475, 19476 | 48856857 | 33 | 7.00E-12 | Cytophaga hutchinsonii | hypothetical protein Chut02000824 [Cytophaga hutchinsonii] | | | | |
| 19477, 19478 | 56675038 | 27 | 8.00E-16 | uncultured bacterium | cellulase [uncultured bacterium] | | | | |
| 19481, 19482 | 48853984 | 38 | 4.00E-22 | Cytophaga hutchinsonii | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | | |
| 19483, 19484 | 39997412 | 34 | 7.00E-35 | Geobacter sulfurreducens PCA | sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gb AAR35690.1 sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] | | | 2.7.3.- | |
| 19485, 19486 | 52853726 | 33 | 9.00E-27 | Psychrobacter sp. 273-4 | COG1479: Uncharacterized conserved protein [Psychrobacter sp. 273-4] | | | | |
| 19487, 19488 | 52425668 | 34 | 6.00E-40 | Mannheimia succiniciproducens MBEL55E | LysC protein [Mannheimia succiniciproducens MBEL55E] gb AAU38220.1 LysC protein [Mannheimia succiniciproducens MBEL55E] | | | 2.7.2.4 | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|---------|
| 19489, 19490 | 45524150 | 59 | 2.00E-95 | Crocospaera watsonii WH 8501 | COG0674: Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit [Crocospaera watsonii WH 8501] | | | | 1.2.7.1 |
| 1949, 1950 | 53795203 | 44 | 5.00E-38 | Chloroflexus aurantiacus | COG1680: Beta-lactamase class C and other penicillin binding proteins [Chloroflexus aurantiacus] | | | | 3.5.2.6 |
| 19491, 19492 | 20808779 | 33 | 5.00E-16 | Thermoanaerobacter tengcongensis MB4 | Transcriptional regulator [Thermoanaerobacter tengcongensis MB4] | | | | 2.7.1.2 |
| 195, 196 | 48854506 | 45 | 2.00E-26 | Cytophaga hutchinsonii | hypothetical protein Chut02002705 [Cytophaga hutchinsonii] | | | | 3.6.1.- |
| 19501, 19502 | 48863156 | 44 | 4.00E-22 | Microbulbifer degradans 2-40 | COG4067: Uncharacterized protein conserved in archaea [Microbulbifer degradans 2-40] | | | | |
| 19503, 19504 | 54032693 | 33 | 3.00E-09 | Polaromonas sp. JS666 | COG3616: Predicted amino acid aldolase or racemase [Polaromonas sp. JS666] | | | | |
| 19507, 19508 | 34397138 | 40 | 5.00E-15 | Porphyrromonas gingivalis W83 | DNA-binding response regulator RprY [Porphyrromonas gingivalis W83] | | | | |
| 19509, 19510 | 48855901 | 53 | 4.00E-80 | Cytophaga hutchinsonii | COG1482: Phosphomannose isomerase [Cytophaga hutchinsonii] | | | | 5.3.1.8 |
| 1951, 1952 | 45659189 | 52 | 5.00E-89 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gb AA51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gb AAS71912.1 sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | 2.7.7.4 |
| 19511, 19512 | | | | | Desc:DNA encoding novel human diagnostic protein #27879. Org:Homo sapiens | | 94 | 3.00E-14 | |
| 19513, 19514 | 42527309 | 49 | 3.00E-17 | Treponema denticola ATCC 35405 | hypothetical protein TDE1803 [Treponema denticola ATCC 35405] gb AAS12318.1 conserved hypothetical protein [Treponema denticola ATCC 35405] | | | | |
| 19515, 19516 | 29349133 | 33 | 1.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78830.1 putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 19517, 19518 | 24213772 | 43 | 1.00E-39 | Leptospira interrogans serovar Lai str. 56601 | hypothetical protein LA1072 [Leptospira interrogans serovar Lai str. 56601] gb AA48271.1 unknown protein [Leptospira interrogans serovar lai str. 56601] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|--|---|--|--|----------|
| 19523, | AAU6761 | 27 | 2.00E-22 | | | Desc:Propionibacterium acnes immunogenic protein #28510. Org:Propionibacterium acnes | | | |
| 19524 | 4 | | | Microbulbifer | | COG2951: Membrane-bound lytic murein transglycosylase B [Microbulbifer | | | |
| 19527, | 48863961 | 55 | 2.00E-63 | degradans 2-40 | | | | | 3.2.1.- |
| 19528 | | | | Wolinella | | hypothetical protein WS2184 [Wolinella succinogenes DSM 1740] | | | |
| 19529, | 34558460 | 53 | 2.00E-81 | succinogenes DSM | | emb CAE11175.1 CONSERVED HYPOTHETICAL PROTEIN [Wolinella | | | |
| 19530 | | | | 1740 | | succinogenes] | | | |
| 1953, | | | | Yersinia | | possible restriction modification enzyme [Yersinia pseudotuberculosis IP | | | |
| 1954 | 51598166 | 39 | 4.00E-20 | IP 32953 | | 32953] emb CAH23119.1 possible restriction modification enzyme [Yersinia | | | |
| | | | | pseudotuberculosis | | pseudotuberculosis IP 32953] | | | 3.1.21.3 |
| 19531, | | | | Rhodopseudomonas | | possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] | | | |
| 19532 | 39936881 | 49 | 4.00E-40 | s palustris CGA009 | | emb CAE29361.1 possible ADP-heptose synthase [Rhodopseudomonas | | | |
| 19535, | | | | Cytophaga | | palustris CGA009] | | | 2.7.7.39 |
| 19536 | 48854159 | 26 | 2.00E-09 | hutchinsonii | | COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase | | | |
| 19539, | | | | Porphyromonas | | superfamily) [Cytophaga hutchinsonii] | | | 3.1.1.24 |
| 19540 | 34397427 | 31 | 8.00E-28 | gingivalis W83 | | ATPase, putative [Porphyromonas gingivalis W83] ref NP_905590.1 | | | |
| | | | | ATPase, putative [Porphyromonas gingivalis W83] | | ATPase, putative [Porphyromonas gingivalis W83] | | | |
| 19541, | | | | Bacteroides | | hypothetical protein BT0083 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 19542 | 29345493 | 37 | 2.00E-21 | thetataomicron | | gb AAO75190.1 conserved hypothetical protein [Bacteroides | | | |
| | | | | VPI-5482 | | thetataomicron VPI-5482] | | | |
| 19543, | | | | Bacteroides fragilis | | putative glycosyltransferase [Bacteroides fragilis YCH46] db BAD49674.1 | | | |
| 19544 | 53714216 | 38 | 2.00E-25 | YCH46 | | putative glycosyltransferase [Bacteroides fragilis YCH46] | | | |
| 19545, | | | | Cytophaga | | COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga | | | 2.3.2.- |
| 19546 | 48854578 | 41 | 8.00E-55 | hutchinsonii | | hutchinsonii] | | | |
| 19547, | | | | Cytophaga | | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga | | | |
| 19548 | 48856112 | 40 | 2.00E-62 | hutchinsonii | | hutchinsonii] | | | |
| 19549, | | | | Geobacillus | | cystathionine beta-lyase [Geobacillus kaustophilus HTA426] | | | |
| 19550 | 56419402 | 42 | 8.00E-57 | kaustophilus | | db BAD75152.1 cystathionine beta-lyase [Geobacillus kaustophilus | | | 4.2.99.9 |
| | | | | HTA426 | | HTA426] | | | |
| 19551, | | | | Microbulbifer | | COG2972: Predicted signal transduction protein with a C-terminal ATPase | | | |
| 19552 | 48862505 | 40 | 4.00E-35 | degradans 2-40 | | domain [Microbulbifer degradans 2-40] | | | 2.7.3.- |
| 19553, | ABB8477 | | | | | Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ | | | |
| 19554 | 1 | 34 | 3.00E-39 | | | ID:144. Org: Cytophaga hutchinsonii | | | 2.7.7.7 |
| 19555, | | | | Cytophaga | | COG0793: Periplasmic protease [Cytophaga hutchinsonii] | | | 3.4.21.- |
| 19556 | 48853807 | 47 | 6.00E-70 | hutchinsonii | | | | | |
| | | | | Bacteroides | | | | | |
| 19561, | | | | thetataomicron | | Ribonuclease G [Bacteroides thetaiotaomicron VPI-5482] gb AAO76607.1 | | | |
| 19562 | 29346910 | 52 | 1.00E-32 | VPI-5482 | | Ribonuclease G [Bacteroides thetaiotaomicron VPI-5482] | | | 3.1.4.- |
| 19563, | | | | Chryseobacterium | | PI-repressible alkaline phosphatase PatA [Chryseobacterium | | | |
| 19564 | 8886019 | 51 | 3.00E-55 | meningosepticum | | meningosepticum] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|---|----|----------|----------|
| 19569, 19570 | 19704590 | 43 | 4.00E-29 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | NagD protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95451.1 NagD protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | 3.1.3.41 |
| 1957, 1958 | 45508953 | 41 | 3.00E-19 | Anabaena variabilis ATCC 29413 | COG4636: Uncharacterized protein conserved in cyanobacteria [Anabaena variabilis ATCC 29413] | | | | |
| 19573, 19574 | 33596386 | 33 | 1.00E-07 | Bordetella parapertussis 12822 | putative lipoprotein [Bordetella parapertussis 12822] emb CAE37057.1 putative lipoprotein [Bordetella parapertussis] | | | | |
| 19575, 19576 | 32474694 | 30 | 6.00E-11 | Rhodopirellula baltica SH 1 | probable penicillin resistance regulatory protein [Rhodopirellula baltica SH 1] emb CAD75235.1 probable penicillin resistance regulatory protein [Pirellula sp.] | | | | |
| 19579, 19580 | 46141189 | 43 | 6.00E-44 | Psychrobacter sp. 273-4 | hypothetical protein Psc03002392 [Psychrobacter sp. 273-4] | | | | |
| 19583, 19584 | 48854401 | 49 | 7.00E-41 | Cytophaga hutchinsonii | COG1475: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | | |
| 19585, 19586 | 52853548 | 29 | 8.00E-10 | Psychrobacter sp. 273-4 | COG0668: Small-conductance mechanosensitive channel [Psychrobacter sp. 273-4] | | | | |
| 1959, 1960 | 21228318 | 42 | 4.00E-21 | Methanosarcina mazei Go1 | Glucose-1-phosphate thymidyltransferase [Methanosarcina mazei Go1] gb AAM31912.1 Glucose-1-phosphate thymidyltransferase [Methanosarcina mazei Goe1] | | | | 2.7.7.24 |
| 19591, 19592 | 27382256 | 42 | 1.00E-22 | Bradyrhizobium japonicum USDA 110 | hypothetical protein bli7145 [Bradyrhizobium japonicum USDA 110] dbj BAC52410.1 bli7145 [Bradyrhizobium japonicum USDA 110] | | | | |
| 19595, 19596 | 9947830 | 68 | 9.00E-94 | Pseudomonas aeruginosa PAO1 | methionine synthase [Pseudomonas aeruginosa PAO1] ref NP_250534.1 methionine synthase [Pseudomonas aeruginosa PAO1] pir E83415 methionine synthase PA1843 [imported] - Pseudomonas aeruginosa (strain PAO1) | Vibrio fischeri gene for cobalamin- dependent methionine synthase, Na ⁺ /H ⁺ antiporter and aspartokinase III, partial and complete cds | 82 | 1.00E-11 | 2.1.1.13 |
| 19603, 19604 | 53714398 | 27 | 9.00E-26 | Bacteroides fragilis YCH46 | putative patatin-like phospholipase [Bacteroides fragilis YCH46] dbj BAD49856.1 putative patatin-like phospholipase [Bacteroides fragilis YCH46] | | | | 3.4.21.- |
| 19605, 19606 | 53712844 | 46 | 4.00E-30 | Bacteroides fragilis YCH46 | ribonuclease G [Bacteroides fragilis YCH46] dbj BAD48302.1 ribonuclease G [Bacteroides fragilis YCH46] | | | | 3.1.4.- |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|----------|
| 19607, 19608 | 53712144 | 37 | 1.00E-10 | Bacteroides fragilis YCH46 | hypothetical protein BF0851 [Bacteroides fragilis YCH46] dbj BAD47602.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 19609, 19610 | 18310494 | 24 | 2.00E-16 | Clostridium perfringens str. 13 | two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] dbj BAB81218.1 two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] | | | |
| 1961, 1962 | 53714371 | 36 | 4.00E-29 | Bacteroides fragilis YCH46 | putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] dbj BAD49829.1 putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] | | | |
| 19611, 19612 | 52079413 | 34 | 2.00E-18 | Bacillus licheniformis ATCC 14580 | putative transcriptional regulator [Bacillus licheniformis ATCC 14580] gb AAU22566.1 putative transcriptional regulator [Bacillus licheniformis ATCC 14580] ref YP_090602.1 YhcZ [Bacillus licheniformis ATCC 14580] gb AAU39909.1 YhcZ [Bacillus licheniformis DSM 13] | | | |
| 19615, 19616 | 53712519 | 36 | 3.00E-38 | Bacteroides fragilis YCH46 | hypothetical protein BF1227 [Bacteroides fragilis YCH46] dbj BAD47977.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 19617, 19618 | 48856396 | 46 | 2.00E-22 | Cytophaga hutchinsonii | COG1579: Zn-ribbon protein, possibly nucleic acid-binding [Cytophaga hutchinsonii] | | | |
| 19619, 19620 | 53715653 | 27 | 4.00E-12 | Bacteroides fragilis YCH46 | hypothetical protein BF4373 [Bacteroides fragilis YCH46] dbj BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 19621, 19622 | 29350071 | 30 | 1.00E-13 | Bacteroides thetataoimicron VPI-5482 | two-component system sensor histidine kinase/response [Bacteroides thetataoimicron VPI-5482] gb AAO79768.1 two-component system sensor histidine kinase/response [Bacteroides thetataoimicron VPI-5482] | | | 2.7.3.- |
| 19625, 19626 | 31194451 | 62 | 4.00E-93 | Anopheles gambiae | ENSANGP00000015516 [Anopheles gambiae] | | | 3.4.21.- |
| 19627, 19628 | 48853783 | 38 | 2.00E-27 | Cytophaga hutchinsonii | COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] | | | 2.7.7.7 |
| 19629, 19630 | 48854335 | 52 | 1.00E-29 | Cytophaga hutchinsonii | COG3762: Predicted membrane protein [Cytophaga hutchinsonii] | | | |
| 1963, 1964 | 28211857 | 27 | 8.00E-15 | Clostridium tetani E88 | glycosyl transferase [Clostridium tetani E88] gb AAO36738.1 glycosyl transferase [Clostridium tetani E88] | | | 2.4.1.- |
| 19631, 19632 | 56459804 | 29 | 3.00E-33 | Idiomarina loihensis L2TR | Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR] | | | |
| 19633, 19634 | 48853480 | 47 | 2.00E-19 | Cytophaga hutchinsonii | COG1187: 16S rRNA uridine-516 pseudouridylation synthase and related pseudouridylation synthases [Cytophaga hutchinsonii] | | | 4.2.1.70 |

| | | | | | | | | | |
|-----------------|----------|----|-----------|--|--|--|--|--|----------|
| 19635, 19636 | 52842257 | 29 | 1.00E-13 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | mevalonate diphosphate decarboxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] decarboxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | 4.1.1.33 |
| 19639, 19640 | 29349999 | 38 | 1.00E-48 | Bacteroides thetaiotaomicron VPI-5482 | putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 19641, 19642 | 48892769 | 26 | 1.00E-12 | Trichodesmium erythraeum IMS101 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] | | | | |
| 19643, 19644 | 48854025 | 51 | 4.00E-19 | Cytophaga hutchinsonii | hypothetical protein Chut02003116 [Cytophaga hutchinsonii] | | | | |
| 19645, 19646 | 32475496 | 42 | 9.00E-55 | Rhodopirellula baltica SH 1 | chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1] emb CAD75867.1 chloromuconate cycloisomerase YkfB1 [Pirellula sp.] | | | | 5.5.-.- |
| 1965, 1966 | 17230329 | 35 | 4.00E-17 | Nostoc sp. PCC 7120 | glycosyltransferase [Nostoc sp. PCC 7120] pir AF2160 glycosyltransferase alr2837 [imported] - Nostoc sp. (strain PCC 7120) db BAB74536.1 glycosyltransferase [Nostoc sp. PCC 7120] | | | | 2.-.-.- |
| 19651, 19652 | 45657936 | 53 | 6.00E-23 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | response regulator [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70659.1 response regulator [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 19653, 19654 | 21674101 | 51 | 1.00E-36 | Chlorobium tepidum TLS | peptide methionine sulfoxide reductase [Chlorobium tepidum TLS] gb AAM72508.1 peptide methionine sulfoxide reductase [Chlorobium tepidum TLS] | | | | 1.8.4.6 |
| 19655, 19656 | 48853937 | 65 | 1.00E-110 | Cytophaga hutchinsonii | COG0482: Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase, contains the PP-loop ATPase domain [Cytophaga hutchinsonii] | | | | 2.1.1.61 |
| 19659, 19660 | 48853990 | 24 | 5.00E-15 | Cytophaga hutchinsonii | COG1196: Chromosome segregation ATPases [Cytophaga hutchinsonii] | | | | |
| 19661, 19662 | 23125186 | 34 | 2.00E-16 | Nostoc punctiforme PCC 73102 | hypothetical protein Npun02006402 [Nostoc punctiforme PCC 73102] | | | | |
| 19663, 19664 | 51892061 | 38 | 2.00E-34 | Symbiobacterium thermophilum IAM 14863 | two-component response regulator [Symbiobacterium thermophilum IAM 14863] dbj BAD39908.1 two-component response regulator [Symbiobacterium thermophilum IAM 14863] | | | | 3.1.1.61 |
| 19665, 19666 | 53613391 | 22 | 7.00E-12 | Azotobacter vinelandii | COG1357: Uncharacterized low-complexity proteins [Azotobacter vinelandii] | | | | |

| | | | | | | | | |
|--------|----------|----|----------|-------------------------------------|--|--|----|-------------------|
| 19667, | 48856618 | 40 | 2.00E-14 | Cytophaga hutchinsonii | COG1562: Phytoene/squalene synthetase [Cytophaga hutchinsonii] | | | |
| 19668 | | | | | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | |
| 19669, | 48853984 | 33 | 9.00E-21 | Cytophaga hutchinsonii | | | | |
| 19670 | | | | | | | | |
| 1967, | 53685350 | 31 | 2.00E-12 | Desulfotobacterium hafniense DCB-2 | COG0535: Predicted Fe-S oxidoreductases [Desulfotobacterium hafniense DCB-2] | | | |
| 1968 | | | | | hypothetical protein al12423 [Nostoc sp. PCC 7120] pir AH2108 hypothetical protein al12423 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB74122.1] | | | |
| 19671, | 17229915 | 27 | 2.00E-15 | Nostoc sp. PCC 7120 | al12423 [Nostoc sp. PCC 7120] | | | 2.7.3.- |
| 19672 | | | | | | | | |
| 19673, | | | | Geobacillus kaustophilus HTA426 | formiminoglutamase [Geobacillus kaustophilus HTA426] dbj BAD75650.1] | | | |
| 19674 | 56419900 | 41 | 4.00E-38 | HTA426 | formiminoglutamase [Geobacillus kaustophilus HTA426] | | | 3.5.3.8 |
| 19675, | 48856973 | 32 | 6.00E-17 | Cytophaga hutchinsonii | COG0382: 4-hydroxybenzoate polyprenyltransferase and related prenyltransferases [Cytophaga hutchinsonii] | | | 2.5.1.- |
| 19676 | | | | | conserved hypothetical protein with rhodanese domain [Bacillus licheniformis ATCC 14580] gb AAU25028.1] conserved hypothetical protein with rhodanese domain [Bacillus licheniformis ATCC 14580] ref YP_093092.1] YbQ [Bacillus licheniformis ATCC 14580] gb AAU42399.1] YbQ [Bacillus licheniformis DSM 13] | | | |
| 19677, | 52081875 | 47 | 9.00E-68 | Bacillus licheniformis ATCC 14580 | | | | |
| 19678 | | | | | | | | |
| 19679, | | | | Thermobifida fusca | COG1321: Mn-dependent transcriptional regulator [Thermobifida fusca] | | | |
| 19680 | 48837393 | 40 | 6.00E-39 | Thermobifida fusca | CBS domain protein [Chlorobium tepidum TLS] gb AAM72271.1] CBS domain protein [Chlorobium tepidum TLS] | | | |
| 19681, | | | | Chlorobium tepidum TLS | | | | |
| 19682 | 21673884 | 34 | 4.00E-15 | Chlorobium tepidum TLS | DNA polymerase II, epsilon subunit [Chlorobium tepidum TLS] gb AAM72272.1] DNA polymerase III, epsilon subunit [Chlorobium tepidum TLS] | | | 2.7.7.7 |
| 19683, | 21673865 | 35 | 1.00E-24 | Chlorobium tepidum TLS | | | | |
| 19684 | | | | | | | | |
| 19687, | | | | Bacteroides fragilis YCH46 | hypothetical protein BF2616 [Bacteroides fragilis YCH46] dbj BAD49366.1] conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 19688 | 53713908 | 65 | 2.00E-35 | Bacteroides fragilis YCH46 | | | | |
| | | | | | | | | |
| 1969, | | | | Methanosarcina barkeri str. fusaro | COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro] | | | |
| 1970 | 48839273 | 62 | 1.00E-54 | Methanosarcina barkeri str. fusaro | | | 95 | 1.00E-54 3.1.21.3 |
| | | | | | Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [Clostridium acetobutylicum ATCC 824] gb AAK79263.1] Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [Clostridium acetobutylicum ATCC 824] pir D97059 membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [imported] - Clostridium acetobutylicum | | | |
| 19693, | | | | Clostridium acetobutylicum ATCC 824 | | | | |
| 19694 | 15894574 | 41 | 5.00E-38 | ATCC 824 | | | | |

| | | | | | | | | | | |
|-----------------|--------------|----|----------|---|--|---|---|----|----------|----------|
| 19695, 19696 | ABP3834 7 | 43 | 1.00E-14 | | | Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3192. Org:Staphylococcus epidermidis | | | | |
| 19697, 19698 | 27364115 | 45 | 9.00E-21 | Vibrio vulnificus CMCP6 | | hypothetical protein VV10658 [Vibrio vulnificus CMCP6] gb AAO09170.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] | | | | |
| 19699, 19700 | 29345776 | 27 | 7.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | | two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482] gb AAO75473.1 two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |
| 19701, 19702 | 29348012 | 47 | 3.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | | putative maturase/reverse transcriptase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77709.1 putative maturase/reverse transcriptase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 19707, 19708 | 34556775 | 71 | 5.00E-99 | Wolinella succinogenes DSM 1740 | | UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09490.1 UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE [Wolinella succinogenes] | Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome | 81 | 6.00E-07 | 2.7.7.9 |
| 19709, 19710 | 34397507 | 36 | 1.00E-19 | Porphyromonas gingivalis W83 | | hypothetical protein PG1529 [Porphyromonas gingivalis W83] ref NP_905670.1 hypothetical protein PG1529 [Porphyromonas gingivalis W83] | | | | |
| 1971, 1972 | 48838982 | 67 | 2.00E-67 | Methanosarcina barkeri str. fusaro | | COG2043: Uncharacterized protein conserved in archaea [Methanosarcina barkeri str. fusaro] | | | | |
| 19711, 19712 | 15617468 | 26 | 8.00E-09 | Lactococcus lactis | | putative IS-like element [Lactococcus lactis] gb AAL02009.1 putative IS-like element [Lactococcus lactis] pir SS3879 hypothetical protein 1 (insertion sequence-like element) - Lactococcus lactis subsp. lactis biovar diacetylactis gb AAB33915.1 Bacillus stearothermophilus putative IS-like element homolog [Lactococcus lactis] | | | | |
| 19713, 19714 | 21672971 | 55 | 2.00E-65 | Chlorobium tepidum TLS | | glucosamine-fructose-6-phosphate aminotransferase [Chlorobium tepidum TLS] gb AAM71378.1 glucosamine-fructose-6-phosphate aminotransferase [Chlorobium tepidum TLS] sp Q8KG38 GLMS_CHL TE Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase) | | | | 2.6.1.16 |
| 19715, 19716 | 17229771 | 29 | 3.00E-07 | Nostoc sp. PCC 7120 | | two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] pir AH2090 two-component hybrid sensor and regulator alr2279 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73978.1 two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] | | | | |
| 19719, 19720 | 48787144 | 26 | 2.00E-11 | Burkholderia fungorum LB400 | | hypothetical protein Bcep02001927 [Burkholderia fungorum LB400] | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|---|----|----------|---------------|
| 19723, 19724 | 48853434 | 67 | 6.00E-61 | Cytophaga hutchinsonii | | COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] | Chromobacterium violaceum ATCC 12472 section. 15 of 16 of the complete genome | 89 | 4.00E-07 | 2.7.7.24 |
| 19725, 19726 | 29345936 | 52 | 3.00E-68 | Bacteroides thetaiotaomicron VPI-5482 | | L-asparaginase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75633.1 L-asparaginase [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.5.1.1 |
| 19729, 19730 | 19068097 | 50 | 3.00E-51 | Bacteroides fragilis Rubrobacter xylanophilus DSM 9941 | | unknown [Bacteroides fragilis] | | | | |
| 1973, 1974 | 45547683 | 28 | 2.00E-16 | | | COG2802: Uncharacterized protein, similar to the N-terminal domain of Lon protease [Rubrobacter xylanophilus DSM 9941] | | | | 3.4.21.5 3 |
| 19731, 19732 | 48856913 | 52 | 3.00E-63 | Cytophaga hutchinsonii | | COG0647: Predicted sugar phosphatases of the HAD superfamily [Cytophaga hutchinsonii] | | | | 3.1.3.41 |
| 19733, 19734 | 34557000 | 58 | 3.00E-64 | Wolinella succinogenes DSM 1740 | | UDP-GLUCOSE DEHYDROGENASE [Wolinella succinogenes DSM 1740] emb CAE09715.1 UDP-GLUCOSE DEHYDROGENASE [Wolinella succinogenes] | | | | 1.1.1.22 |
| 19735, 19736 | 53712881 | 26 | 1.00E-16 | Bacteroides fragilis YCH46 | | hypothetical protein BF1590 [Bacteroides fragilis YCH46] dbj BAD48339.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 19737, 19738 | 29346555 | 59 | 5.00E-64 | Bacteroides thetaiotaomicron VPI-5482 | | glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76252.1 glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A8M2 GIDB_BACTN Methyltransferase gidB [Glucose inhibited division protein B] | | | | |
| 19739, 19740 | 48853433 | 42 | 2.00E-53 | Cytophaga hutchinsonii | | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714691.1 conserved hypothetical protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51706.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS72145.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 19743, 19744 | 45655699 | 34 | 6.00E-25 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Mesorhizobium sp. BNC1] | | | | |
| 19749, 19750 | 45682916 | 32 | 7.00E-28 | Mesorhizobium sp. BNC1 | | COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Cytophaga hutchinsonii] | | | | 1.8.-.- |
| 1975, 1976 | 48856435 | 71 | 2.00E-78 | Cytophaga hutchinsonii | | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|----|----------|----------|
| 19751, 19752 | 48854648 | 80 | 4.00E-72 | Cytophaga hutchinsonii | COG0059: Ketol-acid reductoisomerase [Cytophaga hutchinsonii] | Desc:Haemophilus influenzae DNA for cellular proliferation protein #127. Org:Haemophilus influenzae | 85 | 2.00E-09 | 1.1.1.86 |
| 19753, 19754 | 29027481 | 62 | 4.00E-82 | Aster yellows phytoplasma | threonine dehydratase [Aster yellows phytoplasma] related to 2-oxoglutarate synthase, subunit KorA [Desulfotalea psychrophila LSv54] emb CAG35621.1 related to 2-oxoglutarate synthase, subunit KorA [Desulfotalea psychrophila LSv54] | Streptococcus mutans UA159 section 21 of 185 of the complete genome | 93 | 3.00E-08 | 4.2.1.16 |
| 19759, 19760 | 51244744 | 55 | 3.00E-66 | Desulfotalea psychrophila LSv54 | | | | | 1.2.7.3 |
| 19763, 19764 | 23126889 | 48 | 7.00E-45 | Nostoc punctiforme PCC 73102 | COG3899: Predicted ATPase [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 19765, 19766 | 14030779 | 35 | 6.00E-29 | Mus musculus | ectonucleotide pyrophosphatase/phosphodiesterase 5 [Mus musculus] pir A59390 probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) 5 - mouse gb AAG49143.1 putative nucleotide pyrophosphatase/phosphodiesterase; NPP5 [Mus musculus] putative helicase [Synecococcus elongatus PCC 6301] db BAD78996.1 putative helicase [Synecococcus elongatus PCC 6301] ref P_00163885.1 COG1061: DNA or RNA helicases of superfamily II [Synecococcus elongatus PCC 7942] | | | 3.1.4.1 | |
| 19767, 19768 | 56750815 | 29 | 1.00E-08 | Synechococcus elongatus PCC 6301 | | | | | |
| 19771, 19772 | 53713904 | 68 | 5.00E-89 | Bacteroides fragilis YCH46 | excinuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD49362.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46] | | | | 1.8.- |
| 19773, 19774 | 21226750 | 25 | 7.00E-07 | Methanosarcina mazel Go1 | glycosyltransferase [Methanosarcina mazel Go1] gb AAM30344.1 glycosyltransferase [Methanosarcina mazel Go1] | | | | 2.4.1.- |
| 19775, 19776 | 56460818 | 50 | 2.00E-65 | Idiomarina lithiensis L2TR | Secreted enzyme, contains two amidohydrolase related domains [Idiomarina lithiensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina lithiensis L2TR] | | | | 3.5.1.5 |
| 19777, 19778 | 38044083 | 38 | 4.00E-25 | Helicobacter pylori Clostridium thermocellum | restriction endonuclease [Helicobacter pylori] | | | | |
| 19781, 19782 | 48858283 | 67 | 2.00E-99 | ATCC 27405 | COG2304: Uncharacterized protein containing a von Willebrand factor type A (vWA) domain [Clostridium thermocellum ATCC 27405] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|--|----------|
| 19787, | 38044083 | 32 | 1.00E-24 | Helicobacter pylori | restriction endonuclease [Helicobacter pylori] | | | | |
| 19788 | | | | | COG0769: UDP-N-acetylmuramyl tripeptide synthase [Cytophaga | | | | |
| 19789, | 48854577 | 56 | 7.00E-83 | hutchinsonii | hutchinsonii] | | | | 6.3.2.13 |
| 19790 | | | | | | | | | |
| 1979, | | | | | hypothetical replication factor C small subunit [Sulfolobus tokodaii str. 7] | | | | |
| 1980 | 15920690 | 46 | 4.00E-69 | Sulfolobus tokodaii str. 7 | spiQ975D3[RFC5_SULTO Replication factor C small subunit (RFC small subunit) (Clamp loader small subunit) dbj BAB65468.1 327aa long | | | | 2.7.7.7 |
| 19791, | | | | | hypothetical replication factor C small subunit [Sulfolobus tokodaii str. 7] | | | | |
| 19792 | 48854578 | 43 | 9.00E-41 | Cytophaga hutchinsonii | COG0768: Cell division protein Fis/penicillin-binding protein 2 [Cytophaga hutchinsonii] | | | | 2.3.2.- |
| 19793, | | | | | | | | | |
| 19794 | 48856707 | 45 | 8.00E-31 | Cytophaga hutchinsonii | COG1300: Uncharacterized membrane protein [Cytophaga hutchinsonii] | | | | |
| 19797, | | | | | | | | | |
| 19798 | 32404060 | 27 | 1.00E-08 | Neurospora crassa | predicted protein [Neurospora crassa] emb CAD70330.1 putative protein [Neurospora crassa] gb EAA27596.1 predicted protein [Neurospora crassa] | | | | |
| 19799, | | | | | two-component response regulator [Nostoc sp. PCC 7120] dbj BAB75465.1 | | | | |
| 19800 | 17231258 | 45 | 3.00E-29 | Nostoc sp. PCC 7120 | two-component response regulator [Nostoc sp. PCC 7120] pir AG2276 two-component response regulator all3766 [imported] - Nostoc sp. (strain PCC 7120) | | | | 2.7.3.- |
| 19801, | | | | | hypothetical protein SPOA0125 [Silicibacter pomeroyi] DSS-3 | | | | |
| 19802 | 56708912 | 28 | 7.00E-13 | Silicibacter pomeroyi DSS-3 | gb AAV97262.1 hypothetical protein SPOA0125 [Silicibacter pomeroyi] DSS-3 | | | | |
| 19805, | | | | | | | | | |
| 19806 | 39996271 | 40 | 7.00E-30 | Geobacter sulfurreducens PCA | hypothetical protein GSU1169 [Geobacter sulfurreducens PCA] gb AAR34545.1 hypothetical protein GSU1169 [Geobacter sulfurreducens PCA] | | | | |
| 19811, | | | | | | | | | |
| 19812 | 45644726 | 37 | 1.00E-25 | uncultured marine gamma proteobacterium EBAC20E09 | predicted 3-oxoacyl-ACP synthase [uncultured marine gamma proteobacterium EBAC20E09] | | | | 2.3.1.41 |
| 19813, | | | | | conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 19814 | 57169064 | 32 | 3.00E-33 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 19815, | | | | | | | | | |
| 19816 | 48854435 | 49 | 7.00E-53 | Cytophaga hutchinsonii | COG1331: Highly conserved protein containing a thioredoxin domain [Cytophaga hutchinsonii] | | | | 2.7.4.9 |
| 19817, | | | | | | | | | |
| 19818 | 54309391 | 58 | 1.00E-81 | Photobacterium profundum SS9 | hypothetical short chain dehydrogenase [Photobacterium profundum SS9] emb CAG20609.1 hypothetical short chain dehydrogenase [Photobacterium profundum] | | | | 1.2.1.31 |
| 19819, | | | | | | | | | |
| 19820 | 24373318 | 35 | 6.00E-35 | Shewanella oneidensis MR-1 | membrane protein, putative [Shewanella oneidensis MR-1] gb AAN54805.1 membrane protein, putative [Shewanella oneidensis MR-1] | | | | |

| | | | | | | | | | |
|-----------------|-----------|----|----------|---|---|--|--|--|----------|
| 19821, 19822 | 21675068 | 43 | 9.00E-72 | Chlorobium tepidum TLS | ribonuclease G [Chlorobium tepidum TLS] | | | | 3.1.4.- |
| 19823, 19824 | 29346171 | 33 | 6.00E-15 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0761 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75868.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 19825, 19826 | 50120667 | 35 | 2.00E-11 | Erwinia carotovora subsp. atroseptica SCRI1043 | hypothetical protein ECA1734 [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG74639.1 conserved hypothetical protein [Erwinia carotovora subsp. atroseptica SCRI1043] | | | | |
| 19827, 19828 | 48834834 | 53 | 1.00E-61 | Thermobifida fusca | COG1611: Predicted Rossmann fold nucleotide-binding protein [Thermobifida fusca] | | | | 1.1.1.85 |
| 1983, 1984 | 15922432 | 26 | 2.00E-12 | Sulfolobus tokodaii str. 7 | hypothetical protein ST2106 [Sulfolobus tokodaii str. 7] dbj BAB67210.1 495aa long conserved hypothetical protein [Sulfolobus tokodaii str. 7] | | | | |
| 19831, 19832 | 48853849 | 30 | 2.00E-10 | Cytophaga hutchinsonii | COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii] | | | | |
| 19835, 19836 | 343997507 | 32 | 6.00E-28 | Porphyromonas gingivalis W83 | hypothetical protein PG1529 [Porphyromonas gingivalis W83] ref NP_905670.1 hypothetical protein PG1529 [Porphyromonas gingivalis W83] | | | | |
| 19837, 19838 | 47565344 | 38 | 2.00E-50 | Bacillus cereus G9241 | hypothetical protein protein [Bacillus cereus G9241] gb EAL16024.1 hypothetical protein protein [Bacillus cereus G9241] | | | | |
| 19841, 19842 | 56459804 | 32 | 1.00E-36 | Idiomarina loihlensis L2TR | Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihlensis L2TR] protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihlensis L2TR] | | | | |
| 19843, 19844 | 32476735 | 28 | 6.00E-10 | Rhodopirellula baltica SH 1 | probable serine/threonine protein kinase [Rhodopirellula baltica SH 1] emb CAD77107.1 probable serine/threonine protein kinase [Pirellula sp.] | | | | 2.7.1.- |
| 19847, 19848 | 48854120 | 34 | 8.00E-12 | Cytophaga hutchinsonii | COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] | | | | 6.2.1.3 |
| 19849, 19850 | 37525769 | 41 | 1.00E-31 | Photorhabdus luminescens subsp. laumondii TTO1 | hypothetical protein plu1836 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE14129.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] | | | | |
| 1985, 1986 | 46199730 | 40 | 4.00E-20 | Thermus thermophilus HB27 | hypothetical protein TTC1428 [Thermus thermophilus HB27] gb AAS81770.1 hypothetical protein TTC1428 [Thermus thermophilus HB27] | | | | |

| | | | | | | | | | | | |
|-----------------|--------------|----|----------|--|---|--|--|---|----|----------|----------|
| 19855, 19856 | AAV7437 7 | 38 | 3.00E-08 | | | | Desc: <i>Neisseria gonorrhoeae</i> ORF 073 protein sequence SEQ ID NO:230. Org: <i>Neisseria gonorrhoeae</i> | Anopheles gambiae ENSANGP000000000 0381 (ENSANGG0000000 00361) mRNA, partial cds | 87 | 4.00E-10 | |
| 19857, 19858 | 46188929 | 42 | 8.00E-23 | | <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a | | COG0702: Predicted nucleoside-diphosphate-sugar epimerases [<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a] | | | | |
| 19859, 19860 | 28899147 | 33 | 1.00E-31 | | <i>Vibrio parahaemolyticus</i> RIMD 2210633 | | exodeoxyribonuclease V, 67 kDa subunit [Vibrio parahaemolyticus RIMD 2210633] dbj BAC60636.1 exodeoxyribonuclease V, 67 kDa subunit [Vibrio parahaemolyticus] | | | 3.1.1.15 | |
| 19861, 19862 | 32330663 | 29 | 4.00E-13 | | <i>Solenopsis invicta</i> Thermoanaerobacter tengcongensis | | glutathione S-transferase [Solenopsis invicta] Hypoxanthine-guanine phosphoribosyltransferase [Thermoanaerobacter tengcongensis MB4] gb AAM25533.1 Hypoxanthine-guanine phosphoribosyltransferase [Thermoanaerobacter tengcongensis MB4] | | | 2.5.1.18 | |
| 19863, 19864 | 20808758 | 47 | 6.00E-43 | | <i>Bacteroides thetaiotaomicron</i> VPI-5482 | | ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78944.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | 2.4.2.8 | |
| 19869, 19870 | 29349247 | 60 | 6.00E-60 | | <i>Oceanobacillus thetaiotaomicron</i> HTE831 | | hypothetical protein OB2676 [Oceanobacillus thetaiotaomicron HTE831] dbj BAC14632.1 hypothetical conserved protein [Oceanobacillus thetaiotaomicron HTE831] | | | 1.8.-.- | |
| 19871, 19872 | 23100131 | 34 | 1.00E-26 | | <i>Bacillus thuringiensis</i> | | putative transposase [Bacillus thuringiensis] gb AAL86920.1 putative transposase [Bacillus thuringiensis] | | | 6.3.4.6 | |
| 19875, 19876 | 44894463 | 35 | 1.00E-17 | | <i>Leptospira interrogans</i> serovar Lai str. 56601 | | hypothetical protein LA1980 [Leptospira interrogans serovar Lai str. 56601] gb AAN49179.1 hypothetical protein [Leptospira interrogans serovar Lai str. 56601] | | | | |
| 19877, 19878 | 24214680 | 38 | 3.00E-26 | | <i>Wolinella succinogenes</i> DSM 1740 | | HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella succinogenes DSM 1740] emb CAE10219.1 HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella succinogenes] | Nostoc sp. PCC 7120 DNA, complete genome | 84 | 4.00E-08 | 3.1.21.3 |
| 19881, 19882 | 34557504 | 63 | 1.00E-97 | | uncultured archaeon GZfos12E1 | | conserved hypothetical protein [uncultured archaeon GZfos12E1] | | | | |
| 19889, 19890 | 52632010 | 40 | 2.00E-23 | | <i>Silicibacter</i> sp. TM1040 | | COG0262: Dihydrofolate reductase [Silicibacter sp. TM1040] | | | | 3.4.24.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|--|---------------|
| 19893, 19894 | 51244744 | 58 | 2.00E-68 | Desulfotalea psychrophila LSV54 | related to 2-oxoglutarate synthase, subunit KorA [Desulfotalea psychrophila LSV54] emb CAG35621.1 related to 2-oxoglutarate synthase, subunit KorA [Desulfotalea psychrophila LSV54] | | | | 1.2.7.3 |
| 19895, 19896 | 34397542 | 37 | 1.00E-34 | Porphyromonas gingivalis W83 | transcriptional regulator, Crp family [Porphyromonas gingivalis W83] ref NP_005705.1 transcriptional regulator, Crp family [Porphyromonas gingivalis W83] | | | | |
| 19897, 19898 | 15606303 | 51 | 3.00E-76 | Aquifex aeolicus VF5 | long-chain-fatty-acid CoA ligase [Aquifex aeolicus VF5] gb AAC07072.1 long-chain-fatty-acid CoA ligase [Aquifex aeolicus VF5] pir D70386 probable polyketide synthetase [similarity] - Aquifex aeolicus | | | | 6.2.1.3 |
| 19899, 19900 | 34763672 | 41 | 2.00E-28 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | Long-chain-fatty-acid-CoA ligase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23796.1 Long-chain-fatty-acid-CoA ligase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | | 6.2.1.3 |
| 199, 200 | 48854665 | 44 | 1.00E-39 | Cytophaga hutchinsonii | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | | |
| 19901, 19902 | 53712448 | 32 | 7.00E-20 | Bacteroides fragilis YCH46 | hypothetical protein BF1156 [Bacteroides fragilis YCH46] dbj BAD47906.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 19903, 19904 | 29346729 | 35 | 9.00E-17 | Bacteroides thetaiotaomicron VPI-5482 | two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO76426.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 19907, 19908 | 56678876 | 32 | 2.00E-28 | Silicibacter pomeroi DSS-3 | hypothetical protein SPO2278 [Silicibacter pomeroi DSS-3] ref YP_167502.1 hypothetical protein SPO2278 [Silicibacter pomeroi DSS-3] | | | | |
| 19913, 19914 | 48855430 | 31 | 8.00E-38 | Cytophaga hutchinsonii | hypothetical protein Chut02001765 [Cytophaga hutchinsonii] | | | | |
| 19917, 19918 | 53711756 | 25 | 6.00E-09 | Bacteroides fragilis YCH46 | hypothetical protein BF0465 [Bacteroides fragilis YCH46] dbj BAD47214.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 19921, 19922 | 24374550 | 29 | 5.00E-18 | Shewanella oneidensis MR-1 | hypothetical protein SO3025 [Shewanella oneidensis MR-1] gb AAN56037.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | | |
| 1993, 1994 | 37526903 | 28 | 5.00E-16 | Photorhabdus luminescens subsp. laumondii TTO1 | hypothetical protein plu3015 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15389.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] | | | | 2.4.1.16 6 |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|--|---------|
| 19931, 19932 | 53712348 | 33 | 8.00E-15 | Bacteroides fragilis YCH46 | putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47806.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] | | | |
| 19937, 19938 | 16126741 | 37 | 5.00E-34 | Caulobacter crescentus CB15 | peptidase M20/M25/M40 family protein [Caulobacter crescentus CB15] gb AAK24473.1 peptidase M20/M25/M40 family protein [Caulobacter crescentus CB15] pir [E87559] peptidase M20/M25/M40 family protein [Imported] - Caulobacter crescentus | | | |
| 19939, 19940 | 48855337 | 53 | 2.00E-62 | Cytophaga hutchinsonii | COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii] | | | |
| 19943, 19944 | 48854288 | 41 | 7.00E-32 | Cytophaga hutchinsonii | COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii] | | | |
| 19945, 19946 | 48854286 | 29 | 4.00E-10 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 19947, 19948 | 48856513 | 57 | 2.00E-29 | Cytophaga hutchinsonii | COG0307: Riboflavin synthase alpha chain [Cytophaga hutchinsonii] | | | 2.5.1.9 |
| 19949, 19950 | 56544347 | 45 | 1.00E-24 | Zymomonas mobilis subsp. mobilis ZM4 | glutamine cyclotransferase [Zymomonas mobilis subsp. mobilis ZM4] ref YP_163612.1 glutamine cyclotransferase [Zymomonas mobilis subsp. mobilis ZM4] | | | |
| 1995, 1996 | 53713033 | 59 | 1.00E-114 | Bacteroides fragilis YCH46 | ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD48491.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] | | | |
| 19951, 19952 | 17934032 | 44 | 1.00E-28 | Agrobacterium tumefaciens str. C58 | two component sensor kinase [Agrobacterium tumefaciens str. C58] gb AAL41138.1 two component sensor kinase [Agrobacterium tumefaciens str. C58] pir [AD2590] two component sensor kinase dctB [Imported] - Agrobacterium tumefaciens (strain C58, Dupont) | | | 2.7.3.- |
| 19957, 19958 | 29347086 | 44 | 8.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | Maf protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76783.1 Maf protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A749 YG76_BACTN Maf-like protein BT1676 | | | |
| 19959, 19960 | 48855136 | 58 | 7.00E-62 | Cytophaga hutchinsonii | COG0118: Glutamine amidotransferase [Cytophaga hutchinsonii] | | | 2.4.2.- |
| 19961, 19962 | 29345612 | 51 | 3.00E-52 | Bacteroides thetaiotaomicron VPI-5482 | histidinol-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO75309.1 histidinol-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8ABA8 HIS8_BACTN Histidinol-phosphate aminotransferase [imidazole acetol-phosphate transaminase] | | | 2.6.1.9 |
| 19967, 19968 | 12024595 | 63 | 2.00E-63 | Flavobacterium johnsoniae | GldE [Flavobacterium johnsoniae] | | | |
| 19969, 19970 | 39937015 | 67 | 4.00E-52 | Rhodopseudomonas palustris CGA009 | thioredoxin reductase [Rhodopseudomonas palustris CGA009] emb CAE29395.1 thioredoxin reductase [Rhodopseudomonas palustris CGA009] | | | 1.6.4.5 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|----------|
| 1997, 1998 | 56963167 | 26 | 2.00E-08 | Bacillus clausii KSM-K16 | penicillin-binding protein 4 [Bacillus clausii KSM-K16] dbj BAD63934.1 penicillin-binding protein 4 [Bacillus clausii KSM-K16] | | | | |
| 19973, 19974 | 21674329 | 68 | 6.00E-31 | Chlorobium tepidum TLS | CAAX prenyl protease 1, putative [Chlorobium tepidum TLS] gb AAM72736.1 CAAX prenyl protease 1, putative [Chlorobium tepidum TLS] | | | | 3.4.24.- |
| 19975, 19976 | 15899493 | 31 | 7.00E-11 | Sulfolobus solfataricus P2 | hypothetical protein SSO2778 [Sulfolobus solfataricus P2] gb AAK42888.1 Conserved hypothetical protein [Sulfolobus solfataricus P2] pir A90454 conserved hypothetical protein [imported] - Sulfolobus solfataricus | | | | |
| 19977, 19978 | 56707657 | 63 | 1.00E-58 | Francisella tularensis subsp. tularensis Schu 4 | hypothetical protein FT10522 [Francisella tularensis subsp. tularensis Schu 4] emb CAG45155.1 conserved hypothetical protein [Francisella tularensis subsp. tularensis] | | | | 2.1.1.72 |
| 19979, 19980 | 53796853 | 41 | 8.00E-37 | Chloroflexus aurantiacus | COG0210: Superfamily I DNA and RNA helicases [Chloroflexus aurantiacus] | | | | 3.6.1.- |
| 19981, 19982 | 21243533 | 31 | 4.00E-23 | Xanthomonas axonopodis pv. citri str. 306 | beta-lactamase [Xanthomonas axonopodis pv. citri str. 306] gb AAM37651.1 beta-lactamase [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 19983, 19984 | 48855481 | 34 | 5.00E-29 | Cytophaga hutchinsonii | hypothetical protein Chut02001820 [Cytophaga hutchinsonii] putative protoporphyrinogen oxidase [Bacteroides fragilis YCH46] | | | | |
| 19987, 19988 | 53711799 | 51 | 1.00E-21 | Bacteroides fragilis YCH46 | dbj BAD47257.1 putative protoporphyrinogen oxidase [Bacteroides fragilis YCH46] | | | | 2.1.1.- |
| 19989, 19990 | 52008034 | 33 | 1.00E-18 | Thiobacillus denitrificans ATCC 25259 | COG2202: FOG: PAS/PAC domain [Thiobacillus denitrificans ATCC 25259] | | | | 2.7.3.- |
| 1999, 2000 | AAR0646 | 87 | 1.00E-97 | | Desc:Pancreatic islet cell antigen (ICA) encoding cDNA (clone ICA-302). Org: Homo sapiens | | 80 | 2.00E-50 | 2.7.7.8 |
| 19991, 19992 | 57240784 | 50 | 7.00E-44 | Campylobacter lari RM2100 | Desc:Derived protein from clone ICA302 (ATCC 40551). Org: Homo sapiens conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55177.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | 3.4.13.9 |
| 19993, 19994 | 29347851 | 27 | 5.00E-12 | Bacteroides thetaiotaomicron VPI-5482 | putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77548.1 putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.1.3.5 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 19997, 19998 | 15884727 | 36 | 1.00E-18 | Clostridium acetobutylicum ATCC 824 | tetracycline resistance protein, tetQ family, GTPase [Clostridium acetobutylicum ATCC 824] gb AAK79416.1 tetracycline resistance protein, tetQ family, GTPase [Clostridium acetobutylicum ATCC 824] pti E97078 tetracycline resistance protein, tetQ family, GTPase [imported] - Clostridium acetobutylicum | | | 3.6.1.48 |
| 19999, 20000 | 23014264 | 44 | 1.00E-43 | Magnetospirillum magnetotacticum MS-1 | COG0019: Diaminopimelate decarboxylase [Magnetospirillum magnetotacticum MS-1] | | | 4.1.1.20 |
| 20003, 20004 | 13488054 | 29 | 3.00E-11 | Mesorhizobium loti MAFF303099 | hypothetical protein ml9010 [Mesorhizobium loti MAFF303099] dbj BAB5444.1 ml9010 [Mesorhizobium loti MAFF303099] | | | 4.2.1.79 |
| 20009, 20010 | 53799012 | 31 | 1.00E-13 | Chloroflexus aurantiacus | COG2936: Predicted acyl esterases [Chloroflexus aurantiacus] | | | |
| 2001, 2002 | 52548759 | 51 | 3.00E-69 | uncultured archaeon GZfos18F2 | putative glycosyl transferase [uncultured archaeon GZfos18F2] | | | 2.--- |
| 20013, 20014 | 48853712 | 59 | 6.00E-56 | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | |
| 20015, 20016 | 48856025 | 35 | 5.00E-20 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |
| 20017, 20018 | 48846974 | 47 | 2.00E-19 | Geobacter metallireducens GS-15 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 20019, 20020 | 20807152 | 43 | 2.00E-34 | Thermoanaerobact er tengcongensis MB4 | UDP-N-acetylglucosamine 2-epimerase [Thermoanaerobacter tengcongensis MB4] gb AAM23927.1 UDP-N-acetylglucosamine 2- epimerase [Thermoanaerobacter tengcongensis MB4] | | | 5.1.3.14 |
| 20021, 20022 | 47526988 | 33 | 2.00E-11 | Bacillus anthracis str. 'Ames Ancestor' | tpg/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] | | | |
| 20025, 20026 | 34558474 | 40 | 2.00E-48 | Wolfinella succinogenes DSM 1740 | hypothetical protein WS2199 [Wolfinella succinogenes DSM 1740] emb CAE11189.1 conserved hypothetical protein [Wolfinella succinogenes] | | | |
| 20027, 20028 | 55540738 | 23 | 2.00E-07 | Flavobacterium columnare | Fpo24 [Flavobacterium columnare] | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|-----------------|---|--|----------|--|--|--|
| 20029, 20030 | 16077248 | 38 | 1.00E-30 | 168 | Bacillus subtilis subsp. subtilis str. | DNA-3-methyladenine glycosylase [Bacillus subtilis str. 168] emb CAB11956.1 DNA-3-methyladenine glycosylase [Bacillus subtilis subsp. subtilis str. 168] pir E69584 3-methyladenine DNA glycosylase (EC 3.2.2.-) - Bacillus subtilis sp P37878 3MGA_BACSU DNA-3-methyladenine glycosylase (3-methyladenine-DNA glycosidase) dbj BAA03361.1 3-methyladenine DNA glycosylase [Bacillus subtilis] dbj BAA33073.1 3-METHYLADENINE DNA GLYCOSYLASE [Bacillus subtilis] | 3.2.2.21 | | | |
| 2003, 2004 | 29347199 | 27 | 2.00E-13 | VPI-5482 | Bacteroides thetataomicron | aminopeptidase C (bleomycin hydrolase) [Bacteroides thetataomicron VPI-5482] gb AAO76896.1 aminopeptidase C (bleomycin hydrolase) [Bacteroides thetataomicron VPI-5482] | | | | |
| 20031, 20032 | 21672847 | 46 | 3.00E-45 | tepidum TLS | Chlorobium | Oxa1/60 kDa IMP family protein [Chlorobium tepidum TLS] | | | | |
| 20033, 20034 | 21885294 | 44 | 7.00E-43 | Vibrio cholerae | | putative histidine kinase [Vibrio cholerae] | 2.7.3.- | | | |
| 20035, 20036 | 48853472 | 32 | 1.00E-23 | hutchinsonii | Cytophaga | hypothetical protein Chut02003804 [Cytophaga hutchinsonii] | | | | |
| 20037, 20038 | 23127700 | 36 | 2.00E-42 | PCC 73102 | Nostoc punctiforme | COG1357: Uncharacterized low-complexity proteins [Nostoc punctiforme PCC 73102] | | | | |
| 20039, 20040 | 15894108 | 33 | 8.00E-09 | ATCC 824 | Clostridium acetobutylicum | Transcriptional regulator (TetR/AcrR family) [Clostridium acetobutylicum ATCC 824] gb AAK78797.1 Transcriptional regulator (TetR/AcrR family) [Clostridium acetobutylicum ATCC 824] pir E97001 transcription regulator (TetR/AcrR family) [Imported] - Clostridium acetobutylicum | | | | |
| 20043, 20044 | 34397911 | 28 | 3.00E-13 | gingivalis W83 | Porphyromonas | signal peptidase I [Porphyromonas gingivalis W83] ref NP_906073.1 signal peptidase I [Porphyromonas gingivalis W83] | | | | |
| 20045, 20046 | 20091299 | 25 | 3.00E-08 | acetivorans C2A | Methanosarcina | hypothetical protein MA2468 [Methanosarcina acetivorans C2A] gb AAM05854.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | | |
| 20047, 20048 | 48856576 | 32 | 4.00E-24 | hutchinsonii | Cytophaga | COG1071: Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit [Cytophaga hutchinsonii] | | | | |
| 20049, 20050 | 40062939 | 30 | 4.00E-29 | bacterium 443 | uncultured | DNA polymerase IV [uncultured bacterium 443] | 2.7.7.7 | | | |
| 2005, 2006 | 53714487 | 56 | 3.00E-44 | YCH46 | Bacteroides fragilis | SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD49945.1 SsrA-binding protein [Bacteroides fragilis YCH46] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 20051, 20052 | 21229991 | 39 | 1.00E-16 | Xanthomonas campestris pv. campestris str. ATCC 33913 | hypothetical protein XCC0516 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39832.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_905527.1 hypothetical protein PG1362 [Porphyromonas gingivalis W83] | | | | |
| 20053, 20054 | 34397363 | 35 | 2.00E-14 | Porphyromonas gingivalis W83 | | | | | |
| 20055, 20056 | 23474790 | 41 | 2.00E-17 | Desulfovibrio desulfuricans G20 | COG1157: Flagellar biosynthesis type III secretory pathway ATPase [Desulfovibrio desulfuricans G20] | | | | |
| 20057, 20058 | 32473614 | 33 | 1.00E-27 | Rhodopirella baltica SH 1 | D-amino acid dehydrogenase, small chain [Rhodopirella baltica SH 1] emb CAD78389.1 D-amino acid dehydrogenase, small chain [Pirellula sp.] | | | | 1.4.99.1 |
| 20061, 20062 | 24373267 | 23 | 2.00E-12 | Shewanella oneidensis MR-1 | transcriptional regulator [Shewanella oneidensis MR-1] gb AAN54754.1 transcriptional regulator [Shewanella oneidensis MR-1] | | | | |
| 20063, 20064 | 24637507 | 30 | 3.00E-19 | Streptococcus thermophilus | Eps10P [Streptococcus thermophilus] | | | | |
| 20065, 20066 | 52081208 | 48 | 2.00E-43 | Bacillus licheniformis ATCC 14580 | cystathionine gamma-lyase YrhB [Bacillus licheniformis ATCC 14580] gb AAU24359.1 cystathionine gamma-lyase YrhB [Bacillus licheniformis ATCC 14580] ref YP_092416.1 YrhB [Bacillus licheniformis ATCC 14580] gb AAU41723.1 YrhB [Bacillus licheniformis DSM 13] | | | | 4.2.99.9 |
| 2007, 2008 | 57234396 | 41 | 7.00E-44 | Dehalococcoides ethenogenes 195 | ABC transporter, ATP-binding protein [Dehalococcoides ethenogenes 195] gb AAW39901.1 ABC transporter, ATP-binding protein [Dehalococcoides ethenogenes 195] | | | | 1.8.-.- |
| 20071, 20072 | 48853602 | 54 | 2.00E-76 | Cytophaga hutchinsonii | COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii] | | | | |
| 20073, 20074 | 53712286 | 50 | 3.00E-49 | Bacteroides fragilis YCH46 | putative S-adenosylmethionine-dependent methyltransferase [Bacteroides fragilis YCH46] db BAD47724.1 putative S-adenosylmethionine-dependent methyltransferase [Bacteroides fragilis YCH46] | | | | 2.1.1.- |
| 20075, 20076 | 16331457 | 23 | 2.00E-10 | Synechocystis sp. PCC 6803 | hypothetical protein sl0405 [Synechocystis sp. PCC 6803] db BAA10255.1 sl0405 [Synechocystis sp. PCC 6803] pir S74337 hypothetical protein sl0405 - Synechocystis sp. (strain PCC 6803) | | | | |
| 20077, 20078 | 50929757 | 43 | 2.00E-33 | Oryza sativa (japonica cultivar-group) | OSJNBa0088H09.2 [Oryza sativa (japonica cultivar-group)] emb CAE03444.1 OSJNBa0088H09.2 [Oryza sativa (japonica cultivar-group)] | | | | 6.2.1.3 |
| 20085, 20086 | 53796853 | 41 | 7.00E-38 | Chloroflexus aurantiacus | COG0210: Superfamily I DNA and RNA helicases [Chloroflexus aurantiacus] | | | | 3.6.1.- |
| 20087, 20088 | 29346486 | 44 | 8.00E-46 | Bacteroides thetaiotaomicron VPI-5482 | two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO76183.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 20093, 20094 | 48855702 | 38 | 3.00E-16 | Cytophaga hutchinsonii | COG3279: Response regulator of the LysR/AlgR family [Cytophaga hutchinsonii] | | | |
| 20095, 20096 | 52843085 | 50 | 1.00E-41 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | glucose inhibited division protein B [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28937.1 glucose inhibited division protein B [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] probable 5-formyltetrahydrofolate cyclo-ligase [Clostridium perfringens str. 13] dbj BAB82030.1 probable 5-formyltetrahydrofolate cyclo-ligase | | | |
| 20099, 20100 | 18311306 | 34 | 2.00E-19 | Clostridium perfringens str. 13 | [Clostridium perfringens str. 13] RNA polymerase ECF-type sigma factor [Oceanobacillus ihayensis HTE831] dbj BAC14616.1 RNA polymerase ECF-type sigma factor [Oceanobacillus ihayensis HTE831] | | | 6.3.3.2 |
| 20105, 20106 | 23100115 | 32 | 5.00E-14 | Oceanobacillus ihayensis HTE831 | COG5343: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 20107, 20108 | 48855790 | 33 | 3.00E-15 | Cytophaga hutchinsonii | hypothetical protein [Staphylococcus aureus] | | | |
| 20109, 20110 | 28465878 | 37 | 5.00E-07 | Staphylococcus aureus | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 20111, 20112 | 48854665 | 44 | 4.00E-61 | Cytophaga hutchinsonii | hypothetical protein DP1860 [Desulfotalea psychrophila LSV54] emb CAG36589.1 hypothetical protein [Desulfotalea psychrophila LSV54] response regulator receiver:histidine kinase [Rhodopseudomonas palustris CGA009] emb CAE30230.1 response regulator receiver:histidine kinase | | | 1.3.- |
| 20117, 20118 | 51245712 | 36 | 2.00E-18 | Desulfotalea psychrophila LSV54 | [Rhodopseudomonas palustris CGA009] hypothetical protein SPOA0125 [Silicibacter pomeroyi DSS-3] gb AAV97262.1 hypothetical protein SPOA0125 [Silicibacter pomeroyi DSS-3] | | | 2.7.3.- |
| 20121, 20122 | 39937848 | 48 | 2.00E-19 | Rhodopseudomona s palustris CGA009 | COG2202: FOG: PAS/PAC domain [Anabaena variabilis ATCC 29413] COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | 2.7.3.- |
| 20127, 20128 | 56708912 | 28 | 5.00E-13 | Silicibacter pomeroyi DSS-3 | hypothetical protein BF1151 [Bacteroides fragilis YCH46] dbj BAD47901.1 conserved hypothetical protein [Bacteroides fragilis YCH46] glycerol-3-phosphate dehydrogenase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO77230.1 glycerol-3-phosphate dehydrogenase [Bacteroides thetaitaomicron VPI-5482] | | | 1.1.1.94 |
| 2013, 2014 | 53763805 | 36 | 5.00E-38 | Anabaena variabilis ATCC 29413 | | | | |
| 20131, 20132 | 48859543 | 35 | 7.00E-32 | Clostridium thermocellum ATCC 27405 | | | | |
| 20135, 20136 | 53712443 | 33 | 1.00E-36 | Bacteroides fragilis YCH46 | | | | |
| 20137, 20138 | 29347533 | 39 | 7.00E-18 | Bacteroides thetaitaomicron VPI-5482 | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|----------|
| 20139, 20140 | 23502026 | 78 | 2.00E-68 | Brucella suis 1330 | citrate synthase [Brucella suis 1330] gb AAN30068.1 citrate synthase [Brucella suis 1330] | Salmonella typhimurium LT2, section 37 of 220 of the complete genome | 89 | 4.00E-25 | 4.1.3.7 |
| 20147, 20148 | 36955665 | 86 | 2.00E-63 | Polaribacter filamentus | kynureninase [Polaribacter filamentus] | Polaribacter filamentus kynureninase gene, complete cds | 83 | 1.00E-61 | 3.7.1.3 |
| 20149, 20150 | 48854546 | 40 | 4.00E-16 | Cytophaga hutchinsonii | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | | |
| 20151, 20152 | 33862008 | 30 | 9.00E-17 | Prochlorococcus marinus subsp. pastoris str. CCMP1986 | ATP synthase, delta (OSCP) subunit [Prochlorococcus marinus subsp. pastoris str. CCMP1986] | | | | 3.6.3.14 |
| 20153, 20154 | 29348769 | 57 | 9.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78466.1 phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.1.2.2 |
| 20155, 20156 | 32474967 | 41 | 1.00E-40 | Rhodopirellula baltica SH 1 | hypothetical protein RB7682 [Rhodopirellula baltica SH 1] emb CAD75508.1 hypothetical protein [Pirellula sp.] | | | | |
| 20157, 20158 | 21674971 | 51 | 2.00E-30 | Chlorobium tepidum TLS | DNA-directed RNA polymerase, alpha subunit [Chlorobium tepidum TLS] gb AAM73378.1 DNA-directed RNA polymerase, alpha subunit [Chlorobium tepidum TLS] sp Q8KAA8 RPOA_CHLTE DNA-directed RNA polymerase alpha chain (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit) | | | | 2.7.7.6 |
| 20163, 20164 | 14602144 | 27 | 1.00E-09 | Aeropyrum pernix K1 | hypothetical protein APE2556 [Aeropyrum pernix K1] dbj BAA81573.1 1007aa long hypothetical protein [Aeropyrum pernix K1] pir E72489 hypothetical protein APE2556 - Aeropyrum pernix (strain K1) | | | | 1.2.1.2 |
| 20165, 20166 | 23014654 | 43 | 7.00E-15 | Magnetospirillum magnetotacticum MS-1 | hypothetical protein Magn03009102 [Magnetospirillum magnetotacticum MS-1] | | | | |
| 20167, 20168 | 21672847 | 34 | 6.00E-43 | Chlorobium tepidum TLS | Oxa1/60 kDa IMP family protein [Chlorobium tepidum TLS] gb AAM71254.1 Oxa1/60 kDa IMP family protein [Chlorobium tepidum TLS] sp Q8KGG2 OXA1_CHLTE inner membrane protein oxaA | | | | |
| 20169, 20170 | 27366639 | 39 | 2.00E-22 | Vibrio vulnificus CMCP6 | Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] gb AAO07156.1 Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|--|---|----|----------|----------|
| 2017, 2018 | 53715477 | 58 | 5.00E-99 | Bacteroides fragilis YCH46 | DNA-directed RNA polymerase beta chain [Bacteroides fragilis YCH46] dbj BAD50935.1 DNA-directed RNA polymerase beta chain [Bacteroides fragilis YCH46] | Bacteroides thetalaotamiron VPI-5482, section 12 of 21 of the complete genome | 87 | 2.00E-22 | 2.7.7.6 |
| 20173, 20174 | 20559952 | 37 | 1.00E-06 | Pseudomonas aeruginosa | ORF_12; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa] gb AAM27564.1 ORF_12; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa] | | | | |
| 20175, 20176 | 20559952 | 42 | 1.00E-29 | Pseudomonas aeruginosa | ORF_12; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa] gb AAM27564.1 ORF_12; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa] | | | | |
| 20179, 20180 | 53712067 | 28 | 7.00E-18 | Bacteroides fragilis YCH46 | AAA-metalloprotease FtsH with ATPase domain [Bacteroides fragilis YCH46] dbj BAD47525.1 AAA-metalloprotease FtsH with ATPase domain [Bacteroides fragilis YCH46] | | | | 3.4.24.- |
| 20181, 20182 | 42524039 | 36 | 3.00E-13 | Bdellovibrio bacteriovorus HD100 | transcriptional regulator, LysR family [Bdellovibrio bacteriovorus HD100] emb CAE8041.1 transcriptional regulator, LysR family [Bdellovibrio bacteriovorus HD100] | | | | |
| 20183, 20184 | 48853811 | 46 | 1.00E-52 | Cytophaga hutchinsonii | COG0587: DNA polymerase III, alpha subunit [Cytophaga hutchinsonii] | | | | 2.7.7.7 |
| 20185, 20186 | 48731833 | 73 | 1.00E-120 | Pseudomonas fluorescens PFO-1 | COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Pseudomonas fluorescens PFO-1] | Pseudomonas syringae pv. tomato str. DC3000 section 14 of 21 of the complete genome | 80 | 5.00E-11 | 2.4.2.14 |
| 20187, 20188 | 48856687 | 30 | 1.00E-25 | Cytophaga hutchinsonii | COG2834: Outer membrane lipoprotein-sorting protein [Cytophaga hutchinsonii] | | | | |
| 20189, 20190 | 30249328 | 37 | 3.00E-11 | Nitrosomonas europaea ATCC 19718 | hypothetical protein NE1349 [Nitrosomonas europaea ATCC 19718] emb CAD85260.1 conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] | | | | |
| 20191, 20192 | 45656787 | 49 | 7.00E-49 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_710808.1 Putative glycosyl transferase [Leptospira interrogans serovar Lai str. 56601] gb AAN47826.1 Putative glycosyl transferase [Leptospira interrogans serovar lai str. 56601] gb AAS71510.1 glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | |
| 20193, 20194 | 48853832 | 56 | 5.00E-49 | Cytophaga hutchinsonii | COG0484: DnaJ-class molecular chaperone with C-terminal Zn finger domain [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|--|--|--|--|----------|
| 20195, 20196 | 52079641 | 43 | 1.00E-21 | Bacillus licheniformis ATCC 14580 | oligopeptide ABC transporter (binding protein) [Bacillus licheniformis ATCC 14580] gb AAU22794.1 oligopeptide ABC transporter (binding protein) [Bacillus licheniformis ATCC 14580] ref YP_090833.1 OppA [Bacillus licheniformis ATCC 14580] gb AAU40140.1 OppA [Bacillus licheniformis DSM 13] | | | | |
| 20197, 20198 | 28899115 | 53 | 4.00E-79 | Vibrio parahaemolyticus RIMD 2210633 | putative ATP-dependent DNA helicase RecQ [Vibrio parahaemolyticus RIMD 2210633] dbj BAC0604.1 putative ATP-dependent DNA helicase RecQ [Vibrio parahaemolyticus] | | | | 3.6.1.- |
| 20199, 20200 | 48763874 | 64 | 1.00E-26 | Rhodospirillum rubrum | COG0762: Predicted integral membrane protein [Rhodospirillum rubrum] | | | | |
| 20201, 20202 | 34332873 | 28 | 6.00E-16 | Chromobacterium violaceum ATCC 12472 | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_902918.1 hypothetical protein CV3248 [Chromobacterium violaceum ATCC 12472] | | | | 2.7.3.- |
| 20205, 20206 | 15614300 | 42 | 8.00E-35 | Bacillus halodurans C-125 | homoserine dehydrogenase [Bacillus halodurans C-125] dbj BAB05456.1 homoserine dehydrogenase [Bacillus halodurans C-125] pir A83867 homoserine dehydrogenase BH1737 [Imported] - Bacillus halodurans (strain C-125) | | | | 1.1.1.3 |
| 20207, 20208 | 57158331 | 34 | 1.00E-34 | Thermococcus kodakaraensis | tungsten-containing oxidoreductase [Thermococcus kodakaraensis] ref YP_182485.1 tungsten-containing oxidoreductase [Thermococcus kodakaraensis] | | | | 1.2.7.- |
| 20209, 20210 | 48860188 | 39 | 3.00E-17 | Clostridium thermocellum ATCC 27405 | COG1539: Dihydropyrimidin aldolase [Clostridium thermocellum ATCC 27405] | | | | 4.1.2.25 |
| 2021, 2022 | 29350162 | 26 | 8.00E-17 | Bacteroides thetaiotaomicron VPI-5482 | putative cytosine-specific methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79859.1 putative cytosine-specific methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.1.1.73 |
| 20211, 20212 | ABP7815 0 | 51 | 7.00E-32 | | Desc:N. gonorrhoeae amino acid sequence SEQ ID 2830. Org:Neisseria gonorrhoeae | | | | |
| 20215, 20216 | 21228805 | 29 | 1.00E-07 | Methanosarcina mazei Go1 | type I restriction-modification system specificity subunit [Methanosarcina mazei Go1] gb AAM323399.1 type I restriction-modification system specificity subunit [Methanosarcina mazei Go1] | | | | 3.1.21.3 |
| 20217, 20218 | 48856451 | 50 | 8.00E-72 | Cytophaga hutchinsonii | COG0040: ATP phosphoribosyltransferase [Cytophaga hutchinsonii] | | | | 2.4.2.17 |
| 20223, 20224 | 53712340 | 62 | 3.00E-60 | Bacteroides fragilis YCH46 | hypothetical protein BF1048 [Bacteroides fragilis YCH46] dbj BAD47798.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 20225, 20226 | 48856445 | 46 | 2.00E-43 | Cytophaga hutchinsonii | hypothetical protein Chut02000167 [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|--|---|--|----|----------|---------------|
| 2023, | 42521765 | 58 | 3.00E-63 | Bdellovibrio bacteriovorus HD100 | Acetylornithine/succinyl-diaminopimelate aminotransferase [Bdellovibrio bacteriovorus HD100] emb CAE77799.1] | | | | 2.6.1.11 |
| 20231, | 48856539 | 30 | 4.00E-14 | Cytophaga hutchinsonii | COG0791: Cell wall-associated hydrolases (invasion-associated proteins) [Cytophaga hutchinsonii] | | | | |
| 20233, | 29348479 | 47 | 3.00E-60 | Bacteroides thetaiotaomicron VPI-5482 | Smf protein DNA processing chain A [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78176.1] Smf protein DNA processing chain A [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 20235, | 48854415 | 61 | 3.00E-77 | Cytophaga hutchinsonii | COG3279: Response regulator of the LytR/AlgR family [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 20237, | 16077744 | 39 | 4.00E-21 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU06760 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12496.1] yeeA [Bacillus subtilis subsp. subtilis str. 168] pir E69792 conserved hypothetical protein yeeA - Bacillus subtilis | | | | |
| 20239, | 48853949 | 60 | 1.00E-43 | Cytophaga hutchinsonii | COG0187: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit [Cytophaga hutchinsonii] | | | | 5.99.1.3 |
| 20241, | 48854339 | 75 | 1.00E-53 | Cytophaga hutchinsonii | COG0178: Exonuclease ATPase subunit [Cytophaga hutchinsonii] | Desc: Genomic sequence of Lactococcus lactis IL1403. | 81 | 2.00E-11 | |
| 20243, | 48861416 | 77 | 3.00E-43 | Microbulbifer degradans 2-40 | COG0177: Predicted EndoIII-related endonuclease [Microbulbifer degradans 2-40] | | | | 4.2.99.1 8 |
| 20245, | 53711581 | 61 | 9.00E-31 | Bacteroides fragilis YCH46 | ribonuclease HII [Bacteroides fragilis YCH46] dbj BAD47039.1] ribonuclease HII [Bacteroides fragilis YCH46] | | | | 3.1.26.4 |
| 20249, | 46132462 | 74 | 1.00E-104 | Ralstonia eutropha JMP134 | COG0714: MoxR-like ATPases [Ralstonia eutropha JMP134] | Pseudomonas aeruginosa PAO1, section 259 of 529 of the complete genome | 80 | 5.00E-32 | |
| 2025, | 53763802 | 33 | 4.00E-25 | Anabaena variabilis ATCC 29413 | COG2319: FOG: WD40 repeat [Anabaena variabilis ATCC 29413] | | | | 2.7.1.37 |
| 20251, | 31790565 | 61 | 3.00E-73 | marine bacterium P99-3 | phytoene desaturase [marine bacterium P99-3] | | | | |
| 20253, | AAV7501 | 44 | 4.00E-29 | | Desc: Neisseria meningitidis ORF 525 protein sequence SEQ ID NO:1498. Org: Neisseria meningitidis | | | | |
| 20255, | 29346875 | 28 | 2.00E-18 | Bacteroides thetaiotaomicron VPI-5482 | putative ABC transporter permease [Bacteroides thetaiotaomicron VPI-5482] gb AAO76572.1] putative ABC transporter permease [Bacteroides thetaiotaomicron VPI-5482] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|---|----------|---------------|--|
| 20257, 20258 | 37912867 | 42 | 1.00E-20 | uncultured marine proteobacterium ANT8C10 | predicted acetyltransferase [uncultured marine proteobacterium ANT8C10] | | | | |
| 20259, 20260 | 2411488 | 68 | 9.00E-94 | Klebsiella pneumoniae | HsdR [Klebsiella pneumoniae] pir[T30329 hsdR protein - Klebsiella pneumoniae] | S. enterica hsdM, hsdS & hsdR genes 83 | 6.00E-10 | 3.1.21.3 | |
| 20263, 20264 | 53689679 | 35 | 4.00E-43 | Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293 | COG1540: Uncharacterized proteins, homologs of lactam utilization protein B [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293] | | | | |
| 20265, 20266 | 39997172 | 35 | 5.00E-11 | Geobacter sulfurreducens PCA | PPIC-type PPIASE domain protein [Geobacter sulfurreducens PCA] | | | | |
| 2027, 2028 | 48854724 | 37 | 2.00E-25 | Cytophaga hutchinsonii | gb AAR35450.1 PPIC-type PPIASE domain protein [Geobacter sulfurreducens PCA] | | | 5.2.1.8 | |
| 20277, 20278 | 16125143 | 31 | 1.00E-11 | Caulobacter crescentus CB15 | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- | |
| 20279, 20280 | 56677851 | 30 | 3.00E-21 | Silicibacter pomeroiyi DSS-3 | hypothetical protein CO0890 [Caulobacter crescentus CB15] | | | | |
| 20283, 20284 | 48855019 | 47 | 2.00E-31 | Cytophaga hutchinsonii | gb AAK22875.1 hypothetical protein [Caulobacter crescentus CB15] pir G87359 hypothetical protein CO0890 [imported] - Caulobacter crescentus site-specific recombinase, resolvase family [Silicibacter pomeroiyi DSS-3] ref YP_166469.1 site-specific recombinase, resolvase family [Silicibacter pomeroiyi DSS-3] | | | 2.4.1.18 2 | |
| 2029, 2030 | 45659045 | 56 | 1.00E-54 | Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130 | COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii] | | | | |
| 20291, 20292 | 48854156 | 41 | 9.00E-46 | Cytophaga hutchinsonii | Inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] ref NP_714220.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar Lai str. 56601] gb AAN51238.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar lai str. 56601] sp Q8E221 IPYR_LEPIN Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (Pase) gb AAS71768.1 inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] | | | 3.6.1.1 | |
| 20293, 20294 | 53712087 | 36 | 7.00E-42 | Bacteroides fragilis YCH46 | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] putative transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD47545.1 putative transcriptional regulator [Bacteroides fragilis YCH46] | | | 2.7.3.- | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|----------|
| 20295, 20296 | 34397292 | 50 | 6.00E-53 | Porphyromonas gingivalis W83 | translation elongation factor P [Porphyromonas gingivalis W83] ref NP_905456.1 translation elongation factor P [Porphyromonas gingivalis W83] sp Q7MV32 EFP2 PORGI Elongation factor P 2 (EF-P 2) | Union yellows phytoplasma OY-M DNA, complete genome | 91 | 4.00E-10 | |
| 20299, 20300 | 15894950 | 57 | 6.00E-86 | Clostridium acetobutylicum ATCC 824 | Large subunit of NADH-dependent glutamate synthase [Clostridium acetobutylicum ATCC 824] gb AAK79639.1 Large subunit of NADH- dependent glutamate synthase [Clostridium acetobutylicum ATCC 824] pir D97106 large chain of NADH-dependent glutamate synthase CAC1673 [Imported] - Clostridium acetobutylicum | Clostridium saccharobutylicum glutamate synthase operon, complete sequence | 83 | 2.00E-10 | 1.4.1.13 |
| 20305, 20306 | 31195963 | 63 | 4.00E-70 | Anopheles gambiae | ENSANGP00000000454 [Anopheles gambiae] | | | | 4.2.1.22 |
| 20307, 20308 | 53759487 | 25 | 1.00E-15 | Methylobacillus flagellatus KT | COG1587: Uroporphyrinogen-III synthase [Methylobacillus flagellatus KT] | | | | 4.2.1.75 |
| 2031, 2032 | 45160119 | 54 | 1.00E-45 | Tetrahymena thermophila | mitogen activated protein kinase 4 [Tetrahymena thermophila] | | | | 2.7.1.- |
| 20311, 20312 | 53714594 | 30 | 2.00E-22 | Bacteroides fragilis YCH46 | LacI family transcriptional regulator [Bacteroides fragilis YCH46] db BAD50052.1 LacI family transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 20315, 20316 | 48856573 | 61 | 3.00E-31 | Cytophaga hutchinsonii | COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii] | | | | 2.1.1.63 |
| 20317, 20318 | 28876472 | 31 | 8.00E-16 | Streptococcus pyogenes phage 315.6 | putative DNA primase/helicase [Streptococcus pyogenes phage 315.6] ref NP_801685.1 putative DNA primase (phage associated) [Streptococcus pyogenes SSI-1] ref YP_059353.1 virulence-associated protein E [Streptococcus pyogenes MGAS10394] ref NP_665246.1 putative DNA primase/helicase - phage associated [Streptococcus pyogenes MGAS315] gb AA786170.1 virulence-associated protein E [Streptococcus pyogenes MGAS10394] gb AAM80049.1 putative DNA primase/helicase - phage associated [Streptococcus pyogenes phage 315.6] db BAC63518.1 putative DNA primase (phage associated) [Streptococcus pyogenes SSI-1] | | | | |
| 20321, 20322 | 56460815 | 57 | 2.00E-24 | Idiomarina loihlensis L2TR | Anti-anti-sigma regulatory factor [Idiomarina loihlensis L2TR] gb AAV82547.1 Anti-anti-sigma regulatory factor [Idiomarina loihlensis L2TR] | Idiomarina loihlensis L2TR, complete genome | 88 | 9.00E-07 | |
| 20327, 20328 | 48853783 | 56 | 5.00E-37 | Cytophaga hutchinsonii | COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] | | | | 2.7.7.7 |
| 20329, 20330 | 54031199 | 49 | 2.00E-51 | Polaromonas sp. JS666 | COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Polaromonas sp. JS666] | | | | 6.2.1.3 |
| 20331, 20332 | 31194819 | 59 | 6.00E-78 | Anopheles gambiae | ENSANGP000000002020 [Anopheles gambiae] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|---------------|
| 20333, 20334 | 34398069 | 29 | 2.00E-10 | Porphyrionas gingivalis W83 | NADH:ubiquinone oxidoreductase, C subunit [Porphyrionas gingivalis W83] ref NP_096230.1 NADH:ubiquinone oxidoreductase, C subunit [Porphyrionas gingivalis W83] | | | | |
| 20335, 20336 | 21673146 | 54 | 3.00E-35 | Chlorobium tepidum TLS | dTDP-4-dehydrohamnose reductase [Chlorobium tepidum TLS] gb AAM71553.1 dTDP-4-dehydrohamnose reductase [Chlorobium tepidum TLS] | | | | 1.1.1.13 3 |
| 20337, 20338 | 49482438 | 46 | 6.00E-21 | Staphylococcus aureus subsp. aureus MRSA252 | hypothetical protein SAR0197 [Staphylococcus aureus subsp. aureus MRSA252] emb CAG39224.1 hypothetical protein [Staphylococcus aureus subsp. aureus MRSA252] | | | | |
| 20339, 20340 | 37812000 | 37 | 1.00E-18 | Aeromonas hydrophila | hypothetical protein [Aeromonas hydrophila] | | | | |
| 20341, 20342 | 53714775 | 34 | 6.00E-33 | Bacteroides fragilis YCH46 | transcription regulator [Bacteroides fragilis YCH46] db BAD50233.1 transcription regulator [Bacteroides fragilis YCH46] | | | | |
| 20343, 20344 | 23126871 | 36 | 7.00E-22 | Nostoc punctiforme PCC 73102 | COG0514: Superfamily II DNA helicase [Nostoc punctiforme PCC 73102] | | | | 3.6.1.- |
| 20347, 20348 | 45916344 | 50 | 1.00E-48 | Mesorhizobium sp. BNC1 | COG2220: Predicted Zn-dependent hydrolases of the beta-lactamase fold [Mesorhizobium sp. BNC1] | | | | |
| 2035, 2036 | 29347576 | 46 | 1.00E-41 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77273.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |
| 20351, 20352 | 57159654 | 30 | 3.00E-08 | Thermococcus kodakaraensis | predicted ATP-dependent endonuclease, OLD family [Thermococcus kodakaraensis] ref YP_183808.1 predicted ATP-dependent endonuclease, OLD family [Thermococcus kodakaraensis] | | | | |
| 20355, 20356 | 53797086 | 36 | 5.00E-44 | Chloroflexus aurantiacus | COG0814: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus] | | | | |
| 20359, 20360 | 45512718 | 41 | 3.00E-15 | Synechococcus elongatus PCC 7942 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Synechococcus elongatus PCC 7942] | | | | |
| 20363, 20364 | 48854281 | 26 | 3.00E-16 | Cytophaga hutchinsonii | COG3182: Uncharacterized iron-regulated membrane protein [Cytophaga hutchinsonii] | | | | 1.8.1.2 |
| 20367, 20368 | 30249527 | 50 | 3.00E-27 | Nitrosomonas europaea ATCC 19718 | putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718] | | | | |
| 20369, 20370 | 30249527 | 50 | 3.00E-27 | Nitrosomonas europaea ATCC 19718 | putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718] | | | | |

| | | | | | | | | |
|---|--|--|--|--|---|---|----------------|----------|
| 20373, 20374 20375, 20376 | 37678997 2879819 | 72 47 | 9.00E-42 3.00E-45 | Vibrio vulnificus YJ016 Pseudoalteromonas haloplanktis | type I site-specific restriction-modification system, R (restriction) subunit [Vibrio vulnificus YJ016] dbj BAC93577.1 type I site-specific restriction- modification system, R (restriction) subunit [Vibrio vulnificus YJ016] hypothetical protein [Pseudoalteromonas haloplanktis] | Mycoplasma mobile 163K complete genome | 85 4.00E-09 | 3.1.21.3 |
| 20377, 20378 | 30268405 | 99 | 2.00E-95 | Acinetobacter lwoffii | putative cation efflux system protein [Acinetobacter lwoffii] | Acinetobacter lwoffii plasmid pKLH202 including an aberrant mercury resistance transposon and insertion sequences IS1006.1, IS1006.D1 and IS1009 | 99 0 | 2.1.1.52 |
| 20379, 20380 20381, 20382 20383, 20384 20385, 20386 20389, 20390 20391, 20392 20393, 20394 | 53717736 48853602 48855539 48855760 48853597 48856222 53734766 | 40 45 67 65 55 25 39 | 3.00E-09 3.00E-43 4.00E-71 2.00E-67 4.00E-32 8.00E-07 7.00E-35 | Burkholderia pseudomallei K96243 Cytophaga hutchinsonii Cytophaga hutchinsonii Cytophaga hutchinsonii Crocospaera watsonii WH 8501 | putative cation efflux system protein [Acinetobacter lwoffii] spermidine n(1)-acetyltransferase [Burkholderia pseudomallei K96243] emb CAH34080.1 spermidine n(1)-acetyltransferase [Burkholderia pseudomallei K96243] COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii] COG0142: Geranylgeranyl pyrophosphate synthase [Cytophaga hutchinsonii] COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii] COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] COG0438: Glycosyltransferase [Cytophaga hutchinsonii] COG0857: BioD-like N-terminal domain of phosphotransacetylase [Crocospaera watsonii WH 8501] acetate kinase [Thermotoga maritima MSB8] gb AAD35363.1 acetate kinase [Thermotoga maritima MSB8] sp Q9WYB1 ACKA_THEME Acetate kinase (Acetokinase) pir H72397 acetate kinase - Thermotoga maritima (strain MSB8) | | | |
| 20395, 20396 | 15643044 | 50 | 4.00E-53 | Thermotoga maritima MSB8 | poly(polyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 poly(polyglutamate synthase [Bacteroides fragilis YCH46]) | | | 2.7.2.1 |
| 20399, 20400 | 53714264 | 59 | 1.00E-66 | Bacteroides fragilis YCH46 | | | | 6.3.2.17 |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|---|--|--|--|----------|
| 20401, | 48854489 | 34 | 8.00E-14 | Cytophaga hutchinsonii | hypothetical protein Chut02002688 [Cytophaga hutchinsonii] | | | | |
| 20402 | | | | Nitrosomonas europaea ATCC 19718 | putative transposase [Nitrosomonas europaea ATCC 19718] | | | | |
| 20403, | 30249527 | 47 | 2.00E-25 | | emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718] | | | | |
| 20404 | | | | | | | | | |
| 20405, | 53714651 | 46 | 3.00E-58 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] | | | | 3.1.1.61 |
| 20406 | | | | | | | | | |
| 20407, | | | | Thiobacillus denitrificans ATCC 25259 | COG2189: Adenine specific DNA methylase Mod [Thiobacillus denitrificans ATCC 25259] | | | | 2.1.1.72 |
| 20408 | 52006160 | 38 | 2.00E-52 | | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Exiguobacterium sp. 255-15] | | | | |
| 20409, | 46114055 | 37 | 7.00E-19 | Exiguobacterium sp. 255-15 | Desc:Putative P. abyssal orotidine-5'-phosphate decarboxylase. | | | | |
| 2041, | AAB9655 | 29 | 1.00E-19 | | Org:Pyrococcus abyssi | | | | 4.1.1.23 |
| 2042 | 2 | | | | | | | | |
| 20411, | | | | Tetraodon | unnamed protein product [Tetraodon nigroviridis] | | | | |
| 20412 | 47226257 | 26 | 4.00E-14 | Tetraodon nigroviridis | | | | | |
| 20417, | | | | Ralstonia metallidurans CH34 | hypothetical protein Reut02000359 [Ralstonia metallidurans CH34] | | | | |
| 20418 | 48771615 | 25 | 5.00E-09 | | | | | | |
| 20419, | | | | Flavobacterium johnsoniae | GldD [Flavobacterium johnsoniae] | | | | |
| 20420 | 9837393 | 50 | 3.00E-42 | | | | | | |
| | | | | | | | | | |
| 20421, | | | | | | | | | |
| 20422 | 48854355 | 66 | 8.00E-44 | Cytophaga hutchinsonii | COG1200: RecG-like helicase [Cytophaga hutchinsonii] | | | | |
| 20425, | | | | | | | | | |
| 20426 | 48854339 | 62 | 6.00E-92 | Cytophaga hutchinsonii | COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii] | | | | |
| | | | | | | | | | |
| 20427, | | | | | | | | | |
| 20428 | 48854339 | 75 | 2.00E-64 | Cytophaga hutchinsonii | COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii] | | | | |
| 20429, | | | | | | | | | |
| 20430 | 48856125 | 44 | 9.00E-37 | Cytophaga hutchinsonii | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] | | | | |
| | | | | | | | | | |
| 20427, | | | | | | | | | |
| 20428 | 48854339 | 75 | 2.00E-64 | Cytophaga hutchinsonii | COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii] | | | | |
| 20429, | | | | | | | | | |
| 20430 | 48856125 | 44 | 9.00E-37 | Cytophaga hutchinsonii | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] | | | | |
| | | | | | | | | | |
| 2043, | | | | | | | | | |
| 2044 | 15899135 | 33 | 2.00E-09 | Sulfolobus solfataricus P2 | hypothetical protein SSO2382 [Sulfolobus solfataricus P2] gb AAK42530.1 Conserved hypothetical protein [Sulfolobus solfataricus P2] pir C90409 conserved hypothetical protein [imported] - Sulfolobus solfataricus | | | | |
| 20431, | | | | | | | | | |
| 20432 | 50590629 | 46 | 1.00E-43 | Streptococcus suis 89/1591 | COG4922: Uncharacterized protein conserved in bacteria [Streptococcus suis 89/1591] | | | | |

| | | | | | | | | |
|--------|----------|----|----------|---|---|---|----|----------|
| 20433, | 52008442 | 39 | 2.00E-10 | Thiobacillus denitrificans ATCC 25259 | COG4301: Uncharacterized conserved protein [Thiobacillus denitrificans ATCC 25259] | | | |
| 20437, | | | | Cytophaga hutchinsonii | COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii] | | | |
| 20438, | 48854312 | 31 | 1.00E-21 | Flavobacterium | | | | |
| 20441, | | | | johnsoniae | GldE [Flavobacterium johnsoniae] | | | |
| 20442 | 12024595 | 65 | 2.00E-64 | | | Desc:Listeria Innocua DNA sequence #684. Org:Listeria Innocua | 90 | 1.00E-06 |
| 20443, | | | | Flavobacterium | | | | |
| 20444 | 12024595 | 65 | 2.00E-56 | johnsoniae | GldE [Flavobacterium johnsoniae] | | | |
| 20445, | | | | Chlorobium | phosphoserine phosphatase [Chlorobium tepidum TLS] gb AAM71421.1 | | | 3.1.3.3 |
| 20446 | 21673014 | 55 | 1.00E-26 | tepidum TLS | phosphoserine phosphatase [Chlorobium tepidum TLS] | | | |
| 20447, | | | | Chlorobium | phosphoserine phosphatase [Chlorobium tepidum TLS] gb AAM71421.1 | | | 3.1.3.3 |
| 20448 | 21673014 | 55 | 1.00E-26 | tepidum TLS | phosphoserine phosphatase [Chlorobium tepidum TLS] | | | |
| 20449, | AAG3969 | | | | Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 49152. | | | |
| 20450 | 3 | 58 | 2.00E-39 | | Org:Arabidopsis thaliana | | | 1.6.4.- |
| 20451, | | | | Bacteroides | mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 20452 | 29345783 | 63 | 1.00E-39 | thetaiotaomicron VPI-5482 | gb AAO75480.1 mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482] | | | 5.3.1.8 |
| 20453, | | | | Bacteroides fragilis | exonuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 | | | |
| 20454 | 53713904 | 55 | 2.00E-56 | YCH46 | exonuclease ABC subunit A [Bacteroides fragilis YCH46] | | | |
| 20455, | | | | Cytophaga | | | | |
| 20456 | 48856624 | 33 | 6.00E-07 | hutchinsonii | COG5520: O-Glycosyl hydrolase [Cytophaga hutchinsonii] | | | |
| | | | | Xanthomonas | Mg-protoporphyrin IX monomethyl ester oxidative cyclase [Xanthomonas axonopodis pv. citri str. 306] gb AAM36569.1 Mg-protoporphyrin IX monomethyl ester oxidative cyclase [Xanthomonas axonopodis pv. citri str. 306] | | | 1.97.1.4 |
| 20457, | 21242451 | 30 | 5.00E-26 | str. 306 | putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] | | | |
| 20458 | | | | Bacteroides fragilis | dbj BAD49829.1 putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] | | | |
| 20459, | | | | YCH46 | | | | |
| 20460 | 53714371 | 23 | 2.00E-11 | | | | | |
| 20461, | | | | Cytophaga | | | | |
| 20462 | 48855075 | 45 | 7.00E-25 | hutchinsonii | COG0302: GTP cyclohydrolase I [Cytophaga hutchinsonii] | | | 3.5.4.16 |
| 20463, | | | | Cytophaga | COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Cytophaga hutchinsonii] | | | 1.1.1.18 |
| 20464 | 48854735 | 42 | 9.00E-35 | hutchinsonii | | | | 4 |
| 20465, | | | | Cytophaga | COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Cytophaga hutchinsonii] | | | 1.1.1.18 |
| 20466 | 48854735 | 42 | 9.00E-35 | hutchinsonii | | | | 4 |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---------------------------------------|--|--|---|--|---------|----------------------|
| 20467, 20468 | 53713193 | 25 | 1.00E-10 | Bacteroides fragilis YCH46 | hypothetical protein BF1903 [Bacteroides fragilis YCH46] dbj BAD48651.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | | |
| 20469, 20470 | 29347576 | 43 | 2.00E-47 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77273.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] | | : | | 2.7.3.- | |
| 20471, 20472 | 29349611 | 46 | 6.00E-61 | Bacteroides thetaiotaomicron VPI-5482 | tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79308.1 tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A018 IMIAA_BACTN tRNA delta(2)-isopentenylpyrophosphate transferase (IPP transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase) (IPTase) (IPT) | | | | 2.5.1.8 | |
| 20475, 20476 | 12082815 | 45 | 8.00E-50 | Streptomyces venezuelae | cystathionine beta-synthase [Streptomyces venezuelae] | | | | | 4.2.1.22 |
| 20481, 20482 | 48860637 | 54 | 7.00E-41 | Microbulbifer degradans 2-40 | COG1638: TRAP-type C4-dicarboxylate transport system, periplasmic component [Microbulbifer degradans 2-40] | | | | | |
| 20483, 20484 | 52007804 | 39 | 3.00E-38 | Thiobacillus denitrificans ATCC 25259 | hypothetical protein TdenA01000099 [Thiobacillus denitrificans ATCC 25259] | | | | | |
| 20489, 20490 | 48782075 | 28 | 3.00E-15 | Burkholderia fungorum LB400 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Burkholderia fungorum LB400] | | | | | 2.-.-.- |
| 20491, 20492 | 48853898 | 48 | 2.00E-50 | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | | | 2.1.1.- |
| 20493, 20494 | 48853898 | 48 | 2.00E-49 | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | | | 2.1.1.- |
| 20495, 20496 | ABB4747 | 37 | 8.00E-33 | | Desc:Listeria monocytogenes protein #181. Org:Listeria monocytogenes | | | | | 1.8.-.- |
| 20497, 20498 | 53687332 | 27 | 9.00E-07 | Nostoc punctiforme PCC 73102 | COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102] | | | | | |
| 20499, 20500 | 48862689 | 50 | 3.00E-37 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02001782 [Microbulbifer degradans 2-40] | | | | | |
| 205, 206 | 15894850 | 67 | 2.00E-84 | Clostridium acetobutylicum ATCC 824 | Fructose-1,6-bisphosphatase (Yyde B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] gb AAK79539.1 Fructose-1,6-bisphosphatase (Yyde B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] pir JH97093 fructose-bisphosphatase (EC 3.1.3.11) [similarity] - Clostridium acetobutylicum | Desc:Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1485. Org:Staphylococcus epidermidis | | | | 85 5.00E-13 3.1.3.11 |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|---------------|
| 20503, 20504 | 51246763 | 40 | 1.00E-48 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb[CAG37640.1] conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 20505, 20506 | 51246763 | 37 | 1.00E-35 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb[CAG37640.1] conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 20507, 20508 | 34762717 | 26 | 2.00E-09 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | TETRA TRICOPEPTIDE REPEAT FAMILY PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24895.1 TETRA TRICOPEPTIDE REPEAT FAMILY PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | |
| 20509, 20510 | 6498214 | 42 | 7.00E-21 | Agrobacterium tumefaciens | tior41 [Agrobacterium tumefaciens] ref NP_053281.1 Hypothetical gene [Agrobacterium tumefaciens] | | | |
| 2051, 2052 | 21673647 | 59 | 2.00E-35 | Chlorobium tepidum TLS | peptide chain release factor 3 [Chlorobium tepidum TLS] gb AAM72054.1 peptide chain release factor 3 [Chlorobium tepidum TLS] | | | |
| 20511, 20512 | 48854805 | 36 | 3.00E-13 | Cytophaga hutchinsonii | hypothetical protein Chui02002487 [Cytophaga hutchinsonii] | | | |
| 20513, 20514 | 29349663 | 56 | 8.00E-48 | Bacteroides thetaiotaomicron VPI-5482 | DNA replication and repair protein RecF, ABC family ATPase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79360.1 DNA replication and repair protein RecF, ABC family ATPase [Bacteroides thetaiotaomicron VPI-5482] sp Q89ZW6 REC_F_BACTN DNA replication and repair protein recF | | | |
| 20515, 20516 | 48854136 | 23 | 4.00E-11 | Cytophaga hutchinsonii | COG1566: Multidrug resistance efflux pump [Cytophaga hutchinsonii] | | | |
| 20517, 20518 | 48854136 | 25 | 7.00E-11 | Cytophaga hutchinsonii | COG1566: Multidrug resistance efflux pump [Cytophaga hutchinsonii] | | | |
| 20521, 20522 | 53715653 | 26 | 1.00E-08 | Bacteroides fragilis YCH46 | hypothetical protein BF4373 [Bacteroides fragilis YCH46] dbj BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 20525, 20526 | 52853848 | 64 | 3.00E-29 | Psychrobacter sp. 273-4 | COG0818: Diacylglycerol kinase [Psychrobacter sp. 273-4] | | | 2.7.1.10 7 |
| 20527, 20528 | 48854088 | 31 | 2.00E-10 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | |
| 20529, 20530 | 48854088 | 32 | 1.00E-12 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | |
| 2053, 2054 | 50083323 | 25 | 2.00E-14 | Acinetobacter sp. ADP1 | putative amidohydrolase (isochorismatase) [Acinetobacter sp. ADP1] emb CAG67011.1 putative amidohydrolase (isochorismatase) | | | 3.3.2.1 |
| 20531, 20532 | 53712055 | 43 | 1.00E-46 | Bacteroides fragilis YCH46 | [Acinetobacter sp. ADP1] putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46] | | | 3.5.1.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|----------|
| 20533, 20534 | 37519796 | 26 | 7.00E-07 | Gloebacter violaceus PCC 7421 | hypothetical protein glr0227 [Gloebacter violaceus PCC 7421] dbj BAC88168.1 glr0227 [Gloebacter violaceus PCC 7421] | | | | |
| 20535, 20536 | 51245433 | 32 | 5.00E-19 | Desulfotalea psychrophila LSv54 | hypothetical protein DP1581 [Desulfotalea psychrophila LSv54] emb CAG36310.1 unknown protein [Desulfotalea psychrophila LSv54] | | | | |
| 20537, 20538 | 33595943 | 41 | 1.00E-40 | Bordetella parapertussis 12822 | hypothetical protein BPP1276 [Bordetella parapertussis 12822] emb CAE36577.1 conserved hypothetical protein [Bordetella parapertussis] | | | | |
| 20539, 20540 | 33595943 | 41 | 1.00E-40 | Bordetella parapertussis 12822 | hypothetical protein BPP1276 [Bordetella parapertussis 12822] emb CAE36577.1 conserved hypothetical protein [Bordetella parapertussis] | | | | |
| 20543, 20544 | 48854899 | 55 | 2.00E-51 | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | | 2.1.1.- |
| 20545, 20546 | 26989001 | 28 | 3.00E-16 | Pseudomonas putida KT2440 | hypothetical protein PP2277 [Pseudomonas putida KT2440] gb AAAN67890.1 hypothetical protein [Pseudomonas putida KT2440] Methylated DNA-protein cysteine methyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK81195.1 Methylated DNA-protein cysteine methyltransferase [Clostridium acetobutylicum ATCC 824] pir H97300 methylated DNA-protein cysteine methyltransferase [imported] - Clostridium acetobutylicum | | | | 2.1.1.63 |
| 20553, 20554 | 48854014 | 54 | 8.00E-52 | Cytophaga hutchinsonii | COG1104: Cysteine sulfinate desulfinate/cysteine desulfurase and related enzymes [Cytophaga hutchinsonii] | | | | 4.4.1.- |
| 20555, 20556 | 48853459 | 42 | 2.00E-13 | Cytophaga hutchinsonii | COG0247: Fe-S oxidoreductase [Cytophaga hutchinsonii] | | | | |
| 20557, 20558 | 29345486 | 53 | 3.00E-45 | Bacteroides thetaiotaomicron VPI-5482 | transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75183.1 transposase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 20559, 20560 | 48855592 | 25 | 1.00E-09 | Cytophaga hutchinsonii | COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Cytophaga hutchinsonii] | | | | |
| 20561, 20562 | 15608970 | 54 | 2.00E-10 | Mycobacterium tuberculosis H37Rv | Possible haloalkane dehalogenase [Mycobacterium tuberculosis H37Rv] ref NP_855516.1 Possible haloalkane dehalogenase [Mycobacterium bovis AF2122/97] ref NP_336339.1 haloalkane dehalogenase [Mycobacterium tuberculosis CDC1551] gb AAK46153.1 haloalkane dehalogenase [Mycobacterium tuberculosis CDC1551] sp P64303 DHA2_MYCTU Haloalkane dehalogenase 2 pir B70722 hypothetical protein Rv1833c - Mycobacterium tuberculosis (strain H37Rv) emb CAB01469.1 Possible haloalkane dehalogenase [Mycobacterium tuberculosis H37Rv] emb CAD94567.1 Possible haloalkane dehalogenase [Mycobacterium bovis AF2122/97] sp P64304 DHA2_MYCBO Haloalkane dehalogenase 2 | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|---|---|--|--|--|----------|
| 20563, | 48854215 | 43 | 5.00E-50 | Cytophaga hutchinsonii | COG1646: Predicted phosphate-binding enzymes, TIM-barrel fold [Cytophaga hutchinsonii] | | | | |
| 20564 | | | | | flavoprotein NADH-dependent oxidoreductase [Azoarcus sp. EbN1] emb CAI08136.1 Flavoprotein NADH-dependent oxidoreductase [Azoarcus sp. EbN1] | | | | 1.--- |
| 20565, | 56477448 | 51 | 4.00E-75 | Azoarcus sp. EbN1 | adenylate cyclase-related protein [Shewanella oneidensis MR-1] gb AA054394.1 adenylate cyclase-related protein [Shewanella oneidensis MR-1] | | | | 4.6.1.1 |
| 20567, | 24372907 | 29 | 9.00E-14 | Shewanella oneidensis MR-1 | COG2141: Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases [Rubrobacter xylanophilus DSM 9941] | | | | 1.5.99.9 |
| 20568 | 53766201 | 42 | 1.00E-49 | Rubrobacter xylanophilus DSM 9941 | pyruvate carboxylase [Geobacillus stearothermophilus] | | | | 6.4.1.1 |
| 20573, | 1695686 | 45 | 2.00E-27 | Geobacillus stearothermophilus | pyruvate carboxylase [Geobacillus stearothermophilus] | | | | 6.4.1.1 |
| 20575, | | | | Geobacillus stearothermophilus | pyruvate carboxylase [Geobacillus stearothermophilus] | | | | 6.4.1.1 |
| 20576 | 1695686 | 42 | 8.00E-40 | Geobacillus stearothermophilus | COG1533: DNA repair photolyase [Cytophaga hutchinsonii] | | | | |
| 20577, | | | | Cytophaga hutchinsonii | COG1533: DNA repair photolyase [Cytophaga hutchinsonii] | | | | |
| 20578 | 48856872 | 52 | 9.00E-70 | Cytophaga hutchinsonii | COG1533: DNA repair photolyase [Cytophaga hutchinsonii] | | | | |
| 20579, | | | | Cytophaga hutchinsonii | putative DNA-binding protein [Erwinia carotovora subsp. atroseptica SCR1043] emb CAG75811.1 putative DNA-binding protein [Erwinia carotovora subsp. atroseptica SCR1043] | | | | |
| 20580 | 48856872 | 54 | 1.00E-66 | Erwinia carotovora subsp. atroseptica SCR1043 | COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii] | | | | |
| 20585, | | | | Erwinia carotovora subsp. atroseptica SCR1043 | COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii] | | | | |
| 20586 | 50121835 | 48 | 1.00E-34 | Cytophaga hutchinsonii | COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii] | | | | |
| 20589, | 48855375 | 41 | 7.00E-17 | Cytophaga hutchinsonii | type I restriction enzyme R protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58658.1 type I restriction enzyme R protein [Vibrio parahaemolyticus] | | | | |
| 20590 | | | | Cytophaga hutchinsonii | hypothetical protein nfa45100 [Nocardia farcinica IFM 10152] dbj BAD59361.1 hypothetical protein [Nocardia farcinica IFM 10152] | | | | |
| 20591, | | | | Cytophaga hutchinsonii | hypothetical protein nfa45100 [Nocardia farcinica IFM 10152] dbj BAD59361.1 hypothetical protein [Nocardia farcinica IFM 10152] | | | | |
| 20592 | 48855375 | 41 | 2.00E-16 | Cytophaga hutchinsonii | Transcriptional regulatory protein degU gb AAC41439.1 transcriptional activator protein pir J9835 transcription activator - Bacillus brevis | | | | 3.1.1.61 |
| 20595, | | | | Vibrio parahaemolyticus RIMD 2210633 | | | | | |
| 20596 | 28897169 | 83 | 1.00E-120 | Vibrio parahaemolyticus RIMD 2210633 | | | | | |
| 20601, | | | | Nocardia farcinica IFM 10152 | | | | | |
| 20602 | 54026483 | 41 | 2.00E-48 | Nocardia farcinica IFM 10152 | | | | | |
| 20603, | | | | Nocardia farcinica IFM 10152 | | | | | |
| 20604 | 54026483 | 41 | 6.00E-49 | Nocardia farcinica IFM 10152 | | | | | |
| 20605, | | | | | | | | | |
| 20606 | 1706361 | 35 | 3.00E-20 | | | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|---------------------------------------|--|------------------------------|----|----------|----------|
| 20607, | 27365565 | 36 | 7.00E-21 | Vibrio vulnificus CMCP6 | Transcriptional regulator [Vibrio vulnificus CMCP6] ref NP_934898.1 | | | | 3.1.1.61 |
| 20608 | | | | | Transcriptional regulator [Vibrio vulnificus YJ016] gb AAO10620.1 | | | | |
| 20619, | | | | | Transcriptional regulator [Vibrio vulnificus CMCP6] gb AAK31574.1 | | | | |
| 20620 | 53711964 | 31 | 3.00E-09 | Bacteroides fragilis YCH46 | regulator [Vibrio vulnificus YJ016] | | | | |
| 20621, | | | | | aminopeptidase N [Bacteroides fragilis YCH46] dbj BAD47422.1 | | | | |
| 20622 | 48855430 | 25 | 8.00E-14 | Cytophaga hutchinsonii | aminopeptidase N [Bacteroides fragilis YCH46] | | | | |
| 20623, | | | | | hypothetical protein Chut02001765 [Cytophaga hutchinsonii] | | | | |
| 20624 | 48855430 | 25 | 1.00E-15 | Cytophaga hutchinsonii | hypothetical protein Chut02001765 [Cytophaga hutchinsonii] | | | | |
| 20625, | | | | | hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1 | Photobacterium profundum SS9 | | | |
| 20626 | 54302486 | 69 | 1.00E-102 | Photobacterium profundum SS9 | hypothetical maturase [Photobacterium profundum] | chromosome 2; segment 3/7 | 84 | 1.00E-14 | 2.7.7.49 |
| 20627, | | | | | COG2258: Uncharacterized protein conserved in bacteria [Nostoc punctiforme PCC 73102] | | | | |
| 20628 | 23124249 | 38 | 2.00E-39 | Nostoc punctiforme PCC 73102 | dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] | | | | |
| 20629, | | | | | dbj BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] | | | | 2.4.1.83 |
| 20630 | 53714728 | 67 | 4.00E-57 | Bacteroides fragilis YCH46 | response regulator [Porphyromonas gingivalis W83] ref NP_905164.1 | | | | |
| 2063, | | | | | response regulator [Porphyromonas gingivalis W83] | | | | |
| 2064 | 34396999 | 57 | 2.00E-53 | Porphyromonas gingivalis W83 | response regulator [Porphyromonas gingivalis W83] | | | | |
| 20639, | | | | | COG1475: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | | |
| 20640 | 48854401 | 49 | 3.00E-40 | Cytophaga hutchinsonii | inorganic pyrophosphatase [Methanosarcina acetivorans C2A] | | | | |
| 20641, | | | | | gb AAO06052.1 inorganic pyrophosphatase [Methanosarcina acetivorans str. C2A] sp Q8TMI3 PYR_METAC inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase) | | | | 3.6.1.1 |
| 20642 | 20091497 | 60 | 2.00E-49 | Methanosarcina acetivorans C2A | probable two-component response regulator [Chromobacterium violaceum ATCC 12472] ref NP_903174.1 probable two-component response regulator [Chromobacterium violaceum ATCC 12472] | | | | 2.7.3.- |
| 20645, | | | | | regulator [Chromobacterium violaceum ATCC 12472] | | | | |
| 20646 | 34104808 | 42 | 2.00E-30 | Chromobacterium violaceum ATCC 12472 | COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii] | | | | |
| 20649, | | | | | hutchinsonii | | | | |
| 20650 | 48853602 | 51 | 2.00E-69 | Cytophaga hutchinsonii | riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 20651, | | | | | gb AAO78833.1 riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 20652 | 29349136 | 44 | 1.00E-11 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein NMA0240 [Neisseria meningitidis Z2491] | | | | |
| 20653, | | | | | emb CAB83548.1 hypothetical protein NMA0240 [Neisseria meningitidis Z2491] pir D82018 hypothetical protein NMA0240 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) | | | | 3.4.13.9 |
| 20654 | 15793258 | 54 | 1.00E-38 | Neisseria meningitidis Z2491 | | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|---|--|--|--|----|----------------|
| 20657, | 46580426 | 72 | 1.00E-104 | Desulfovibrio vulgaris subsp. vulgaris str. | hypothetical protein DVU2019 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AA596494.1] conserved hypothetical protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | 3.4.21.5 3 |
| 20659, | 48854181 | 30 | 4.00E-17 | Cytophaga hutchinsonii | COG0323: DNA mismatch repair enzyme (predicted ATPase) [Cytophaga hutchinsonii] | | | | |
| 20663, | | | | Bacteroides fragilis | two-component system sensor histidine kinase [Bacteroides fragilis YCH46] | | | | 2.7.3.- |
| 20664 | 53715149 | 42 | 2.00E-32 | YCH46 | dbj BAD50607.1] two-component system sensor histidine kinase [Bacteroides fragilis YCH46] sp Q09408 PRX BACFR Sensor protein rprX | | | | |
| 20667, | 2500093 | 75 | 6.00E-69 | | RecA protein (Recombinase A) gb AAC44506.1] RecA | | | | |
| 20668 | | | | | COG0131: Imidazoleglycerol-phosphate dehydratase [Cytophaga hutchinsonii] | | | 91 | 2.00E-15 3.1.- |
| 20670 | 48855137 | 64 | 4.00E-27 | Cytophaga hutchinsonii | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | | 3.1.3.15 |
| 2067, | 48855683 | 56 | 4.00E-39 | Cytophaga hutchinsonii | phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 20671, | | | | Bacteroides thetaitaomicron | gb AAO76486.1] phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 20672 | 29346789 | 62 | 1.00E-56 | VPI-5482 | sp Q8A725 HIS4_BACTN 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase (Phosphoribosylformimino-5-aminimidazole carboxamide ribotide isomerase) | | | | 5.3.1.16 |
| 20673, | | | | Francisella | glycosyl transferases group 1 family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45868.1] glycosyl transferases group 1 family protein [Francisella tularensis subsp. tularensis] | | | | 2.-.-.- |
| 20674, | 56708297 | 29 | 1.00E-11 | tularensis subsp. tularensis Schu 4 | hypothetical protein Chut02000065 [Cytophaga hutchinsonii] | | | | |
| 20675, | 48856350 | 31 | 1.00E-15 | Cytophaga hutchinsonii | phenylacetyl-CoA ligase [Thermus thermophilus HB27] gb AAS0950.1] | | | | 6.2.1.30 |
| 20681, | | | | Thermus | phenylacetyl-CoA ligase [Thermus thermophilus HB27] | | | | |
| 20682 | 46198910 | 64 | 1.00E-52 | thermophilus HB27 | COG2304: Uncharacterized protein containing a von Willebrand factor type A (vWA) domain [Clostridium thermocellum ATCC 27405] | | | | |
| 20685, | | | | Clostridium | | | | | |
| 20686 | 48858283 | 57 | 1.00E-40 | ATCC 27405 | | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|---|---|----|----------|----------|
| 20687, | 53715279 | 43 | 1.00E-48 | Bacteroides fragilis YCH46 | putative methyltransferase [Bacteroides fragilis YCH46] dbj BAD50737.1 putative methyltransferase [Bacteroides fragilis YCH46] | | | | 2.4.99.- |
| 20688, | 53795507 | 59 | 2.00E-34 | Chloroflexus aurantiacus | COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Chloroflexus aurantiacus] | | | | 1.6.6.9 |
| 20691, | 50084651 | 38 | 2.00E-14 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD1480 [Acinetobacter sp. ADP1] emb CAG368339.1 hypothetical protein [Acinetobacter sp. ADP1] | | | | |
| 20692 | | | | Bacteroides thetaiotaomicron VPI-5482 | putative Tricorn-like protease [Bacteroides thetaiotaomicron VPI-5482] gb AAO76515.1 putative Tricorn-like protease [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 20693, | 29346818 | 28 | 7.00E-19 | | | | | | |
| 20694 | | | | Idiomarina loihiensis L2TR | Prolyl 4-hydroxylase alpha subunit homolog, 2OG-Fe(II) oxygenase family [Idiomarina loihiensis L2TR] gb AAV81086.1 Prolyl 4-hydroxylase alpha subunit homolog, 2OG-Fe(II) oxygenase family [Idiomarina loihiensis L2TR] | | | | |
| 20697, | 56459354 | 38 | 8.00E-29 | Cytophaga hutchinsonii | COG0644: Dehydrogenases (flavoproteins) [Cytophaga hutchinsonii] | | | | |
| 20698, | 48854244 | 35 | 2.00E-42 | | | | | | |
| 20700 | | | | Clostridium acetobutylicum ATCC 824 | Fructose-1,6-bisphosphatase (YyDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] gb AAK79539.1 Fructose-1,6-bisphosphatase (YyDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] pir H97093 fructose-bisphosphatase (EC 3.1.3.11) [similarity] - Clostridium acetobutylicum | Desc:Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1485. Org:Staphylococcus epidermidis | 88 | 4.00E-11 | 3.1.3.11 |
| 20701, | 15994850 | 69 | 9.00E-94 | Streptomyces avermitilis MA-4680 | putative type III polyketide synthase [Streptomyces avermitilis MA-4680] ref NP_828307.1 putative type III polyketide synthase [Streptomyces avermitilis MA-4680] dbj BAB69299.1 PhD homolog (polyketide synthase) [Streptomyces avermitilis] | | | | 2.3.1.74 |
| 20702 | 29610797 | 40 | 1.00E-19 | Oceanobacillus ihayensis HTE831 | hypothetical protein OB2278 [Oceanobacillus ihayensis HTE831] dbj BAC14234.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831] | | | | |
| 20705, | 23099733 | 42 | 8.00E-14 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714691.1 conserved hyperthermophilic protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51706.1 conserved hyperthermophilic protein [Leptospira interrogans serovar lai str. 56601] gb AAS72145.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | |
| 20709, | 45655699 | 35 | 2.00E-33 | Cytophaga hutchinsonii | hypothetical protein Chut02000044 [Cytophaga hutchinsonii] | | | | |
| 20710 | | | | | | | | | |
| 2071, | 48856332 | 52 | 2.00E-26 | | | | | | |
| 2072 | | | | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|---------------|
| 20713, 20714 | 16263990 | 37 | 1.00E-52 | Sinorhizobium meliloti 1021 | hypothetical protein Smb20252 [Sinorhizobium meliloti 1021] pir[B95872 hypothetical protein [Imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb[CAC48642.1] HYPOTHETICAL PROTEIN [Sinorhizobium meliloti 1021] | | | 1.12.99. 1 |
| 20715, 20716 | 49478996 | 40 | 1.00E-20 | Bacillus thuringiensis serovar konkukian str. 97-27 | beta-1,3-N-acetylglucosaminyltransferase [Bacillus thuringiensis serovar konkukian str. 97-27] gb/AA761198.1 beta-1,3-N- acetylglucosaminyltransferase [Bacillus thuringiensis serovar konkukian str. 97-27] | | | 2.-.-.- |
| 20717, 20718 | 48787592 | 29 | 1.00E-21 | Burkholderia fungorum LB400 | COG3593: Predicted ATP-dependent endonuclease of the OLD family [Burkholderia fungorum LB400] | | | |
| 20721, 20722 | 48863242 | 36 | 2.00E-08 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02001316 [Microbulbifer degradans 2-40] | | | |
| 20723, 20724 | 29349346 | 46 | 1.00E-47 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb/AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | 3.6.1.- |
| 20725, 20726 | 53715187 | 40 | 6.00E-31 | Bacteroides fragilis YCH46 | methionyl-tRNA formyltransferase [Bacteroides fragilis YCH46] dbj BAD50645.1 methionyl-tRNA formyltransferase [Bacteroides fragilis YCH46] | | | 2.1.2.9 |
| 20727, 20728 | 21230408 | 64 | 9.00E-31 | Xanthomonas campestris pv. campestris str. ATCC 33913 | 2-amino-3-ketobutyrate CoA ligase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb/AAAM40249.1 2-amino-3-ketobutyrate CoA ligase [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | 2.3.1.29 |
| 2073, 2074 | 48847412 | 28 | 1.00E-06 | Geobacter metallireducens GS-15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | |
| 20731, 20732 | 48855267 | 39 | 2.00E-13 | Cytophaga hutchinsonii | COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Cytophaga hutchinsonii] | | | |
| 20733, 20734 | 29350148 | 31 | 2.00E-07 | Bacteroides thetaiotaomicron VPI-5482 | transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_812706.1 transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_811980.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] ref NP_810669.1 transposase, invertase [Bacteroides thetaiotaomicron VPI- 5482] ref NP_810516.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] ref NP_809398.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb/AAO79845.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb/AAO78900.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb/AAO78174.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] gb/AAO76863.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] gb/AAO76710.1 transposase [Bacteroides thetaiotaomicron VPI-5482] gb/AAO75592.1 transposase [Bacteroides thetaiotaomicron VPI-5482] | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|------------------------|--|---------------------|----|----------|----------|
| 20735, | 48855460 | 26 | 6.00E-09 | Cytophaga hutchinsonii | hypothetical protein Chut02001797 [Cytophaga hutchinsonii] | | | | |
| 20736 | | | | | | | | | |
| 20737, | | | | Bacteroides fragilis | tRNA/rRNA methyltransferase [Bacteroides fragilis YCH46] dbj BAD49725.1 | | | | 2.1.1.34 |
| 20738 | 53714267 | 40 | 1.00E-08 | YCH46 | tRNA/rRNA methyltransferase [Bacteroides fragilis YCH46] | | | | |
| 20739, | | | | Bacteroides | ATP-dependent DNA helicase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 20740 | 29346067 | 45 | 8.00E-30 | thetaitotaomicron | gb AAO75764.1 ATP-dependent DNA helicase [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.6.1.- |
| 20741, | AAG2841 | 2 | 1.00E-06 | | Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 33619. | | | | |
| 20742 | 2 | 25 | 1.00E-06 | | Org:Arabidopsis thaliana | | | | |
| 20743, | | | | Psychrobacter sp. | | | | | |
| 20744 | 52853852 | 33 | 5.00E-34 | 273-4 | COG0442: Polyl-rRNA synthetase [Psychrobacter sp. 273-4] | | | | |
| 20745, | | | | Bacteroides fragilis | hypothetical protein BF1758 [Bacteroides fragilis YCH46] dbj BAD48505.1 | | | | |
| 20746 | 53713047 | 82 | 2.00E-54 | YCH46 | conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 20751, | | | | Cytophaga | | | | | |
| 20752 | 48855690 | 47 | 2.00E-39 | hutchinsonii | COG0352: Thiamine monophosphate synthase [Cytophaga hutchinsonii] | | | | 2.5.1.3 |
| 20753, | | | | Escherichia coli | Hypothetical protein ydhs [Escherichia coli CFT073] gb AAN80520.1 | | | | |
| 20754 | 26247915 | 34 | 7.00E-21 | CFT073 | Hypothetical protein ydhs [Escherichia coli CFT073] | | | | |
| 20755, | | | | Tannerella | | | | | |
| 20756 | 28274157 | 32 | 3.00E-17 | forsythensis | HexA [Tannerella forsythensis] | | | | |
| 20759, | AAW2308 | 5 | 2.00E-50 | | Desc:Microscilla furvescens esterase 53sc2. Org:Microscilla furvescens | | | | 3.1.1.47 |
| 20760 | 5 | 50 | 2.00E-50 | | COG1463: ABC-type transport system involved in resistance to organic | | | | |
| 20763, | | | | Cytophaga | solvents, periplasmic component [Cytophaga hutchinsonii] | | | | |
| 20764 | 48853578 | 32 | 1.00E-26 | hutchinsonii | | | | | |
| 20765, | | | | | | Escherichia coli | | | |
| 20766 | | | | | | locus of enterocyte | | | |
| | | | | | | effacement, right | | | |
| | | | | | | hand side | 93 | 1.00E-09 | |
| 20767, | | | | Bacteroides | D-alanine--D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 20768 | 29349121 | 41 | 4.00E-55 | thetaitotaomicron | gb AAO78818.1 D-alanine--D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine--D-alanine ligase (D- | | | | 6.3.2.4 |
| 20769, | | | | VPI-5482 | alanylalanine synthetase) (D-Ala-D-Ala ligase) | | | | |
| 20770 | 48853465 | 53 | 9.00E-24 | Cytophaga | COG0653: Preprotein translocase subunit SecA (ATPase, RNA helicase) | | | | |
| | | | | hutchinsonii | [Cytophaga hutchinsonii] | | | | |
| 2077, | | | | Bacteroides fragilis | ATP-dependent Clp protease ATP-binding subunit [Bacteroides fragilis YCH46] dbj BAD50819.1 ATP-dependent Clp protease ATP-binding subunit | | | | |
| 2078 | 53715361 | 65 | 1.00E-112 | YCH46 | [Bacteroides fragilis YCH46] | | | | 3.4.24.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|----|----------|----------|
| 20771, 20772 | 29348669 | 56 | 5.00E-65 | Bacteroides thetaiotaomicron VPI-5482 | DNA polymerase I [Bacteroides thetaiotaomicron VPI-5482] gb AA078366.1 DNA polymerase I [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.7.7 |
| 20773, 20774 | 53715279 | 48 | 3.00E-53 | Bacteroides fragilis YCH46 | putative methyltransferase [Bacteroides fragilis YCH46] db BAD50737.1 putative methyltransferase [Bacteroides fragilis YCH46] | Desc:Empedobacter r brevis aminopeptidase related coding sequence SEQ ID NO: 15. Org:Empedobacter r brevis | 92 | 8.00E-09 | 2.1.1.- |
| 20777, 20778 | 48853807 | 50 | 2.00E-64 | Cytophaga hutchinsonii | COG0793: Periplasmic protease [Cytophaga hutchinsonii] | | | | 3.4.21.- |
| 20779, 20780 | 24637483 | 33 | 7.00E-17 | Streptococcus thermophilus | Eps9K [Streptococcus thermophilus] | | | | |
| 20781, 20782 | 33861469 | 45 | 5.00E-60 | Prochlorococcus marinus subsp. pastoris str. CCMP1986 | Pyruvate kinase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19371.1 Pyrivate kinase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] | Bacillus sphaericus putative acetyl-CoA carboxylase alpha subunit (accA) gene, partial cds; 6- phosphofructokinase (pfk) gene, complete cds; and putative pyruvate kinase (pykA) gene, partial cds | 91 | 7.00E-10 | 2.7.1.40 |
| 20787, 20788 | 48855782 | 30 | 3.00E-08 | Cytophaga hutchinsonii | hypothetical protein Chut02000991 [Cytophaga hutchinsonii] | | | | |
| 20789, 20790 | 50983054 | 64 | 7.00E-41 | Dictyostellum discoideum | glucose-6-phosphate isomerase [Dictyostellum discoideum] | Vibrio cholerae O1 blovar eltor str. N16961 chromosome I, section 33 of 251 of the complete chromosome | 88 | 7.00E-11 | 5.3.1.9 |
| 2079, 2080 | 54022239 | 25 | 8.00E-07 | Nocardia farcinica IFM 10152 | hypothetical protein nfa2750 [Nocardia farcinica IFM 10152] db BAD55117.1 hypothetical protein [Nocardia farcinica IFM 10152] | | | | |
| 20791, 20792 | 45523117 | 41 | 5.00E-43 | Crocospaera watsonii WH 8501 | COG4301: Uncharacterized conserved protein [Crocospaera watsonii WH 8501] | | | | |

| | | | | | | | | |
|--------|----------|----|----------|--|--|--|--|----------|
| 20793, | 20092474 | 28 | 4.00E-08 | Methanosarcina acetivorans C2A | N-acetyltransferase [Methanosarcina acetivorans C2A] gb AAM07029.1 N-acetyltransferase [Methanosarcina acetivorans str. C2A] | | | |
| 20794 | 52853377 | 78 | 7.00E-94 | Psychrobacter sp. 273-4 | COG0845: Membrane-fusion protein [Psychrobacter sp. 273-4] | | | |
| 20795, | | | | Bradyrhizobium japonicum USDA 110 | hypothetical protein bir7549 [Bradyrhizobium japonicum USDA 110] dbj BAC52814.1 bir7549 [Bradyrhizobium japonicum USDA 110] | | | |
| 20796 | 27382660 | 29 | 1.00E-12 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0909 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76016.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 20797, | 29346319 | 55 | 9.00E-66 | Salmonella enterica | Sty SBLI [Salmonella enterica] | | | 3.1.21.3 |
| 20798 | 1679868 | 69 | 3.00E-97 | Bacteroides uniformis | Tn10-like transposase [Bacteroides uniformis] | | | |
| 20799, | 37962667 | 46 | 6.00E-45 | Gloeobacter violaceus PCC 7421 | hypothetical protein gll0560 [Gloeobacter violaceus PCC 7421] dbj BAC88501.1 gll0560 [Gloeobacter violaceus PCC 7421] | | | |
| 20800 | 37520129 | 33 | 4.00E-11 | Geobacter metallireducens GS-15 | COG1463: ABC-type transport system involved in resistance to organic solvents, periplasmic component [Geobacter metallireducens GS-15] | | | |
| 20801, | 48844754 | 30 | 9.00E-29 | Cytophaga hutchinsonii | COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | |
| 20802 | 48853637 | 26 | 1.00E-08 | Bacteroides fragilis YCH46 | hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 20803, | 53712708 | 60 | 1.00E-63 | Microbulbifer degradans 2-40 | COG4067: Uncharacterized protein conserved in archaea [Microbulbifer degradans 2-40] | | | |
| 20804 | 48863156 | 33 | 8.00E-13 | Haemophilus influenzae R2866 | COG2865: Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen [Haemophilus influenzae R2866] | | | |
| 20805, | 42632161 | 59 | 3.00E-63 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb CA37640.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 20806 | 51246763 | 40 | 2.00E-32 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | 2.7.3.- |
| 20807, | 45657883 | 42 | 5.00E-37 | Microbulbifer degradans 2-40 | COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40] | | | 2.7.3.- |
| 20808 | 48864300 | 45 | 6.00E-59 | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|---|--|--|----------|
| 20829, 20830 | 39995426 | 40 | 2.00E-16 | Geobacter sulfurreducens PCA | hypothetical protein GSU0317 [Geobacter sulfurreducens PCA] gb AAR33650.1 conserved hypothetical protein [Geobacter sulfurreducens PCA] | | | |
| 2083, 2084 | 53715372 | 48 | 1.00E-68 | Bacteroides fragilis YCH46 | putative GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD50830.1 putative GTP-binding protein [Bacteroides fragilis YCH46] | | | |
| 20831, 20832 | 34330256 | 41 | 4.00E-33 | Chromobacterium violaceum ATCC 12472 | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_899878.1 hypothetical protein CV0208 [Chromobacterium violaceum ATCC 12472] | | | 2.7.3.- |
| 20833, 20834 | 27228587 | 36 | 3.00E-15 | Pseudomonas resinovorans | helicase [Pseudomonas resinovorans] dbj BAC41615.1 helicase | | | |
| 20835, 20836 | 48853912 | 55 | 2.00E-68 | Cytophaga hutchinsonii | COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii] | | | 4.1.1.19 |
| 20837, 20838 | 48854312 | 30 | 2.00E-13 | Cytophaga hutchinsonii | COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii] | | | |
| 20839, 20840 | 48855972 | 49 | 8.00E-22 | Cytophaga hutchinsonii | hypothetical protein Chut02001199 [Cytophaga hutchinsonii] | | | |
| 20841, 20842 | 44004501 | 46 | 3.00E-35 | Bacillus cereus ATCC 10987 | acetyltransferase, GNAT family protein [Bacillus cereus ATCC 10987] gb AAS45012.1 acetyltransferase, GNAT family protein [Bacillus cereus ATCC 10987] | | | 2.3.1.- |
| 20843, 20844 | 48856970 | 57 | 2.00E-82 | Cytophaga hutchinsonii | COG1077: Actin-like ATPase involved in cell morphogenesis [Cytophaga hutchinsonii] | | | |
| 20845, 20846 | 48856970 | 67 | 1.00E-29 | Cytophaga hutchinsonii | COG1077: Actin-like ATPase involved in cell morphogenesis [Cytophaga hutchinsonii] | | | |
| 20847, 20848 | 52853377 | 78 | 1.00E-117 | Psychrobacter sp. 273-4 | COG0845: Membrane-fusion protein [Psychrobacter sp. 273-4] | | | |
| 20849, 20850 | 14579394 | 72 | 2.00E-84 | Yersinia enterocolitica | unknown [Yersinia enterocolitica] ref NP_863558.1 unknown [Yersinia enterocolitica] | | | |
| 20853, 20854 | 52550522 | 31 | 9.00E-13 | uncultured archaeon GZfos9D8 | Bpml endonuclease-methyltransferase fusion protein type IIg [uncultured archaeon GZfos9D8] | | | |
| 20855, 20856 | 53758942 | 42 | 4.00E-11 | Methylococcus capsulatus str. Bath | conserved domain protein [Methylococcus capsulatus str. Bath] ref YP_113621.1 hypothetical protein MCA1152 [Methylococcus capsulatus str. Bath] | | | |
| 20857, 20858 | 53712850 | 36 | 3.00E-09 | Bacteroides fragilis YCH46 | siderophore (sulfactin) biosynthesis regulatory protein [Bacteroides fragilis YCH46] dbj BAD48308.1 siderophore (sulfactin) biosynthesis regulatory protein [Bacteroides fragilis YCH46] | | | |
| 20859, 20860 | 32470723 | 43 | 3.00E-43 | Rhodopirellula ballica SH 1 | probable acylaminoacyl-peptidase [Rhodopirellula ballica SH 1] emb CAD71387.1 probable acylaminoacyl-peptidase [Pirellula sp.] | | | |
| 20861, 20862 | 48855767 | 57 | 4.00E-37 | Cytophaga hutchinsonii | COG0123: Deacetylases, including yeast histone deacetylase and acetoin utilization protein [Cytophaga hutchinsonii] | | | |

| | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|----------|
| 20865, | 53735944 | 36 | 3.00E-26 | Crocospaera watsonii WH 8501 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Crocospaera watsonii WH 8501] | | | 2.7.7.6 |
| 20866 | 53735944 | 36 | 3.00E-26 | Chloroflexus aurantiacus | COG0665: Glycine/D-amino acid oxidases (deaminating) [Chloroflexus aurantiacus] | | | |
| 2087, | 53795653 | 28 | 9.00E-09 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1527 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2088 | 29346937 | 29 | 2.00E-08 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | hypothetical protein lpg1073 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | |
| 20875, | 52841307 | 37 | 4.00E-09 | Bacteroides fragilis YCH46 | peptidyl-tRNA hydrolase [Bacteroides fragilis YCH46] | | | |
| 20876 | 53712488 | 62 | 2.00E-41 | Flavobacterium johnsoniae | peptidyl-tRNA hydrolase [Bacteroides fragilis YCH46] | | | 3.1.1.29 |
| 20879, | 5360168 | 38 | 3.00E-44 | Microbulbifer degradans 2-40 | GidB [Flavobacterium johnsoniae] | | | |
| 20880 | 48862596 | 51 | 3.00E-64 | Bacteroides thetaiotaomicron VPI-5482 | COG3022: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] | | | |
| 20881, | 29349616 | 43 | 5.00E-37 | Bacteroides fragilis YCH46 | phosphohydrolase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 20882 | 53712874 | 42 | 7.00E-30 | Bacteroides fragilis YCH46 | phosphohydrolase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 20883, | 46114055 | 50 | 3.00E-11 | Exiguobacterium sp. 255-15 | ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] | | | |
| 20884 | 48854337 | 25 | 6.00E-09 | Cytophaga hutchinsonii | dbj[BAD48332.1] ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] | | | |
| 20885, | 53712874 | 42 | 7.00E-30 | Bacteroides fragilis YCH46 | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Exiguobacterium sp. 255-15] | | | |
| 20886 | 46114055 | 50 | 3.00E-11 | Exiguobacterium sp. 255-15 | COG1280: Putative threonine efflux protein [Cytophaga hutchinsonii] | | | |
| 20887, | 48854337 | 25 | 6.00E-09 | Cytophaga hutchinsonii | COG4529: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 20888 | 48856773 | 25 | 1.00E-09 | Bacteroides fragilis YCH46 | DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] | | | |
| 20889, | 53715439 | 74 | 4.00E-67 | Bacteroides fragilis YCH46 | dbj[BAD50897.1] DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] | | | 2.7.7.6 |
| 20890 | 48854337 | 25 | 6.00E-09 | Cytophaga hutchinsonii | ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 20891, | 48856773 | 25 | 1.00E-09 | Bacteroides fragilis YCH46 | dbj[BAD50897.1] ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | 3.6.1.- |
| 20892 | 48856773 | 25 | 1.00E-09 | Bacteroides fragilis YCH46 | COG2202: FOG: PAS/PAC domain [Anabaena variabilis ATCC 29413] | | | 2.7.3.- |
| 20893, | 53715439 | 74 | 4.00E-67 | Bacteroides fragilis YCH46 | | | | |
| 20894 | 53715439 | 74 | 4.00E-67 | Bacteroides fragilis YCH46 | | | | |
| 20895, | 29349252 | 58 | 2.00E-72 | Anabaena variabilis ATCC 29413 | | | | |
| 20896 | 29349252 | 58 | 2.00E-72 | Anabaena variabilis ATCC 29413 | | | | |
| 20897, | 45508610 | 30 | 2.00E-09 | Anabaena variabilis ATCC 29413 | | | | |
| 20898 | 45508610 | 30 | 2.00E-09 | Anabaena variabilis ATCC 29413 | | | | |

| | | | | | | | | |
|-------------|----------|----|----------|---------------------------------------|--|--|---------|----------|
| 209,210 | 53684756 | 57 | 1.00E-61 | Desulfitobacterium hafnense DCB-2 | COG0587: DNA polymerase III, alpha subunit [Desulfitobacterium hafnense DCB-2] | | | 2.7.7.7 |
| 20901,20902 | 28900685 | 50 | 2.00E-16 | Vibrio parahaemolyticus RIMD 2210633 | putative AraC-family transcriptional regulatory protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62173.1 putative AraC-family transcriptional regulatory protein [Vibrio parahaemolyticus] | | | |
| 20903,20904 | 48787592 | 32 | 1.00E-28 | Burkholderia fungorum LB400 | COG3593: Predicted ATP-dependent endonuclease of the OLD family [Burkholderia fungorum LB400] | | | |
| 20905,20906 | 48854967 | 51 | 1.00E-23 | Cytophaga hutchinsonii | COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 20907,20908 | 48855702 | 36 | 3.00E-26 | Cytophaga hutchinsonii | COG3279: Response regulator of the LytR/AigR family [Cytophaga hutchinsonii] | | | |
| 20909,20910 | 23126057 | 32 | 6.00E-12 | Nostoc punctiforme PCC 73102 | COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102] | | | |
| 2091,2092 | 55819298 | 36 | 2.00E-16 | Mimivirus | unknown [Mimivirus] gb AAV50692.1 unknown [Mimivirus] | | | |
| 20911,20912 | 17936631 | 45 | 7.00E-59 | Agrobacterium tumefaciens str. C58 | acyl-CoA thioesterase II [Agrobacterium tumefaciens str. C58] gb AAL43737.1 acyl-CoA thioesterase II [Agrobacterium tumefaciens str. C58] pir AC2915 acyl-CoA thioesterase II [imported] - Agrobacterium tumefaciens (strain C58, Dupont) | | 3.1.2.- | |
| 20913,20914 | 48729722 | 36 | 7.00E-21 | Pseudomonas fluorescens PFO-1 | COG2194: Predicted membrane-associated, metal-dependent hydrolase [Pseudomonas fluorescens PFO-1] | | | |
| 20917,20918 | 53731382 | 73 | 5.00E-62 | Methanococcoides burtonii DSM 6242 | COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Methanococcoides burtonii DSM 6242] | | | 3.1.21.3 |
| 20919,20920 | 48854426 | 65 | 9.00E-62 | Cytophaga hutchinsonii | COG0692: Uracil DNA glycosylase [Cytophaga hutchinsonii] | | | 3.2.2.- |
| 20921,20922 | 48854014 | 50 | 2.00E-56 | Cytophaga hutchinsonii | COG1104: Cysteine sulfinate desulfinate/cysteine desulfurase and related enzymes [Cytophaga hutchinsonii] | | | 4.4.1.- |
| 20923,20924 | 24371964 | 40 | 1.00E-37 | Shewanella oneidensis MR-1 | hypothetical protein SO0366 [Shewanella oneidensis MR-1] gb AAN53451.1 hypothetical protein [Shewanella oneidensis MR-1] | | | |
| 20927,20928 | 29346947 | 42 | 1.00E-52 | Bacteroides thetaiotaomicron VPI-5482 | putative NADH dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76644.1 putative NADH dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] | | | 1.6.99.3 |
| 20929,20930 | 51244305 | 44 | 2.00E-31 | Desulfotalea psychrophila LSv54 | hypothetical protein DP0453 [Desulfotalea psychrophila LSv54] emb CAG35182.1 conserved hypothetical protein [Desulfotalea psychrophila LSv54] | | | |
| 2093,2094 | 14600644 | 25 | 1.00E-06 | Aeropyrum pernix K1 | hypothetical protein APE0340 [Aeropyrum pernix K1] dbj BAA79295.1 749aa long hypothetical protein [Aeropyrum pernix K1] pir C72725 hypothetical protein APE0340 - Aeropyrum pernix (strain K1) | | | |

| | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|---|--|--|----------|
| 20931, | 48853570 | 35 | 1.00E-13 | Cytophaga hutchinsonii | COG0161: Adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Cytophaga hutchinsonii] | | | 2.6.1.62 |
| 20932, | 4164093 | 29 | 2.00E-24 | Bacteroides fragilis | BfmC [Bacteroides fragilis] | | | |
| 20933, | | | | | | | | |
| 20934, | 27367976 | 42 | 1.00E-41 | Vibrio vulnificus CMCP6 | Spermidine synthase [Vibrio vulnificus CMCP6] gb AAO08493.1 Spermidine synthase [Vibrio vulnificus CMCP6] sp Q8D3Q3 SPEE_VIBVU Spermidine synthase (Putrescine aminopropyltransferase) (SPDSY) | | | 2.5.1.16 |
| 20935, | 48856983 | 32 | 2.00E-12 | Cytophaga hutchinsonii | COG0782: Transcription elongation factor [Cytophaga hutchinsonii] | | | |
| 20936, | 53711795 | 43 | 2.00E-36 | Bacteroides fragilis YCH46 | putative outer membrane protein [Bacteroides fragilis YCH46] | | | |
| 20937, | 48856079 | 61 | 3.00E-87 | Cytophaga hutchinsonii | COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | 1.8.- |
| 20938, | 53711856 | 38 | 2.00E-23 | Bacteroides fragilis YCH46 | 5'-nucleotidase precursor [Bacteroides fragilis YCH46] dbj BAD47314.1 5'-nucleotidase precursor [Bacteroides fragilis YCH46] | | | 3.1.3.5 |
| 20939, | 29347250 | 68 | 4.00E-70 | Bacteroides thetaiotaomicron VPI-5482 | histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76947.1 histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A6N7 SYH_BACTN Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS) | | | 6.1.1.21 |
| 20940, | 53712142 | 37 | 1.00E-59 | Bacteroides fragilis YCH46 | putative N-acyl-D-glucosamine 2-epimerase [Bacteroides fragilis YCH46] | | | |
| 20941, | 53759663 | 48 | 7.00E-63 | Methylobacillus flagellatus KT | COG1236: Predicted exonuclease of the beta-lactamase fold involved in RNA processing [Methylobacillus flagellatus KT] | | | 2.7.7.22 |
| 20942, | | | | | | | | |
| 20943, | 51245718 | 43 | 1.00E-27 | Desulfotalea psychrophila LSV54 | related to low molecular weight heat shock protein (Hsp17) [Desulfotalea psychrophila LSV54] emb CAG36595.1 related to low molecular weight heat shock protein (Hsp17) [Desulfotalea psychrophila LSV54] | | | |
| 20944, | 34396493 | 38 | 1.00E-35 | Porphyromonas gingivalis W83 | ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] ref NP_904660.1 ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] | | | 3.6.1.- |
| 20945, | 53715375 | 39 | 2.00E-17 | Bacteroides fragilis YCH46 | hypothetical protein BF4091 [Bacteroides fragilis YCH46] dbj BAD50833.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 20946, | | | | | | | | |
| 20947, | 29349228 | 39 | 1.00E-15 | Bacteroides thetaiotaomicron VPI-5482 | putative DNA polymerase III, delta subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO78925.1 putative DNA polymerase III, delta subunit [Bacteroides thetaiotaomicron VPI-5482] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|----------|----------|
| 20969, 20970 | 53712115 | 35 | 2.00E-41 | acyl-carrier-protein | 3-oxoacyl-[acyl-carrier-protein] synthase [Bacteroides fragilis YCH46] | | | | 2.3.1.41 |
| 2097, 2098 | 48853620 | 32 | 2.00E-19 | Cytophaga hutchinsonii | COG4252: Predicted transmembrane sensor domain [Cytophaga hutchinsonii] | | | | |
| 20971, 20972 | 48862684 | 43 | 4.00E-41 | Microbulbifer degradans 2-40 | COG3228: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] | | | | |
| 20973, 20974 | 53718224 | 50 | 1.00E-49 | Burkholderia pseudomallei K96243 | hypothetical protein BPSL0582 [Burkholderia pseudomallei K96243] | | | | |
| 20977, 20978 | 34763977 | 39 | 2.00E-22 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | Magnesium and cobalt transport protein corA [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23536.1 Magnesium and cobalt transport protein corA [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | | |
| 20979, 20980 | 42526734 | 66 | 8.00E-70 | Treponema denticola ATCC 35405 | zinc ABC transporter, ATP-binding protein [Treponema denticola ATCC 35405] gb AAS11743.1 zinc ABC transporter, ATP-binding protein [Treponema denticola ATCC 35405] | Oceanobacillus ihayensis HTE831 genomic DNA, section 2/13 | 89 | 1.00E-07 | 1.8.-.- |
| 20983, 20984 | 34396491 | 54 | 8.00E-27 | Porphyromonas gingivalis W83 | GTP-binding protein [Porphyromonas gingivalis W83] ref NP_904658.1 GTP-binding protein [Porphyromonas gingivalis W83] | | | | |
| 20985, 20986 | 52143029 | 42 | 4.00E-22 | Bacillus cereus ZK | hypothetical protein BCZK2210 [Bacillus cereus ZK] gb AAU18048.1 conserved hypothetical protein [Bacillus cereus ZK] | | | | |
| 20987, 20988 | 53712846 | 55 | 2.00E-21 | Bacteroides fragilis YCH46 | AG-specific adenine glycosylase [Bacteroides fragilis YCH46] dbj BAD48304.1 AG-specific adenine glycosylase [Bacteroides fragilis YCH46] | | | | 3.2.2.- |
| 20989, 20990 | 58476791 | 37 | 3.00E-24 | Azoarcus sp. EbN1 | adenine specific DNA methylase MOD [Azoarcus sp. EbN1] emb CAI07479.1 Adenine specific DNA methylase MOD [Azoarcus sp. EbN1] | | | | |
| 2099, 2100 | 45358866 | 43 | 6.00E-34 | Methanococcus maripaludis S2 | Sensory transduction histidine kinase [Methanococcus maripaludis S2] emb CAF30859.1 Sensory transduction histidine kinase [Methanococcus maripaludis S2] | | | | 2.7.3.- |
| 20991, 20992 | 31195967 | 82 | 7.00E-43 | Anopheles gambiae | ENSANGP00000016322 [Anopheles gambiae] | | | | 1.6.4.5 |
| 20993, 20994 | 23479053 | 27 | 5.00E-09 | Plasmodium yoelii | mature-parasite-infected erythrocyte surface antigen [Plasmodium yoelii yoelii] | | | | |
| 20995, 20996 | 53711509 | 37 | 3.00E-30 | Bacteroides fragilis YCH46 | ribonuclease III [Bacteroides fragilis YCH46] dbj BAD46967.1 ribonuclease III [Bacteroides fragilis YCH46] | | | | 3.1.26.3 |
| 20997, 20998 | 23103544 | 31 | 4.00E-21 | Azotobacter vinelandii | COG1251: NAD(P)H-nitrite reductase [Azotobacter vinelandii] | | | | 1.6.6.4 |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 20999, 21000 | 29345821 | 52 | 1.00E-64 | Bacteroides thetaiotaomicron VPI-5482 | CysQ, sulfite synthesis pathway protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75518.1 CysQ, sulfite synthesis pathway protein [Bacteroides thetaiotaomicron VPI-5482] | | | 3.1.3.25 |
| 21, 22 | 48854298 | 67 | 6.00E-95 | Cytophaga hutchinsonii | COG4867: Uncharacterized protein with a von Willebrand factor type A (VWA) domain [Cytophaga hutchinsonii] | | | |
| 21001, | | | | Cytophaga | | | | |
| 21002 | 48854958 | 61 | 4.00E-66 | hutchinsonii | COG1432: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 21003, | | | | Rhodopirellula | hypothetical protein RB7682 [Rhodopirellula baltica SH 1] emb CAD75508.1 | | | |
| 21004 | 32474967 | 46 | 3.00E-53 | baltica SH 1 | hypothetical protein [Pirellula sp.] | | | |
| 21005, | | | | Cytophaga | | | | |
| 21006 | 48856607 | 31 | 1.00E-22 | hutchinsonii | COG1321: Mn-dependent transcriptional regulator [Cytophaga hutchinsonii] | | | |
| 21008, | | | | Cytophaga | | | | |
| 21010 | 48856112 | 31 | 2.00E-32 | hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 2101, | | | | Exiguobacterium | | | | |
| 2102 | 45533048 | 40 | 2.00E-16 | sp. 255-15 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Exiguobacterium sp. 255-15] | | | 2.7.3.- |
| 21013, | | | | Aquifex aeolicus | | | | |
| 21014 | 15605827 | 26 | 1.00E-17 | VF5 | hypothetical protein aq_294 [Aquifex aeolicus VF5] gb AAC06602.1 putative protein [Aquifex aeolicus VF5] pir H70326 hypothetical protein aq_294 - Aquifex aeolicus | | | |
| 21017, | | | | Bacteroides fragilis | | | | |
| 21018 | 53712185 | 46 | 2.00E-29 | YCH46 | alanine racemase [Bacteroides fragilis YCH46] | | | 5.1.1.1 |
| 21019, | | | | Rubrobacter | | | | |
| 21020 | 46106876 | 46 | 7.00E-24 | xylanophilus DSM 9941 | COG4585: Signal transduction histidine kinase [Rubrobacter xylanophilus DSM 9941] | | | 2.7.3.- |
| 21021, | | | | Bacteroides | | | | |
| 21022 | 29348881 | 49 | 5.00E-55 | thetaiotaomicron VPI-5482 | putative hydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78578.1 putative hydrogenase [Bacteroides thetaiotaomicron VPI-5482] | | | 1.-.-.- |
| 21023, | | | | Polaromonas sp. | | | | |
| 21024 | 54032941 | 43 | 4.00E-26 | JS666 | COG0225: Peptide methionine sulfoxide reductase [Polaromonas sp. JS666] | | | 1.8.4.6 |
| 21025, | | | | Chlorobium | | | | |
| 21026 | 21674157 | 35 | 5.00E-16 | tepidum TLS | hypothetical protein [Chlorobium tepidum TLS] | | | |
| | | | | Desulfovibrio | | | | |
| 21027, | | | | vulgaris subsp. | hypothetical protein DVU2025 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96500.1 conserved hypothetical protein | | | |
| 21028 | 46580432 | 42 | 6.00E-50 | Hildenborough | [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 21029, | | | | Bacteroides fragilis | | | | |
| 21030 | 53714701 | 59 | 4.00E-58 | YCH46 | histidyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD50159.1 histidyl-tRNA synthetase [Bacteroides fragilis YCH46] | | | 6.1.1.21 |
| 2103, | | | | Exiguobacterium | | | | |
| 2104 | 45533048 | 38 | 1.00E-16 | sp. 255-15 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Exiguobacterium sp. 255-15] | | | 2.7.3.- |

| | | | | | | | | |
|---|----------------|----------|--|--|---|----|-----------|----------|
| 21031, 21032, 21035, 21036, 21037, 21038 | 53713593 68 | 1.00E-44 | Bacteroides fragilis YCH46 | ATP-dependent protease [Bacteroides fragilis YCH46] dbj BAD49051.1 ATP dependent protease [Bacteroides fragilis YCH46] COG3920: Signal transduction histidine kinase [Methanosarcina barkeri str. fusaro] | Pasteurella multocida subsp. multocida str. Pm70 section 201 of 204 of the complete genome | 91 | 1.00E-063 | 3.4.21.5 |
| 21039, 21040 | 48838064 34 | 1.00E-13 | Methanosarcina barkeri str. fusaro | | | | | 2.7.3.- |
| 21041, 21042 | 36955846 64 | 1.00E-60 | Polaribacter filamentus | nicotinate-nucleotide adenyltransferase [Polaribacter filamentus] hypothetical protein BT2236 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77343.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A5K3 YM36_BACTN Hypothetical UPF0102 protein BT2236 | | | | 2.7.7.18 |
| 21045, 21046 | 29347646 42 | 5.00E-18 | Bacteroides thetaiotaomicron VPI-5482 | | | | | 3.1.-.- |
| 21047, 21048 | 50123026 57 | 5.00E-12 | Erwinia carotovora subsp. atroseptica SCRI1043 | phosphoenolpyruvate carboxykinase [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG77003.1 phosphoenolpyruvate carboxykinase [Erwinia carotovora subsp. atroseptica SCRI1043] putative DNA mismatch repair protein [Bacteroides fragilis YCH46] dbj BAD50625.1 putative DNA mismatch repair protein [Bacteroides fragilis YCH46] | | | | 4.1.1.49 |
| 21055, 21056 | 53715167 46 | 9.00E-16 | Bacteroides fragilis YCH46 | DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] dbj BAD51320.1 DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] | | | | |
| 21057, 21058 | 53715862 65 | 3.00E-63 | Bacteroides fragilis YCH46 | asparagine synthetase (asnB) [Methanocaldococcus jannaschii DSM 2661] gb AAB99058.1 asparagine synthetase (asnB) [Methanocaldococcus jannaschii DSM 2661] leucyl-tRNA synthetase [Porphyromonas gingivalis W83] ref NP_905058.1 leucyl-tRNA synthetase [Porphyromonas gingivalis W83] sp Q7MW49 SYL_PORGI Leucyl-tRNA synthetase (Leucine-tRNA ligase) (LeuRS) | | | | 6.3.5.4 |
| 21059, 21060 | 15669245 48 | 6.00E-48 | Porphyromonas gingivalis W83 | oxidoreductase [Bdellovibrio bacteriovorus HD100] emb CAE79695.1 oxidoreductase [Bdellovibrio bacteriovorus HD100] | | | | 6.1.1.4 |
| 21063, 21064 | 34396892 56 | 6.00E-49 | Bdellovibrio bacteriovorus HD100 | hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62612.1 hypothetical protein [Vibrio parahaemolyticus] | | | | 1.1.1.- |
| 21065, 21066 | 42523322 26 | 7.00E-11 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62612.1 hypothetical protein [Vibrio parahaemolyticus] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|----|----------|----------|
| 21069, 21070 | 48855120 | 56 | 6.00E-23 | Cytophaga hutchinsonii | COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii] | | | 6.1.1.4 |
| 2107, 2108 | 1334389 | 69 | 2.00E-45 | Emmericella nidulans | unnamed protein product [Emmericella nidulans] pir D22735 hypothetical nox3 protein - Emmericella nidulans mitochondrion | 83 | 9.00E-57 | |
| 21071, 21072 | 48854784 | 62 | 5.00E-50 | Cytophaga hutchinsonii | COG0044: Dihydroorotase and related cyclic amidohydrolases [Cytophaga hutchinsonii] | | | 3.5.2.3 |
| 21073, 21074 | 15793258 | 57 | 1.00E-38 | Neisseria meningitidis Z2491 | hypothetical protein NMA0240 [Neisseria meningitidis Z2491] emb CAB83548.1 hypothetical protein NMA0240 [Neisseria meningitidis Z2491] pir D82018 hypothetical protein NMA0240 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) | | | 3.4.13.9 |
| 21075, 21076 | 29349136 | 44 | 1.00E-11 | Bacteroides thetaiotaomicron VPI-5482 | riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482] gb AAO78833.1 riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21079, 21080 | 53715167 | 43 | 2.00E-17 | Bacteroides fragilis YCH46 | putative DNA mismatch repair protein [Bacteroides fragilis YCH46] dbj BAD50625.1 putative DNA mismatch repair protein [Bacteroides fragilis YCH46] | | | |
| 21081, 21082 | 48856925 | 24 | 2.00E-12 | Cytophaga hutchinsonii | COG1309: Transcriptional regulator [Cytophaga hutchinsonii] | | | |
| 21085, 21086 | 48853462 | 24 | 3.00E-08 | Cytophaga hutchinsonii | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii] | | | |
| 21089, 21090 | 27366595 | 33 | 6.00E-22 | Vibrio vulnificus CMCP6 | Response regulator [Vibrio vulnificus CMCP6] ref NP_936705.1 probable response regulator [Vibrio vulnificus YJ016] gb AAO07112.1 Response regulator [Vibrio vulnificus CMCP6] dbj BAC96675.1 probable response regulator [Vibrio vulnificus YJ016] | | | 2.7.3.- |
| 21093, 21094 | 48864200 | 26 | 5.00E-32 | Microbulbifer degradans 2-40 | COG0784: FOG; Che Y-like receiver [Microbulbifer degradans 2-40] | | | |
| 21095, 21096 | 8101030 | 42 | 2.00E-66 | Prevotella sp. RS2 | MdsD protein [Prevotella sp. RS2] | | | 3.4.21.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|----------|
| 21097, 21098 | 24372547 | 29 | 1.00E-08 | Shewanella oneidensis MR-1 | hypothetical spermidine synthase [Shewanella oneidensis MR-1] gb AA54034.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | 2.5.1.16 |
| 211, 212 | 48733660 | 52 | 2.00E-59 | Pseudomonas fluorescens PfO-1 | COG1638: TRAP-type C4-dicarboxylate transport system, periplasmic component [Pseudomonas fluorescens PfO-1] | | | |
| 21109, 21110 | 15899493 | 23 | 2.00E-09 | Sulfolobus solfataricus P2 | hypothetical protein SSO2778 [Sulfolobus solfataricus P2] gb AAK42888.1 Conserved hypothetical protein [Sulfolobus solfataricus P2] pir A90454 conserved hypothetical protein [imported] - Sulfolobus solfataricus | | | |
| 21113, 21114 | 53714728 | 61 | 9.00E-65 | Bacteroides fragilis YCH46 | dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] dbj BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] | | | 2.4.1.83 |
| 21117, 21118 | 42526734 | 70 | 2.00E-52 | Treponema denticola ATCC 35405 | zinc ABC transporter, ATP-binding protein [Treponema denticola ATCC 35405] gb AAS11743.1 zinc ABC transporter, ATP-binding protein [Treponema denticola ATCC 35405] | | | 1.8.-- |
| 21119, 21120 | 28210167 | 57 | 3.00E-35 | Clostridium tetani E88 | hypothetical protein CTC00414 [Clostridium tetani E88] gb AAO35048.1 conserved protein [Clostridium tetani E88] | | | |
| 21123, 21124 | 16329878 | 36 | 2.00E-30 | Synechocystis sp. PCC 6803 | hypothetical protein sir1135 [Synechocystis sp. PCC 6803] dbj BAA17286.1 sir1135 [Synechocystis sp. PCC 6803] pir S77439 hypothetical protein sir1135 - Synechocystis sp. (strain PCC 6803) | | | |
| 21127, 21128 | 30249527 | 48 | 4.00E-27 | Nitrosomonas europaea ATCC 19718 | putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718] | | | |
| 21129, 21130 | 34397295 | 53 | 7.00E-45 | Porphyromonas gingivalis W83 | phosphoserine aminotransferase [Porphyromonas gingivalis W83] ref NP_905459.1 phosphoserine aminotransferase [Porphyromonas gingivalis W83] | | | 2.6.1.52 |
| 21131, 21132 | 16263258 | 34 | 3.00E-09 | Sinorhizobium meliloti 1021 | Putative methyltransferase [Sinorhizobium meliloti 1021] gb AAK65463.1 Putative methyltransferase [Sinorhizobium meliloti 1021] pir E95362 probable methyltransferase [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA | | | |
| 21137, 21138 | 48854435 | 42 | 5.00E-44 | Cytophaga hutchinsonii | COG1331: Highly conserved protein containing a thioredoxin domain [Cytophaga hutchinsonii] | | | |
| 21141, 21142 | 45657883 | 54 | 5.00E-35 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | 2.7.3.- |

| | | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|----|-------------------|
| 21143, | 34397331 | 62 | 4.00E-37 | Porphyromonas gingivalis W83 | crossover junction endodeoxyribonuclease RuvC [Porphyromonas gingivalis W83] refNP_905495.1 crossover junction endodeoxyribonuclease RuvC [Porphyromonas gingivalis W83] spIQ7MUZ6[RUV_C_PORGI Crossover junction endodeoxyribonuclease ruvC (Holliday junction nuclease ruvC) (Holliday junction resolvase ruvC)] | | | | 3.1.22.4 |
| 21144, | | | | Cytophaga hutchinsonii | COG0026: Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase) [Cytophaga hutchinsonii] | | | | 4.1.1.21 |
| 21145, | 48854305 | 50 | 3.00E-17 | Pedococcus pentosaceus ATCC 25745 | COG0237: Dephospho-CoA kinase [Pedococcus pentosaceus ATCC 25745] | | | | 2.7.1.24 |
| 21146 | 48870478 | 31 | 2.00E-19 | Cytophaga hutchinsonii | COG0714: MoxR-like ATPases [Cytophaga hutchinsonii] | | | | |
| 21147, | | | | Cytophaga hutchinsonii | COG3386: Gluconolactonase [Cytophaga hutchinsonii] | | | | 3.1.1.17 |
| 21148 | 48856710 | 59 | 2.00E-26 | Cytophaga hutchinsonii | hypothetical maturase [Photobacterium profundum SS9] emb[CAG22679.1] | Photobacterium profundum SS9 chromosome 2; segment 3/7 | | | |
| 21149, | 48854087 | 48 | 3.00E-52 | Cytophaga hutchinsonii | hypothetical maturase [Photobacterium profundum] | | | 82 | 3.00E-14/2.7.7.49 |
| 2115, | | | | | Uvs063 [uncultured bacterium] | | | | |
| 21151, | 54302486 | 73 | 2.00E-88 | Photobacterium profundum SS9 uncultured bacterium | putative transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 21152 | 37222112 | 66 | 4.00E-73 | Bacteroides fragilis YCH46 | dbj[BAD47957.1] putative transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 21153, | | | | | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | | | | |
| 21154 | 53712499 | 39 | 3.00E-36 | Cytophaga hutchinsonii | COG1137: ABC-type (unclassified) transport system, ATPase component [Cytophaga hutchinsonii] | | | | 1.8.- |
| 21157, | 48853518 | 35 | 2.00E-46 | Cytophaga hutchinsonii | phosphohydrolase [Bacteroides fragilis YCH46] | | | | |
| 21161, | 48854368 | 70 | 6.00E-79 | Bacteroides fragilis YCH46 | phosphohydrolase [Bacteroides fragilis YCH46] | | | | |
| 21162 | 53712201 | 59 | 4.00E-60 | | putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj[BAD47634.1] putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] | | | | |
| 21163, | | | | Bacteroides fragilis YCH46 | COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 21164 | 48854368 | 70 | 6.00E-79 | Cytophaga hutchinsonii | hypothetical protein XF1489 [Xylella fastidiosa 9a5c] gbj[AAF84298.1] | | | | |
| 21165, | | | | Xylella fastidiosa 9a5c | hypothetical protein XF1489 [Xylella fastidiosa 9a5c] p[ir][E82675] | | | | |
| 21166 | 53712201 | 59 | 4.00E-60 | Cytophaga hutchinsonii | hypothetical protein XF1489 [imported] - Xylella fastidiosa (strain 9a5c) molybdenum cofactor biosynthesis protein C [Campylobacter coli RM2228] | | | | |
| 21167, | | | | Campylobacter coli RM2228 | gbj[EAL56857.1] molybdenum cofactor biosynthesis protein C [Campylobacter coli RM2228] | | | | |
| 21168 | 53712176 | 32 | 4.00E-13 | Bacteroides fragilis YCH46 | | | | | |
| 21169, | 48855703 | 39 | 1.00E-28 | Cytophaga hutchinsonii | | | | | |
| 21170 | | | | | | | | | |
| 21171, | 15838090 | 29 | 1.00E-10 | Xylella fastidiosa 9a5c | | | | | |
| 21172 | 57168375 | 47 | 9.00E-21 | Campylobacter coli RM2228 | | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|--|----|----------|--|---------|
| 21173, | 28829330 | 38 | 2.00E-26 | Dictyostellum discoidium | hypothetical protein [Dictyostellum discoidium] | | | | 5.2.1.8 |
| 21174, | | | | Dictyostellum discoidium | hypothetical protein [Dictyostellum discoidium] | | | | |
| 21175, | 28829330 | 41 | 7.00E-19 | Dictyostellum discoidium | | | | | |
| 21176, | | | | Shewanella oneidensis MR-1 | HlyD family-related protein [Shewanella oneidensis MR-1] gb AAO54933.1 | | | | |
| 21177, | 24373446 | 29 | 3.00E-09 | Shewanella oneidensis MR-1 | HlyD family-related protein [Shewanella oneidensis MR-1] | | | | |
| 21181, | | | | Vibrio vulnificus | Putative transcriptional regulator [Vibrio vulnificus CMCP6] | | | | |
| 21182, | 27366450 | 64 | 4.00E-30 | CMCP6 | Putative transcriptional regulator [Vibrio vulnificus CMCP6] | | | | |
| 21183, | | | | Cytophaga hutchinsonii | COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii] | | | | 4.1.3.- |
| 21184, | 48856398 | 51 | 3.00E-65 | Cytophaga hutchinsonii | COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii] | | | | 4.1.3.- |
| 21185, | | | | Cytophaga hutchinsonii | COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii] | | | | |
| 21186, | 48856398 | 55 | 1.00E-50 | Cytophaga hutchinsonii | COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii] | | | | |
| 21187, | | | | Cytophaga hutchinsonii | COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii] | | | | |
| 21188, | 48854194 | 45 | 3.00E-38 | Cytophaga hutchinsonii | membrane protein, putative [Porphyromonas gingivalis W83] | | | | |
| 21189, | | | | Cytophaga hutchinsonii | ref NP_904821.1 membrane protein, putative [Porphyromonas gingivalis W83] sp P60036 OXAA_PORG inner membrane protein oxaA | | | | |
| 21191, | | | | Porphyromonas gingivalis W83 | two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21192, | 34396654 | 32 | 3.00E-28 | Porphyromonas gingivalis W83 | regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21193, | | | | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21194, | 29348306 | 40 | 5.00E-22 | Bacteroides thetaiotaomicron VPI-5482 | regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21195, | | | | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21196, | 29348306 | 40 | 6.00E-22 | Bacteroides thetaiotaomicron VPI-5482 | regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21197, | | | | Bacteroides thetaiotaomicron VPI-5482 | conserved hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75921.1 conserved hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21198, | 29346224 | 30 | 2.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | COG1522: Transcriptional regulators [Cytophaga hutchinsonii] | | | | |
| 21201, | | | | Cytophaga hutchinsonii | putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46] | | | | |
| 21202, | 48856980 | 43 | 3.00E-27 | Cytophaga hutchinsonii | putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46] | | | | |
| 21207, | | | | Bacteroides fragilis YCH46 | putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46] | | | | |
| 21208, | 53713469 | 46 | 2.00E-51 | Bacteroides fragilis YCH46 | putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46] | | | | |
| | | | | Acinetobacter sp. ADP1 complete genome | | 91 | 6.00E-07 | | |

| | | | | | | | | |
|-----------------|--------------|----|----------|---|---|--|-------------|----------|
| 21209, 21210 | 53717167 | 27 | 4.00E-23 | Burkholderia mallei ATCC 23344 | sensory box histidine kinase/response regulator [Burkholderia mallei ATCC 23344] gb AAU46707.1 sensory box histidine kinase/response regulator [Burkholderia mallei ATCC 23344] | | | 2.7.- |
| 2121, 2122 | ABU0070 6 | 34 | 3.00E-31 | | Desc:S. pneumoniae type 4 strain protein from coding region #273. Org:Streptococcus pneumoniae type 4 strain | | | 5.1.3.14 |
| 21215, 21216 | 53712889 | 32 | 1.00E-26 | Bacteroides fragilis YCH46 | putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46] | | | |
| 21217, 21218 | 6498243 | 39 | 7.00E-32 | Agrobacterium tumefaciens | tiotf70 [Agrobacterium tumefaciens] ref NP_053310.1 Hypothetical gene [Agrobacterium tumefaciens] | | | |
| 21219, 21220 | 26988659 | 34 | 4.00E-37 | Pseudomonas putida KT2440 | hypothetical protein PP1931 [Pseudomonas putida KT2440] gb AAN67548.1 conserved hypothetical protein [Pseudomonas putida KT2440] | | | |
| 21223, 21224 | 48853912 | 50 | 2.00E-49 | Cytophaga hutchinsonii | COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii] | | | |
| 21225, 21226 | 48853912 | 51 | 2.00E-48 | Cytophaga hutchinsonii | COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii] | | | |
| 21227, 21228 | 9658004 | 59 | 3.00E-45 | Vibrio cholerae O1 biovar eltor str. N16961 | MutT/nudix family protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232982.1 MutT/nudix family protein [Vibrio cholerae O1 biovar eltor str. N16961] pir G82439 MutT/nudix family protein VCA0592 [Imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | |
| 21229, 21230 | 31195231 | 55 | 2.00E-80 | Anopheles gambiae | ENSANGP00000001058 [Anopheles gambiae] gb EAA02216.1 ENSANGP00000001058 [Anopheles gambiae str. PEST] ref XP_561308.1 ENSANGP00000001058 [Anopheles gambiae str. PEST] | | | 1.1.1.34 |
| 2123, 2124 | 48854732 | 25 | 4.00E-15 | Cytophaga hutchinsonii | COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 21231, 21232 | 48855521 | 29 | 2.00E-17 | Cytophaga hutchinsonii | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | |
| 21233, 21234 | 53713656 | 53 | 4.00E-78 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD49114.1 two-component system response regulator [Bacteroides fragilis YCH46] | Desulfotalea psychrophila Lsv54 chromosome | 93 4.00E-08 | |
| 21237, 21238 | 48854416 | 27 | 2.00E-13 | Cytophaga hutchinsonii | COG3275: Putative regulator of cell autolysis [Cytophaga hutchinsonii] | | | 2.7.3- |
| 21239, 21240 | 48854415 | 38 | 1.00E-35 | Cytophaga hutchinsonii | COG3279: Response regulator of the LysR/Algr family [Cytophaga hutchinsonii] | | | |
| 21241, 21242 | 48855448 | 29 | 4.00E-26 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|---------------|
| 21243, 21244 | 37528315 | 48 | 9.00E-76 | Photorhabdus luminescens subsp. laumondii TTO1 | Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_931390.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930919.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930800.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930791.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928662.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928429.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_927713.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_927691.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16866.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16580.1 Transposase, IS4 fa | | | |
| 21245, 21246 | 24373937 | 51 | 9.00E-49 | Shewanella oneidensis MR-1 | CDP-diacylglycerol--serine O-phosphatidyltransferase [Shewanella oneidensis MR-1] gb AAN55424.1 CDP-diacylglycerol--serine O-phosphatidyltransferase [Shewanella oneidensis MR-1] | | | 2.7.8.8 |
| 21247, 21248 | 24373937 | 50 | 6.00E-54 | Shewanella oneidensis MR-1 | CDP-diacylglycerol--serine O-phosphatidyltransferase [Shewanella oneidensis MR-1] gb AAN55424.1 CDP-diacylglycerol--serine O-phosphatidyltransferase [Shewanella oneidensis MR-1] | | | 2.7.8.8 |
| 2125, 2126 | 29349895 | 43 | 1.00E-44 | Bacteroides thetalaotomicron VPI-5482 | putative membrane-bound lytic murein transglycosylase [Bacteroides thetalaotomicron VPI-5482] gb AAO79592.1 putative membrane-bound lytic murein transglycosylase [Bacteroides thetalaotomicron VPI-5482] | | | 3.2.1.- |
| 21253, 21254 | 53764144 | 43 | 3.00E-65 | Anabaena variabilis ATCC 29413 | COG1770: Protease II [Anabaena variabilis ATCC 29413] | | | 3.4.21.8 3 |
| 21255, 21256 | 31195963 | 66 | 1.00E-56 | Anopheles gambiae | ENSANGP00000000454 [Anopheles gambiae] | | | 4.2.1.22 |
| 21257, 21258 | 31195963 | 65 | 2.00E-50 | Anopheles gambiae | ENSANGP00000000454 [Anopheles gambiae] | | | 4.2.1.22 |
| 21259, 21260 | 53686269 | 48 | 8.00E-60 | Desulfotomobacterium hafnense DCB-2 | COG0535: Predicted Fe-S oxidoreductases [Desulfotomobacterium hafnense DCB-2] | | | |
| 21261, 21262 | 53714074 | 49 | 1.00E-47 | Bacteroides fragilis YCH46 | hypothetical protein BF2782 [Bacteroides fragilis YCH46] dbj BAD49532.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 21263, 21264 | 29348700 | 29 | 1.00E-21 | Bacteroides thetalaotomicron VPI-5482 | hypothetical protein BT3291 [Bacteroides thetalaotomicron VPI-5482] gb AAO78397.1 hypothetical protein [Bacteroides thetalaotomicron VPI-5482] | | | |

| | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|---------------|
| 21265, | 46156085 | 27 | 1.00E-10 | Haemophilus sommus 2336 | COG3298: Predicted 3'-5' exonuclease related to the exonuclease domain of PoB [Haemophilus somnus 2336] | | | |
| 21266 | | | | Bacteroides thetaiotaomicron VPI-5482 | putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO75743.1 putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21267, | 29346046 | 30 | 3.00E-29 | Bacteroides thetaiotaomicron VPI-5482 | TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO79003.1 TonB [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21269, | 29349306 | 33 | 3.00E-12 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70144.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.7.3.- |
| 2127, | 45657421 | 42 | 2.00E-13 | Bacteroides fragilis YCH46 | hypothetical protein BF0893 [Bacteroides fragilis YCH46] dbj BAD47644.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 21273, | 53712186 | 42 | 4.00E-13 | Porphyromonas gingivalis W83 | peptide chain release factor 3 [Porphyromonas gingivalis W83] ref NP_904540.1 peptide chain release factor 3 [Porphyromonas gingivalis W83] | | | 3.6.1.48 |
| 21274 | 48854958 | 61 | 9.00E-81 | Cytophaga hutchinsonii | COG1432: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 21279, | 46447426 | 28 | 5.00E-08 | Parachlamydia sp. UWE25 | putative rRNA methylase [Parachlamydia sp. UWE25] emb CAF24516.1 putative rRNA methylase [Parachlamydia sp. UWE25] | | | 2.1.1.- |
| 21280 | | | | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1139 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76246.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21281, | 29346549 | 42 | 4.00E-25 | Idiomarina lohiensis L2TR | Probable aminopeptidase [Idiomarina lohiensis L2TR] gb AAV81546.1 Probable aminopeptidase [Idiomarina lohiensis L2TR] | | | |
| 21285, | 56459814 | 26 | 1.00E-12 | Xanthomonas axonopodis pv. citri str. 306 | hypothetical protein XAC0026 [Xanthomonas axonopodis pv. citri str. 306] gb AAM34918.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] | | | 3.4.17.2 1 |
| 21287, | 21240800 | 28 | 5.00E-24 | Chloroflexus aurantiacus | COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus] | | | |
| 21288 | 53797086 | 36 | 8.00E-47 | Rhodopirellula baltica SH 1 | cryptic haloacid dehalogenase 1 [Rhodopirellula baltica SH 1] emb CAD73861.1 cryptic haloacid dehalogenase 1 [Pirellula sp.] | | | 3.8.1.3 |
| 21290 | 32473181 | 34 | 5.00E-30 | Pseudomonas aeruginosa PAO1 | hypothetical protein PA4882 [Pseudomonas aeruginosa PAO1] pir D83036 hypothetical protein PA4882 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253569.1 hypothetical protein PA4882 [Pseudomonas aeruginosa PAO1] | | | 1.6.6.1 |

| | | | | | | | | |
|-----------------|---------------------|----------|----------------------|---|--|----|-----------|---------------------|
| 21305, 21306 | 36955884 | 78 | 1.00E-51 | Polaribacter filamentus | NAD kinase [Polaribacter filamentus] ATP-dependent helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76161.1 ATP-dependent helicase [Bacteroides thetaiotaomicron VPI-5482] | 84 | 7.00E-42 | 2.7.1.23 |
| 21309, 21310 | 29346464 | 25 | 2.00E-13 | Bacteroides thetaitaomicron VPI-5482 | adenylate cyclase-related protein [Shewanella oneidensis MR-1] gb AAN54394.1 adenylate cyclase-related protein [Shewanella oneidensis MR-1] | | | 3.6.1.- |
| 21311, 21312 | 24372907 | 31 | 1.00E-12 | Shewanella oneidensis MR-1 | | | | 4.6.1.1 |
| 21313, 21314 | 46105876 | 36 | 3.00E-48 | Rubrobacter xylanophilus DSM 9941 | COG0520: Selenocysteine lyase [Rubrobacter xylanophilus DSM 9941] | | | 4.4.1.- |
| 21317, 21318 | 22255857 | 60 | 1.00E-100 | Micromonospora echinospora | CalR4 [Micromonospora echinospora] fusion protein of probable Na-dependent permease domain and histidine kinase domain of putative two-component sensor [Azoarcus sp. EbN1] emb CAI06216.1 Fusion protein of probable Na-dependent permease domain and histidine kinase domain of putative two-component sensor [Azoarcus sp. EbN1] | 88 | 5.00E-173 | 3.4.21.5 |
| 21323, 21324 | 56475528 | 38 | 1.00E-19 | Azoarcus sp. EbN1 | putative anti-sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO76072.1 putative anti-sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21329, 21330 | 29346375 | 31 | 4.00E-18 | Bacteroides thetaitaomicron VPI-5482 | unknown [Branchiostoma floridae] | | | 2.4.2.- |
| 21331, 21332 | 20302775 ABB5457 | 44 52 | 1.00E-36 9.00E-20 | Branchiostoma floridae | Desc: Lactococcus lactis protein ymgC. Org: Lactococcus lactis IL1403 COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Cytophaga hutchinsonii] | | | 1.8.- |
| 21333, 21334 | 48856353 | 72 | 2.00E-78 | Cytophaga hutchinsonii | COG0796: Glutamate racemase [Pseudomonas syringae pv. syringae B728a] COG0710: Acetyltransferase (isoleucine patch superfamily) [Methanosarcina barkeri str. fusaro] COG1012: NAD-dependent aldehyde dehydrogenases [Cytophaga hutchinsonii] COG1012: NAD-dependent aldehyde dehydrogenases [Cytophaga hutchinsonii] | | | 5.1.1.3 2.3.1.18 |
| 21335, 21336 | 46188261 | 44 | 7.00E-52 | Pseudomonas syringae pv. syringae B728a | | | | |
| 21337, 21338 | 48838984 | 70 | 6.00E-59 | Methanosarcina barkeri str. fusaro | | | | |
| 21339, 21340 | 48855746 | 54 | 8.00E-43 | Cytophaga hutchinsonii | | | | |
| 21341, 21342 | 48855746 | 59 | 4.00E-56 | Cytophaga hutchinsonii | | | | 1.2.1.9 |

| | | | | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|--|--|--|--|--|--|----------|
| 21347, | | | | | | | | | hypothetical protein BF3957 [Bacteroides fragilis YCH46] dbj BAD50699.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 21348 | 53715241 | 33 | 5.00E-14 | Bacteroides fragilis YCH46 | | | | | COG0500: SAM-dependent methyltransferases [Ralstonia eutropha JMP134] | | | |
| 21349, | | | | | | | | | COG0178: Exonuclease ATPase subunit [Cytophaga hutchinsonii] | | | |
| 21350 | 53762545 | 40 | 6.00E-35 | Ralstonia eutropha JMP134 | | | | | outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2135, | | | | | | | | | gb AAO75667.1 outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2136 | 48854339 | 55 | 6.00E-85 | Cytophaga hutchinsonii | | | | | putative endonuclease [Bacteroides fragilis YCH46] dbj BAD48430.1 | | | |
| 21351, | | | | | | | | | putative integral membrane protein [Campylobacter jejuni] | | | |
| 21352 | 29345970 | 31 | 7.00E-22 | Bacteroides thetaiotaomicron VPI-5482 | | | | | conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_904597.1 hypothetical protein PG0276 [Porphyromonas gingivalis W83] | | | |
| 21353, | | | | | | | | | ABC transporter, ATP-binding protein [Porphyromonas gingivalis W83] ref NP_905177.1 ABC transporter, ATP-binding protein [Porphyromonas gingivalis W83] | | | 1.8.-.- |
| 21354 | 53712972 | 56 | 7.00E-27 | Bacteroides fragilis YCH46 | | | | | putative glycosylhydrolase [Bacteroides fragilis YCH46] dbj BAD49843.1 | | | 3.2.1.17 |
| 21359, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21360 | 8572750 | 29 | 9.00E-09 | Campylobacter jejuni | | | | | gb AAO77240.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21365, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21366 | 34396430 | 34 | 1.00E-34 | Porphyromonas gingivalis W83 | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21369, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21370 | 34397012 | 66 | 9.00E-74 | Porphyromonas gingivalis W83 | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2137, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2138 | 53714385 | 31 | 2.00E-15 | Bacteroides fragilis YCH46 | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21371, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21372 | 17228761 | 23 | 5.00E-16 | Nostoc sp. PCC 7120 | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21373, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21374 | 29347543 | 34 | 2.00E-29 | Bacteroides thetaiotaomicron VPI-5482 | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21375, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21376 | 29347543 | 36 | 2.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21377, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21378 | 48854733 | 63 | 1.00E-68 | Cytophaga hutchinsonii | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21379, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21380 | 56420623 | 31 | 6.00E-20 | Geobacillus kaustophilus HTA426 | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21381, | | | | | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21382 | 48855054 | 32 | 5.00E-36 | Cytophaga hutchinsonii | | | | | hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|----|----------|
| 2139, | 20808385 | 28 | 6.00E-23 | Thermoanaerobacter tengcongensis MB4 | Diaminopimelate decarboxylase [Thermoanaerobacter tengcongensis MB4] | | | | 4.1.1.20 |
| 2140, | ABP3882 | | | | Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3667. Org:Staphylococcus epidermidis | | | | 2.1.1.61 |
| 21396 | 2 | 55 | 1.00E-36 | | | | | | |
| 21397, | AAU3889 | | | | Desc:C. pneumoniae CT287 homologue CPn0438. Org:Chlamydia pneumoniae | | | | 2.1.1.61 |
| 21398 | 5 | 42 | 3.00E-52 | | Desc:C. pneumoniae CT287 homologue CPn0438. Org:Chlamydia pneumoniae | | | | 2.1.1.61 |
| 21399, | AAU3889 | | | | | | | | |
| 21400 | 5 | 44 | 1.00E-49 | | | | | | |
| 21403, | | | | Vibrio | | | | | |
| 21404 | 28901123 | 46 | 4.00E-38 | parahaemolyticus RIMD 2210633 | hypothetical protein VPA1268 [Vibrio parahaemolyticus RIMD 2210633] dbj[BAC62611.1] hypothetical protein [Vibrio parahaemolyticus] | | | | |
| 21405, | AAU3443 | | | | Desc:Porphyromonas gingivalis protein PG95. Org:Porphyromonas gingivalis | | | | |
| 21406 | 4 | 29 | 5.00E-12 | | | | | | |
| 21409, | | | | Bacillus cereus ATCC 14579 | Cell cycle protein MesJ [Bacillus cereus ATCC 14579] gb AAP07166.1] Cell cycle protein MesJ [Bacillus cereus ATCC 14579] | | | | |
| 21410 | 30018334 | 33 | 2.00E-27 | | glutamine amidotransferase, class-I [Silicibacter pomeroyi ref YP_166322.1] glutamine amidotransferase, class-I [Silicibacter pomeroyi DSS-3] | | | | 6.3.5.2 |
| 21411, | 56677705 | 47 | 5.00E-49 | Silicibacter pomeroyi DSS-3 | | | | | |
| 21412 | | | | | | | | | |
| 21413, | | | | Photobacterium profundum SS9 | hypothetical protein PBPRA1799 [Photobacterium profundum SS9] emb CAG20204.1] hypothetical protein [Photobacterium profundum] | | | 92 | 1.00E-11 |
| 21414 | 54309986 | 46 | 3.00E-58 | | | | | | |
| | | | | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | hypothetical protein lpg1991 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28060.1] hypothetical protein lpg1991 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | |
| 21415, | | | | | peptide ABC transporter, peptide-binding protein, putative [Campylobacter lari RM2100] gb EAL54465.1] peptide ABC transporter, peptide-binding protein, putative [Campylobacter lari RM2100] | | | | |
| 21416 | 52842208 | 22 | 9.00E-08 | | | | | | |
| 21417, | | | | Campylobacter lari RM2100 | | | | | |
| 21418 | 57241353 | 35 | 2.00E-14 | | | | | | |
| 21421, | | | | Haemophilus | | | | | |
| 21422 | 46133173 | 27 | 4.00E-13 | Influenzae R2866 | COG1216: Predicted glycosyltransferases [Haemophilus influenzae R2866] | | | | |
| 21423, | | | | Crocospaera watsonii WH 8501 | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Crocospaera watsonii WH 8501] | | | | |
| 21424 | 53735011 | 37 | 5.00E-33 | | topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] gb AAO78685.1] topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21425, | | | | Bacteroides thetaiotaomicron VPI-5482 | | | | | |
| 21426 | 29348988 | 40 | 3.00E-56 | | putative DNA repair protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75185.1] putative DNA repair protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21429, | | | | Bacteroides thetaiotaomicron VPI-5482 | | | | | |
| 21430 | 29345488 | 49 | 1.00E-26 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|-------------|----------|
| 2143, 2144 | 48853949 | 73 | 1.00E-126 | Cytophaga hutchinsonii | COG0187: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit [Cytophaga hutchinsonii] | | | 5.99.1.- |
| 21437, 21438 | 29346728 | 23 | 1.00E-12 | Bacteroides thetataoimicron VPI-5482 | signaling protein without kinase domain [Bacteroides thetataoimicron VPI- 5482] gb AAO76425.1 signaling protein without kinase domain [Bacteroides thetataoimicron VPI-5482] | | | 2.7.3.- |
| 21439, 21440 | 462651 | 64 | 1.00E-56 | Fusobacterium nucleatum | Modification methylase FnuDI (Cytosine-specific methyltransferase FnuDI) (M.FnuDI) gb AAC05695.1 FnuDI DNA modification methyltransferase [Fusobacterium nucleatum] | Fusobacterium nucleatum adenylosuccinate synthetase (purA), FnuDI restriction endonuclease (fnuDIR), and FnuDI DNA modification methyltransferase (fnuDIM) genes, complete cds | 83 5.00E-07 | 2.1.1.73 |
| 21441, 21442 | 53712295 | 50 | 5.00E-38 | Bacteroides fragilis YCH46 | pantoate-beta-alanine ligase [Bacteroides fragilis YCH46] db BAD47753.1 | | | 6.3.2.1 |
| 21443, 21444 | 4163101 | 37 | 2.00E-20 | Erwinia chrysanthemi | pantoate-beta-alanine ligase [Bacteroides fragilis YCH46] transcriptional activator [Erwinia chrysanthemi] | | | |
| 21445, 21446 | 20807153 | 35 | 3.00E-40 | Thermoanaerobact er tengcongensis MB4 | predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4] gb AAM23928.1 predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4] | | | 2.4.- |
| 21447, 21448 | 48855909 | 39 | 4.00E-22 | Cytophaga hutchinsonii | COG0326: Molecular chaperone, HSP90 family [Cytophaga hutchinsonii] Beta-lactamase class C family protein [Idiomarina loihiensis L2TR] gb AAV80889.1 Beta-lactamase class C family protein [Idiomarina loihiensis L2TR] | | | 3.5.2.6 |
| 2145, 2146 | 56459157 | 41 | 3.00E-33 | Idiomarina loihiensis L2TR | COG0155: Sulfite reductase, beta subunit (hemoprotein) [Cytophaga hutchinsonii] | | | |
| 21451, 21452 | 48854475 | 42 | 7.00E-45 | Cytophaga hutchinsonii | hypothetical protein RB12778 [Rhodopirellula ballica SH 1] emb CAD7775.1 conserved hypothetical protein [Pirellula sp.] | | | |
| 21453, 21454 | 32477704 | 40 | 2.00E-16 | Rhodopirellula ballica SH 1 | transcriptional regulator [Nostoc sp. PCC 7120] db BAB73907.1 transcriptional regulator [Nostoc sp. PCC 7120] pir AB2082 transcription regulator air2208 [imported] - Nostoc sp. (strain PCC 7120) | | | |
| 21455, 21456 | 17229700 | 24 | 9.00E-14 | Nostoc sp. PCC 7120 | peptidyl-dipeptidase [Bacteroides fragilis YCH46] db BAD47716.1 peptidyl- dipeptidase [Bacteroides fragilis YCH46] | | | 3.4.15.5 |
| 21457, 21458 | 53712258 | 54 | 5.00E-38 | Bacteroides fragilis YCH46 | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|---------------|
| 21459, 21460 | 29348812 | 61 | 4.00E-74 | Bacteroides thetataomicron VPI-5482 | putative nitrogen utilization substance protein [Bacteroides thetataomicron VPI-5482] gb AAO78509.1 putative nitrogen utilization substance protein [Bacteroides thetataomicron VPI-5482] | | | |
| 21461, 21462 | 53715107 | 32 | 1.00E-33 | Bacteroides fragilis YCH46 | putative N-acetylmuramoyl-L-alanine amidase AmiA [Bacteroides fragilis YCH46] dbj BAD50565.1 putative N-acetylmuramoyl-L-alanine amidase AmiA [Bacteroides fragilis YCH46] | | | 3.5.1.28 |
| 21463, 21464 | 45510657 | 68 | 8.00E-83 | Anabaena variabilis ATCC 29413 | COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Anabaena variabilis ATCC 29413] | | | 3.1.21.3 |
| 21465, 21466 | 52426179 | 30 | 2.00E-11 | Mannheimia succiniciproducens MBEL55E | hypothetical protein MS2124 [Mannheimia succiniciproducens MBEL55E] gb AAU38731.1 unknown [Mannheimia succiniciproducens MBEL55E] | | | 3.2.1.41 |
| 21469, 21470 | 45657883 | 41 | 3.00E-24 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.7.3.- |
| 21475, 21476 | 48853532 | 37 | 4.00E-24 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 21481, 21482 | 29347959 | 42 | 2.00E-55 | Bacteroides thetataomicron VPI-5482 | putative carboxypeptidase [Bacteroides thetataomicron VPI-5482] gb AAO77656.1 putative carboxypeptidase [Bacteroides thetataomicron VPI-5482] | | | 3.4.17.1 3 |
| 21487, 21488 | 48863883 | 26 | 2.00E-18 | Microbulbifer degradans 2-40 | COG3250: Beta-galactosidase/beta-glucuronidase [Microbulbifer degradans 2-40] | | | |
| 21491, 21492 | 53711667 | 58 | 8.00E-30 | Bacteroides fragilis YCH46 | hypothetical protein BF0376 [Bacteroides fragilis YCH46] dbj BAD47125.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 21493, 21494 | 54308987 | 55 | 7.00E-24 | Photobacterium profundum SS9 | hypothetical protein PBPPRA1800 [Photobacterium profundum SS9] emb CAG20205.1 hypothetical protein [Photobacterium profundum] | | | |
| 21495, 21496 | 29346626 | 26 | 1.00E-10 | Bacteroides thetataomicron VPI-5482 | putative two-component system sensor protein, without kinase domain [Bacteroides thetataomicron VPI-5482] gb AAO76323.1 putative two- component system sensor protein, without kinase domain [Bacteroides thetataomicron VPI-5482] | | | |
| 21499, 21500 | 45658436 | 30 | 1.00E-13 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711250.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AAN48268.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AAS71159.1 alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 3.4.11.5 |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|--|---------------|
| 21505, 21506 | 51246488 | 55 | 1.00E-32 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2836 [Desulfotalea psychrophila LSV54] emb CAG37365.1 hypothetical protein [Desulfotalea psychrophila LSV54] | | | | |
| 21507, 21508 | 53713193 | 33 | 5.00E-15 | Bacteroides fragilis YCH46 | hypothetical protein BF1903 [Bacteroides fragilis YCH46] dbj BAD48651.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 21509, 21510 | 46906236 | 34 | 2.00E-20 | Listeria monocytogenes str. 4b F2365 | diphosphomevalonate decarboxylase [Listeria monocytogenes str. 4b F2365] gb AAT02802.1 diphosphomevalonate decarboxylase [Listeria monocytogenes str. 4b F2365] | | | | 4.1.1.33 |
| 2151, 2152 | 15612940 | 44 | 8.00E-25 | Bacillus halodurans C-125 | hypothetical protein BH0377 [Bacillus halodurans C-125] dbj BAB04096.1 BH0377 [Bacillus halodurans C-125] pir A83697 hypothetical protein BH0377 [imported] - Bacillus halodurans (strain C-125) | | | | |
| 21511, 21512 | 27379522 | 44 | 5.00E-15 | Bradyrhizobium japonicum USDA 110 | hypothetical protein bir4411 [Bradyrhizobium japonicum USDA 110] dbj BAC49676.1 bir4411 [Bradyrhizobium japonicum USDA 110] | | | | |
| 21513, 21514 | 48856112 | 33 | 5.00E-24 | Cytophaga hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 21519, 21520 | 53715398 | 53 | 2.00E-57 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD50856.1 two-component system response regulator [Bacteroides fragilis YCH46] | | | | |
| 21521, 21522 | 32476021 | 59 | 1.00E-62 | Rhodopirellula baltica SH 1 | X-Pro dipeptidyl-peptidase [Rhodopirellula baltica SH 1] emb CAD76400.1 X Pro dipeptidyl-peptidase [Pirellula sp.] sp P59825 PEPX_RHOBA Putative Xaa-Pro dipeptidyl-peptidase (X-Pro dipeptidyl-peptidase) (X-prolyl-dipeptidyl aminopeptidase) (X-PDAP) | | | | 3.4.14.1 1 |
| 21523, 21524 | 42525031 | 36 | 2.00E-32 | Bdellovibrio bacteriovorus HD100 | type I restriction-modification system, S subunit [Bdellovibrio bacteriovorus HD100] emb CAE81065.1 type I restriction-modification system, S subunit [Bdellovibrio bacteriovorus HD100] | | | | 3.1.21.3 |
| 21525, 21526 | 48855000 | 52 | 1.00E-49 | Cytophaga hutchinsonii | COG2509: Uncharacterized FAD-dependent dehydrogenases [Cytophaga hutchinsonii] | | | | |
| 21529, 21530 | 48858932 | 35 | 1.00E-24 | Clostridium thermocellum ATCC 27405 | COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | | 2.7.3.- |
| 2153, 2154 | 17230943 | 35 | 5.00E-32 | Nostoc sp. PCC 7120 | ATP-dependent DNA helicase [Nostoc sp. PCC 7120] pir AD2237 ATP- dependent DNA helicase [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75150.1 ATP-dependent DNA helicase [Nostoc sp. PCC 7120] | | | | |
| 21535, 21536 | 48854182 | 42 | 6.00E-20 | Cytophaga hutchinsonii | COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii] | | | | |
| 21541, 21542 | 48854793 | 43 | 1.00E-54 | Cytophaga hutchinsonii | COG1109: Phosphomannomutase [Cytophaga hutchinsonii] | | | | 5.4.2.8 |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|---|----|-------------------|
| 21543, 21544 | 31194451 | 67 | 1.00E-78 | Anopheles gambiae | ENSANGP0000015516 [Anopheles gambiae] lysine-sensitive aspartokinase III [Haemophilus ducreyi 35000HP] ref NP_873799.1 lysine-sensitive aspartokinase III [Haemophilus ducreyi 35000HP] | | | 3.4.21.- |
| 21545, 21546 | 33148669 | 34 | 1.00E-24 | Haemophilus ducreyi 35000HP | | | | 2.7.2.4 |
| 21547, 21548 | 54302486 | 73 | 6.00E-99 | Photobacterium profundum SS9 | hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1 hypothetical maturase [Photobacterium profundum] | Photobacterium profundum SS9 chromosome 2; segment 3/7 | | |
| 2155, 2156 | 42523179 | 51 | 4.00E-68 | Bdellovibrio bacteriovorus HD100 | putative formyltransferase [Bdellovibrio bacteriovorus HD100] emb CAE79552.1 putative formyltransferase [Bdellovibrio bacteriovorus HD100] | | 84 | 7.00E-19 2.7.7.49 |
| 21551, 21552 | 15613179 | 42 | 5.00E-19 | Bacillus halodurans C-125 | hypothetical protein BH0616 [Bacillus halodurans C-125] dbj BAB04335.1 BH0616 [Bacillus halodurans C-125] pir H83726 hypothetical protein BH0616 [imported] - Bacillus halodurans (strain C-125) | | | 2.1.2.9 |
| 21553, 21554 | 48854781 | 31 | 2.00E-10 | Cytophaga hutchinsonii | hypothetical protein Chut02002457 [Cytophaga hutchinsonii] | | | |
| 21557, 21558 | 24214122 | 41 | 7.00E-32 | Leptospira interrogans serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AA048621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] | | | |
| 21563, 21564 | 19704846 | 31 | 5.00E-08 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Phosphatidylinositol-4-phosphate 5-kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93640.1 hypothetical exported 24-amino acid repeat protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | 2.7.1.88 |
| 21567, 21568 | 46141620 | 59 | 3.00E-28 | Psychrobacter sp. 273-4 | COG3335: Transposase and inactivated derivatives [Psychrobacter sp. 273- 4] | | | |
| 21569, 21570 | 53715439 | 64 | 2.00E-57 | Bacteroides fragilis YCH46 | DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] dbj BAD50897.1 DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] | | | 2.7.7.6 |
| 2157, 2158 | 53714076 | 28 | 4.00E-15 | Bacteroides fragilis YCH46 | putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD49534.1 putative glycosyltransferase [Bacteroides fragilis YCH46] | | | |
| 21571, 21572 | 37525750 | 59 | 9.00E-52 | Photorhabdus luminescens subsp. laumondii TTO1 | hypothetical protein plu1816 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE14109.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] | | | |
| 21573, 21574 | 22094882 | 49 | 3.00E-10 | Flavobacterium johnsoniae | GldH [Flavobacterium johnsoniae] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|---|--|--|--|----------|
| 21577, | 48859857 | 30 | 2.00E-26 | Clostridium thermocellum ATCC 27405 | COG0653: Preprotein translocase subunit SecA (ATPase, RNA helicase) [Clostridium thermocellum ATCC 27405] | | | | |
| 21578 | ABB9930 | | | | Desc:Amino acid sequence of DNA-methyltransferase M.EacI. | | | | |
| 21579, | 9 | 34 | 2.00E-33 | | Org: <i>Eubacterium acidaminophilum</i> | | | | 2.1.1.72 |
| 21580 | | | | | | | | | |
| 21583, | 32473152 | 39 | 5.00E-29 | Rhodospirillum rubrum SH 1 | hypothetical protein RB4512 [Rhodospirillum rubrum SH 1] emb[CAD73832.1] | | | | |
| 21584 | | | | | conserved hypothetical protein [Prelula sp.] | | | | |
| 21585, | | | | | COG1060: Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes [Cytophaga hutchinsonii] | | | | |
| 21586 | 48855692 | 71 | 2.00E-88 | Cytophaga hutchinsonii | | | | | |
| 21587, | | | | | | | | | |
| 21588 | 53715653 | 33 | 3.00E-14 | Bacteroides fragilis YCH46 | hypothetical protein BF4373 [Bacteroides fragilis YCH46] dbj[BAD5111.1] conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 21589, | | | | | LacI family transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21590 | 29349021 | 44 | 8.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | gb AAO78718.1 LacI family transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 2159, | | | | | | | | | |
| 2160 | 29349471 | 47 | 1.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | NADH dehydrogenase I, chain I [Bacteroides thetaiotaomicron VPI-5482] gb AAO79188.1 NADH dehydrogenase I, chain I [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.6.5.3 |
| 21591, | | | | | | | | | |
| 21592 | 16080202 | 45 | 3.00E-29 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU31500 [Bacillus subtilis subsp. subtilis str. 168] emb CAB07916.1 unknown [Bacillus subtilis] emb CAB15139.1 yuxK [Bacillus subtilis subsp. subtilis str. 168] pir B55220 hypothetical protein yuxK - Bacillus subtilis gb AAA64944.1 unknown sp P40761 YUXK_BACSU | | | | |
| 21593, | | | | | | | | | |
| 21594 | 48854071 | 45 | 1.00E-26 | Cytophaga hutchinsonii | Hypothetical protein yuxK (ORF2) COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii] | | | | |
| 21599, | | | | | | | | | |
| 21600 | 39995668 | 26 | 7.00E-22 | Geobacter sulfurreducens PCA | hypothetical protein GSU0561 [Geobacter sulfurreducens PCA] gb AAR33892.1 conserved domain protein [Geobacter sulfurreducens PCA] | | | | |
| 21601, | | | | | | | | | |
| 21602 | 48854901 | 44 | 7.00E-28 | Cytophaga hutchinsonii | COG3696: Putative silver efflux pump [Cytophaga hutchinsonii] | | | | |
| 21603, | | | | | | | | | |
| 21604 | 48856151 | 52 | 1.00E-29 | Cytophaga hutchinsonii | hypothetical protein Chut02001392 [Cytophaga hutchinsonii] | | | | |
| 21605, | | | | | | | | | |
| 21606 | 24371725 | 38 | 2.00E-17 | Shewanella oneidensis MR-1 | hypothetical protein SO0125 [Shewanella oneidensis MR-1] gb AAN53212.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | | |
| 21607, | | | | | | | | | |
| 21608 | 41690520 | 83 | 7.00E-85 | Psychrobacter sp. 273-4 | COG2050: Uncharacterized protein, possibly involved in aromatic compounds catabolism [Psychrobacter sp. 273-4] | | | | |
| 2161, | | | | | | | | | |
| 2162 | 23124542 | 32 | 2.00E-17 | Nostoc punctiforme PCC 73102 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |

| | | | | | | | | |
|--------|----------|----|-----------|---|--|--|----|------------------|
| 21613, | 29347486 | 38 | 3.00E-29 | Bacteroides thetaiotaomicron VPI-5482 | acetohydroxyacid synthase small subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO77183.1 acetohydroxyacid synthase small subunit | | | 4.1.3.18 |
| 21614 | | | | Bacteroides thetaiotaomicron VPI-5482 | putative dTDP-4-dehydrothiamine reductase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76837.1 putative dTDP-4-dehydrothiamine reductase | | | 1.1.1.13 |
| 21615, | 29347140 | 46 | 2.00E-31 | Bacteroides thetaiotaomicron VPI-5482 | UDP-glucose/GDP-mannose dehydrogenase family protein [Chlorobium tepidum TLS] gb AAM71474.1 UDP-glucose/GDP-mannose dehydrogenase family protein [Chlorobium tepidum TLS] | | | 1.1.1.- |
| 21617, | 21673067 | 48 | 2.00E-27 | Chlorobium tepidum TLS | COG2038: NaMN:DMB phosphoribosyltransferase [Microbulbifer degradans 2-40] | | | 2.4.2.21 |
| 21618 | 48861664 | 62 | 3.00E-31 | Microbulbifer degradans 2-40 | hypothetical protein STH2171 [Symbiobacterium thermophilum IAM 14863] dbj BAD41156.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863] | | | |
| 21619, | 51893309 | 37 | 2.00E-14 | Symbiobacterium thermophilum IAM 14863 | COG0686: Alanine dehydrogenase [Cytophaga hutchinsonii] | | | 1.4.1.1 |
| 21620 | 48856852 | 45 | 2.00E-24 | Cytophaga hutchinsonii | pyruvate phosphate dikinase [Porphyromonas gingivalis W83] ref NP_905238.1 pyruvate phosphate dikinase [Porphyromonas gingivalis W83] | | | |
| 21623, | 34397073 | 75 | 2.00E-71 | Porphyromonas gingivalis W83 | hypothetical protein RB6958 [Rhodopirella baltica SH 1] emb CAD75097.1 conserved hypothetical protein [Pirella sp.] | | 87 | 2.00E-15/2.7.9.1 |
| 21624 | 32474556 | 33 | 2.00E-21 | Rhodopirella baltica SH 1 | hypothetical protein Chut0202457 [Cytophaga hutchinsonii] | | | |
| 21625, | 48854781 | 32 | 7.00E-15 | Cytophaga hutchinsonii | COG1404: Subtilisin-like serine proteases [Cytophaga hutchinsonii] | | | |
| 21626 | 48853939 | 32 | 2.00E-07 | Cytophaga hutchinsonii | tpg/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] | | | |
| 21631, | 48854781 | 32 | 7.00E-15 | Cytophaga hutchinsonii | COG0013: Alanyl-tRNA synthetase [Cytophaga hutchinsonii] | | | |
| 21632 | 48854966 | 71 | 1.00E-100 | Cytophaga hutchinsonii | putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46] | | 86 | 4.00E-17/6.1.1.7 |
| 21635, | 47526988 | 29 | 2.00E-10 | Bacillus anthracis str. 'Ames Ancestor' | | | | 3.5.1.- |
| 21636 | | | | | | | | |
| 21637, | | | | | | | | |
| 21638 | | | | | | | | |
| 21641, | | | | | | | | |
| 21642 | 48854966 | 71 | 1.00E-100 | Cytophaga hutchinsonii | | | | |
| 21643, | 53712055 | 48 | 8.00E-38 | Bacteroides fragilis YCH46 | | | | |
| 21644 | | | | | | | | |

| | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|--|--|----------|
| 21645, | 46202712 | 36 | 2.00E-17 | Magnetospirillum magnetotacticum MS-1 | COG4623: Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein [Magnetospirillum magnetotacticum MS-1] | | | 3.2.1.- |
| 21646 | | | | | | | | |
| 21647, | 53714082 | 41 | 4.00E-12 | Bacteroides fragilis YCH46 | putative excisionase [Bacteroides fragilis YCH46] dbj BAD49540.1 putative excisionase [Bacteroides fragilis YCH46] | | | |
| 21648 | | | | | | | | |
| 2165, | | | | | | | | |
| 2165, | 32474556 | 33 | 2.00E-21 | Rhodopirellula batlica SH 1 | hypothetical protein RB6958 [Rhodopirellula batlica SH 1] emb CAD75097.1 conserved hypothetical protein [Pirellula sp.] | | | |
| 21651, | | | | | | | | |
| 21652 | 14531032 | 47 | 2.00E-48 | Flavobacterium johnsoniae | Fjo14 [Flavobacterium johnsoniae] | | | |
| | | | | | | | | |
| 21653, | | | | | | | | |
| 21654 | 29346131 | 37 | 1.00E-48 | Bacteroides thetaiotaomicron VPI-5482 | DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75828.1 DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21655, | | | | | | | | |
| 21656 | 37962667 | 46 | 3.00E-34 | Bacteroides uniformis | Tn10-like transposase [Bacteroides uniformis] | | | |
| | | | | | | | | |
| 21659, | | | | | | | | |
| 21660 | 15793683 | 40 | 9.00E-20 | Neisseria meningitidis Z2491 | hypothetical protein NMA0704 [Neisseria meningitidis Z2491] emb CAB83991.1 hypothetical protein NMA0704 [Neisseria meningitidis Z2491] pir E81913 hypothetical protein NMA0704 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) | | | 4.6.1.10 |
| 21661, | | | | | | | | |
| 21662 | 53714846 | 47 | 8.00E-50 | Bacteroides fragilis YCH46 | putative cation efflux system transmembrane protein [Bacteroides fragilis YCH46] dbj BAD50304.1 putative cation efflux system transmembrane protein [Bacteroides fragilis YCH46] | | | |
| | | | | | | | | |
| 21663, | | | | | | | | |
| 21664 | 33864121 | 37 | 1.00E-20 | Prochlorococcus marinus str. MIT 9313 | LybB protein homolog [Prochlorococcus marinus str. MIT 9313] emb CAE22029.1 LybB protein homolog [Prochlorococcus marinus str. MIT 9313] sp Q7V477 ISPH_PROMM 4-hydroxy-3-methylbut-2-enyl diphosphate reductase | | | |
| 21665, | | | | | | | | |
| 21666 | 48856755 | 59 | 2.00E-61 | Cytophaga hutchinsonii | COG0139: Phosphoribosyl-AMP cyclohydrolase [Cytophaga hutchinsonii] | | | 3.5.4.19 |
| | | | | | | | | |
| 21667, | | | | | | | | |
| 21668 | 51244305 | 43 | 9.00E-41 | Desulfotalea psychrophila LSV54 | hypothetical protein DP0453 [Desulfotalea psychrophila LSV54] emb CAG35182.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 21671, | | | | | | | | |
| 21672 | 48863666 | 32 | 4.00E-07 | Microbulifer degradans 2-40 | COG3428: Predicted membrane protein [Microbulifer degradans 2-40] | | | |
| | | | | | | | | |
| 21673, | | | | | | | | |
| 21674 | 52632010 | 30 | 2.00E-15 | uncultured archaeon GZfos12E1 | conserved hypothetical protein [uncultured archaeon GZfos12E1] | | | |
| | | | | | | | | |
| 21675, | | | | | | | | |
| 21676 | 53714587 | 69 | 3.00E-28 | Bacteroides fragilis YCH46 | 50S ribosomal protein L31 type B [Bacteroides fragilis YCH46] dbj BAD500045.1 50S ribosomal protein L31 type B [Bacteroides fragilis YCH46] | | | |
| 21677, | | | | | | | | |
| 21678 | 56964929 | 50 | 9.00E-11 | Bacillus clausii KSM-K16 | glycosyltransferase [Bacillus clausii KSM-K16] dbj BAD65699.1 glycosyltransferase [Bacillus clausii KSM-K16] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 21679, 21680 | 48855461 | 39 | 1.00E-40 | Cytophaga hutchinsonii | COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 21683, 21684 | 53712087 | 40 | 3.00E-20 | Bacteroides fragilis YCH46 | putative transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 21689, 21690 | 48856079 | 62 | 9.00E-67 | Cytophaga hutchinsonii | COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | 1.8.- |
| 21693, 21694 | 29348486 | 54 | 4.00E-33 | Bacteroides thetataoamicron VPI-5482 | ribonuclease R [Bacteroides thetataoamicron VPI-5482] gb AAO78183.1 ribonuclease R [Bacteroides thetataoamicron VPI-5482] | | | 3.1.- |
| 21695, 21696 | 53712881 | 40 | 1.00E-45 | Bacteroides fragilis YCH46 | hypothetical protein BF1590 [Bacteroides fragilis YCH46] dbj BAD48339.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | 2.- |
| 21697, 21698 | 53713905 | 26 | 7.00E-12 | Bacteroides fragilis YCH46 | LysM-repeat proteins and domains [Bacteroides fragilis YCH46] dbj BAD49363.1 LysM-repeat proteins and domains [Bacteroides fragilis YCH46] | | | |
| 21699, 21700 | 46580228 | 30 | 2.00E-10 | Desulfovibrio vulgaris subsp. YCH46 | protein-export membrane protein SecF [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS9295.1 protein-export membrane protein SecF [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 21701, 21702 | 29347584 | 35 | 4.00E-20 | Bacteroides thetataoamicron VPI-5482 | ABC transporter ATP-binding protein [Bacteroides thetataoamicron VPI-5482] gb AAO77281.1 ABC transporter ATP-binding protein [Bacteroides thetataoamicron VPI-5482] | | | |
| 21703, 21704 | 52841257 | 49 | 7.00E-48 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | ribose-phosphate pyrophosphokinase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27109.1 ribose-phosphate pyrophosphokinase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAM00625.1 unknown [Legionella pneumophila] | | | 2.7.6.1 |
| 21705, 21706 | 53712038 | 32 | 3.00E-26 | Bacteroides fragilis YCH46 | hypothetical protein BF0745 [Bacteroides fragilis YCH46] dbj BAD47496.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 21707, 21708 | 14531035 | 47 | 1.00E-47 | Flavobacterium johnsoniae | gliding motility protein GldG [Flavobacterium johnsoniae] probable: Putative GlcNAc transferase [Azoarcus sp. EbN1] emb CAI06955.1 probable: Putative GlcNAc transferase [Azoarcus sp. EbN1] | | | |
| 21709, 21710 | 56476267 | 38 | 9.00E-10 | Azoarcus sp. EbN1 | putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46] | | | 3.5.1.- |
| 2171, 2172 | 53712055 | 43 | 1.00E-52 | Bacteroides fragilis YCH46 | related to isochorismate synthase (MenF) [Desulfotalea psychrophila LSv54] emb CAG34983.1 related to isochorismate synthase (MenF) [Desulfotalea psychrophila LSv54] | | | |
| 21711, 21712 | 51244106 | 36 | 9.00E-15 | Desulfotalea psychrophila LSv54 | | | | 5.4.99.6 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 21713, 21714 | 48854285 | 35 | 3.00E-39 | Cytophaga hutchinsonii | COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 21715, 21716 | 57229242 | 24 | 2.00E-11 | Cryptococcus neoformans var. neoformans JEC21 | conserved hypothetical protein [Cryptococcus neoformans var. neoformans JEC21] | | | | 2.3.1.51 |
| 21717, 21718 | 29346221 | 43 | 4.00E-42 | Bacteroides thetaiotaomicron VPI-5482 | putative tRNA/rRNA methyltransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO75918.1 putative tRNA/rRNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.1.1.- |
| 21719, 21720 | 24374852 | 54 | 7.00E-41 | Shewanella oneidensis MR-1 | antioxidant, AhpC/TSA family [Shewanella oneidensis MR-1] gb AAN56339.1 antioxidant, AhpC/TSA family [Shewanella oneidensis MR- 1] | | | | 1.11.1.- |
| 21725, 21726 | 32470723 | 51 | 4.00E-84 | Rhodopirellula baltica SH 1 | probable acylaminoacyl-peptidase [Rhodopirellula baltica SH 1] emb CAD71387.1 probable acylaminoacyl-peptidase [Pirellula sp.] | | | | 3.4.19.1 |
| 21727, 21728 | 29345713 | 42 | 9.00E-44 | Bacteroides thetaiotaomicron VPI-5482 | putative patatin-like phospholipase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75410.1 putative patatin-like phospholipase [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.4.21.- |
| 21729, 21730 | 42519768 | 43 | 1.00E-31 | Lactobacillus johnsonii NCC 533 | chromosome partitioning protein ParB [Lactobacillus johnsonii NCC 533] gb AAS09664.1 chromosome partitioning protein ParB [Lactobacillus johnsonii NCC 533] | | | | |
| 2173, 2174 | 48856045 | 24 | 1.00E-08 | Cytophaga hutchinsonii | hypothetical protein Chut02001277 [Cytophaga hutchinsonii] | | | | |
| 21737, 21738 | 39997374 | 32 | 1.00E-21 | Geobacter sulfurreducens PCA | hypothetical protein GSU2276 [Geobacter sulfurreducens PCA] gb AAR35652.1 conserved hypothetical protein [Geobacter sulfurreducens PCA] | | | | |
| 21739, 21740 | 55246965 | 65 | 6.00E-36 | Anopheles gambiae str. PEST | ENSANGP000000000220 [Anopheles gambiae str. PEST] ref XP_561052.1 ENSANGP000000000220 [Anopheles gambiae str. PEST] | | | | |
| 21741, 21742 | 48854452 | 58 | 6.00E-30 | Cytophaga hutchinsonii | COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii] | | | | |
| 21743, 21744 | ABJ19039 | 40 | 9.00E-14 | | Desc:Pathogen specific antigen related staphylococcal protein SEQ ID No 288. Org:Staphylococcus sp | | | | 3.2.1.17 |
| 21745, 21746 | 53711478 | 44 | 1.00E-36 | Bacteroides fragilis YCH46 | hypothetical protein BF0187 [Bacteroides fragilis YCH46] db BAD46936.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 21749, 21750 | 16080777 | 41 | 4.00E-49 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU37240 [Bacillus subtilis subsp. subtilis str. 168] emb CAA90049.1 unknown, similar to E.coli cardiolipin synthase [Bacillus subtilis] emb CAB15752.1 ywiE [Bacillus subtilis subsp. subtilis str. 168] pir S60089 cardiolipin synthetase homolog ywiE - Bacillus subtilis spiP45860 CLS1_BACSU Probable cardiolipin synthetase 1 (Cardiolipin synthase 1) (CL synthase 1) | | | | 2.7.8.- |

| | | | | | | | | |
|--------|----------|----|-----------|--|--|--|--|----------|
| 21757, | 48855885 | 76 | 1.00E-115 | Cytophaga hutchinsonii | COG0209: Ribonucleotide reductase, alpha subunit [Cytophaga hutchinsonii] | | | 1.17.4.1 |
| 21758 | | | | | | | | |
| 21759, | 46316555 | 38 | 3.00E-07 | Burkholderia cepacia R18194 | COG1289: Predicted membrane protein [Burkholderia cepacia R18194] | | | |
| 21760 | | | | | | | | |
| 21765, | 48855808 | 42 | 3.00E-12 | Cytophaga hutchinsonii | COG0694: Thioredoxin-like proteins and domains [Cytophaga hutchinsonii] | | | |
| 21766 | | | | | | | | |
| 21769, | 48853783 | 52 | 7.00E-42 | Cytophaga hutchinsonii | COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] | | | 2.7.7.7 |
| 21770 | | | | | | | | |
| 2177, | | | | uncultured archaeon | | | | |
| 2178 | 52550493 | 45 | 1.00E-51 | GZfos9D8 | conserved hypothetical protein [uncultured archaeon GZfos9D8] | | | 2.8.1.6 |
| 21771, | | | | | | | | |
| 21772 | 34397936 | 29 | 3.00E-14 | Porphyromonas gingivalis W83 | hypothetical protein PG2030 [Porphyromonas gingivalis W83] ref NP_906097.1 hypothetical protein PG2030 [Porphyromonas gingivalis W83] | | | |
| | | | | | | | | |
| 21773, | | | | Symbiobacterium thermophilum IAM 14863 | oligopeptide ABC transporter substrate-binding protein [Symbiobacterium thermophilum IAM 14863] | | | |
| 21774 | 51891266 | 28 | 1.00E-18 | Lactobacillus helveticus | mevalonate diphosphate decarboxylase [Lactobacillus helveticus] | | | 4.1.1.33 |
| 21775, | 15212071 | 31 | 3.00E-16 | Bacteroides fragilis YCH46 | endopeptidase Clp ATP-binding chain B [Bacteroides fragilis YCH46] | | | |
| 21776 | | | | | | | | |
| 21779, | 53712497 | 52 | 9.00E-29 | Trichodesmium erythraeum IMS101 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] | | | |
| 21780 | | | | | transposase [Proteus vulgaris] dbj BAB93648.1 transposase [Proteus vulgaris] | | | |
| 21781, | | | | | | | | |
| 21782 | 48890583 | 30 | 9.00E-21 | Bacillus cereus G9241 | DNA-binding response regulator [Bacillus cereus G9241] gb EAL16839.1 | | | |
| 21787, | 21233748 | 47 | 2.00E-10 | Proteus vulgaris | DNA-binding response regulator [Bacillus cereus G9241] | | | |
| 21788 | | | | | | | | |
| 21789, | 47564364 | 43 | 1.00E-30 | uncultured archaeon | conserved hypothetical protein [uncultured archaeon GZfos9D8] | | | 2.8.1.6 |
| 21790 | 52550493 | 47 | 2.00E-58 | GZfos9D8 | | | | |
| 2179, | | | | | | | | |
| 2180 | 53685139 | 31 | 5.00E-13 | Desulfotribacterium hafniense DCB-2 | hypothetical protein Desu02002249 [Desulfotribacterium hafniense DCB-2] | | | |
| 21793, | | | | | | | | |
| 21794 | | | | Chromobacterium violaceum ATCC 12472 | probable sensory transduction histidine kinase [Chromobacterium violaceum ATCC 12472] ref NP_902929.1 probable sensory transduction histidine kinase [Chromobacterium violaceum ATCC 12472] | | | 2.7.- |
| 21795, | | | | | | | | |
| 21796 | 34104565 | 36 | 4.00E-23 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|--|--|---------------|
| 21797, 21798 | 27366595 | 33 | 2.00E-21 | Vibrio vulnificus CMCP6 | Response regulator [Vibrio vulnificus CMCP6] ref NP_936705.1 probable response regulator [Vibrio vulnificus YJ016] gb AAO07112.1 Response regulator [Vibrio vulnificus CMCP6] dbj BAC96675.1 probable response regulator [Vibrio vulnificus YJ016] | | | | 2.7.3.- |
| 21801, 21802 | 53715865 | 53 | 1.00E-69 | Bacteroides fragilis YCH46 | leucyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD51323.1 leucyl-tRNA synthetase [Bacteroides fragilis YCH46] | | | | 6.1.1.4 |
| 21803, 21804 | 46118176 | 37 | 8.00E-13 | Crocospaera watsonii WH 8501 | COG2207: AraC-type DNA-binding domain-containing proteins | | | | |
| 21805, 21806 | 27817220 | 38 | 2.00E-28 | Nostoc sp. ATCC 53789 | [Crocospaera watsonii WH 8501] | | | | |
| 21809, 21810 | 29349306 | 35 | 8.00E-10 | Bacteroides thetaiotaomicron VPI-5482 | penicillin-binding protein-like protein [Nostoc sp. ATCC 53789] | | | | 3.5.2.6 |
| 2181, 2182 | 18312445 | 46 | 4.00E-48 | Pyrobaculum aerophilum str. IM2 | TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO79003.1 TonB [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 21811, 21812 | 52853435 | 89 | 1.00E-117 | Psychrobacter sp. 273-4 | hypothetical protein PAE1163 [Pyrobaculum aerophilum str. IM2] gb AAL63294.1 conserved hypothetical protein [Pyrobaculum aerophilum str. IM2] | | | | |
| 21815, 21816 | 25011383 | 33 | 4.00E-08 | Streptococcus agalactiae NEM316 | COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] ref ZP_00146915.2 COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] | | | | |
| 21817, 21818 | AAV2914 | 34 | 1.00E-34 | | hypothetical protein gbs1341 [Streptococcus agalactiae NEM316] emb CAD47000.1 unknown [Streptococcus agalactiae NEM316] | | | | |
| 21819, 21820 | 48853536 | 40 | 1.00E-47 | Cytophaga hutchinsonii | Desc:Amino acid sequence of a virulence factor encoded by ORF11738. Org:Pseudomonas aeruginosa | | | | |
| 21821, 21822 | 28897146 | 38 | 5.00E-45 | Vibrio parahaemolyticus RIMD 2210633 | COG1619: Uncharacterized proteins, homologs of microcin C7 resistance protein MccF [Cytophaga hutchinsonii] | | | | 3.4.17.1 3 |
| 21823, 21824 | 29345972 | 70 | 4.00E-47 | Bacteroides thetaiotaomicron VPI-5482 | putative hemolysin [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58635.1 putative hemolysin [Vibrio parahaemolyticus] | | | | |
| 21825, 21826 | 48837702 | 58 | 3.00E-53 | Methanosarcina barkeri str. fusaro | putative ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75669.1 putative ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.8.-.- |
| 21829, 21830 | 38637719 | 26 | 4.00E-10 | Cupriavidus necator | COG1001: Adenine deaminase [Methanosarcina barkeri str. fusaro] | | | | 3.5.4.2 |
| 2183, 2184 | 15644379 | 38 | 1.00E-09 | Thermotoga maritima MSB8 | hypothetical protein PHG054 [Cupriavidus necator] gb AAP85807.1 hypothetical protein PHG054 [Ralstonia eutropha] | | | | |
| | | | | | hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD36698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|---------------|
| 21833, 21834 | 48855019 | 50 | 1.00E-26 | Cytophaga hutchinsonii | COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii] | | | 2.4.1.18 2 |
| 21835, 21836 | 48850961 | 69 | 1.00E-40 | Novosphingobium aromaticivorans DSM 12444 | COG0250: Transcription antiterminator [Novosphingobium aromaticivorans DSM 12444] | | | |
| 21839, 21840 | 1710105 | 55 | 3.00E-65 | Plasmid pWQ799 | UDP-N-acetylglucosamine 2-epimerase (UDP-GlcNAc-2-epimerase) gb AAC98403.1 UDP-N-acetylglucosamine 2-epimerase [Plasmid pWQ799] | | | 5.1.3.14 |
| 21841, 21842 | 51246488 | 36 | 5.00E-29 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2636 [Desulfotalea psychrophila LSV54] emb CAG37365.1 hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 21845, 21846 | 29349812 | 34 | 2.00E-35 | Bacteroides thetaiotaomicron VPI-5482 | putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO79509.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21849, 21850 | 48853433 | 45 | 6.00E-23 | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | |
| 2185, 2186 | 15644379 | 38 | 1.00E-09 | Thermotoga maritima MSB8 | hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD38698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | |
| 21855, 21856 | 53714426 | 34 | 1.00E-06 | Bacteroides fragilis YCH46 | hypothetical protein BF3139 [Bacteroides fragilis YCH46] dbj BAD49884.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 21857, 21858 | 45657883 | 39 | 3.00E-20 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.7.3.- |
| 21859, 21860 | 48854752 | 54 | 2.00E-74 | Cytophaga hutchinsonii | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 21861, 21862 | 29349616 | 42 | 3.00E-28 | Bacteroides thetaiotaomicron VPI-5482 | phosphohydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79313.1 phosphohydrolase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 21863, 21864 | 48855471 | 29 | 8.00E-15 | Cytophaga hutchinsonii | COG1622: Heme/copper-type cytochrome/quinol oxidases, subunit 2 [Cytophaga hutchinsonii] | | | |
| 21865, 21866 | 53711569 | 33 | 4.00E-19 | Bacteroides fragilis YCH46 | hypothetical protein BF0278 [Bacteroides fragilis YCH46] dbj BAD47027.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|---|--|--|--|----------|
| 21867, | 15616393 | 31 | 1.00E-09 | Bacillus halodurans C-125 | hypothetical protein BH3831 [Bacillus halodurans C-125] dbj BAB07550.1 BH3831 [Bacillus halodurans C-125] pir G84128 hypothetical protein BH3831 [imported] - Bacillus halodurans (strain C-125) | | | | |
| 21868 | 28209996 | 40 | 1.00E-21 | Clostridium tetani E88 | putative polysaccharide deacetylase [Clostridium tetani E88] gb AAO34877.1 putative polysaccharide deacetylase [Clostridium tetani E88] | | | | |
| 21875, | 30023301 | 32 | 9.00E-13 | Bacillus cereus ATCC 14579 | Amylovoran biosynthesis AmsK [Bacillus cereus ATCC 14579] gb AAP12133.1 Amylovoran biosynthesis AmsK [Bacillus cereus ATCC 14579] | | | | |
| 21876 | 21674545 | 42 | 2.00E-20 | Chlorobium tepidum TLS | DNA methylase, putative [Chlorobium tepidum TLS] gb AAM72952.1 DNA methylase, putative [Chlorobium tepidum TLS] | | | | |
| 21877, | | | | Bacteroides thetaiotaomicron VPI-5482 | CysQ, sulfite synthesis pathway protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75518.1 CysQ, sulfite synthesis pathway protein [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.1.3.25 |
| 21878 | 29345821 | 47 | 3.00E-39 | Cytophaga hutchinsonii | COG3279: Response regulator of the LytR/AlgR family [Cytophaga hutchinsonii] | | | | 2.7.-.- |
| 21881, | 48855702 | 39 | 9.00E-38 | Clostridium tetani E88 | putative mechanosensitive ion-channel [Clostridium tetani E88] gb AAO35110.1 putative mechanosensitive ion-channel [Clostridium tetani E88] | | | | |
| 21885, | 28210229 | 51 | 1.00E-41 | Bacteroides fragilis YCH46 | phosphohydrolase [Bacteroides fragilis YCH46] dbj BAD47659.1 phosphohydrolase [Bacteroides fragilis YCH46] | | | | |
| 21886 | 53712201 | 61 | 5.00E-61 | Porphyrromonas gingivalis W83 | hypothetical protein PG1908 [Porphyrromonas gingivalis W83] ref NP_905991.1 hypothetical protein PG1908 [Porphyrromonas gingivalis W83] | | | | |
| 21891, | 34397829 | 35 | 1.00E-08 | Rhodopirellula baltica SH 1 | purine nucleoside phosphorylase [Rhodopirellula baltica SH 1] emb CAD74895.1 purine nucleoside phosphorylase [Pirellula sp.] | | | | 2.4.2.1 |
| 21897, | 32474355 | 51 | 8.00E-37 | Bacteroides fragilis YCH46 | putative N-acetylmuramoyl-L-alanine amidase [Bacteroides fragilis YCH46] dbj BAD50289.1 putative N-acetylmuramoyl-L-alanine amidase [Bacteroides fragilis YCH46] | | | | 3.5.1.28 |
| 21898 | 53714831 | 46 | 4.00E-57 | Gloeobacter violaceus PCC 7421 | hypothetical protein gl11812 [Gloeobacter violaceus PCC 7421] dbj BAC89753.1 gl11812 [Gloeobacter violaceus PCC 7421] | | | | |
| 21899, | | | | Thiobacillus denitrificans ATCC 25259 | COG0189: Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase) [Thiobacillus denitrificans ATCC 25259] | | | | |
| 21900 | 37521381 | 27 | 6.00E-13 | Methanococcus burtonii DSM 6242 | COG0381: UDP-N-acetylglucosamine 2-epimerase [Methanococcus burtonii DSM 6242] | | | | 5.1.3.14 |

| | | | | | | | | | |
|------------------------------------|----------------------------------|----------------------|---|--|--|----|----------|----------|---------------|
| 21907, 21908 21909, 21910 | 150457 50 29335922 31 | 1.00E-46 2.00E-21 | Streptomyces aureofaciens Bacteroides thetaitaomicron | chloroperoxidase CPO-A2 [Streptomyces aureofaciens] pir S27614 bromide peroxidase (EC 1.11.1.-) BPO1 - Streptomyces aureofaciens sp P29715 BPA2_STRAU Non-haem bromoperoxidase BPO-A2 (Bromide peroxidase) (BPO2) mobilization protein C [Bacteroides thetaiotaomicron] ref NP_818961.1 mobilization protein C [Bacteroides thetaiotaomicron] | | | | | 1.11.1.1 0 |
| 21911, 21912 21913, 21914 | 29348628 71 48854577 56 | 2.00E-92 4.00E-39 | Bacteroides thetaitaomicron VPI-5482 Cytophaga hutchinsonii | S-adenosylmethionine synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78325.1 S-adenosylmethionine synthetase [Bacteroides thetaitaomicron VPI-5482] sp Q8A2T6 METK_BACTN S- adenosylmethionine synthetase (Methionine adenosyltransferase) (AdoMet synthetase) (MAT) COG0769: UDP-N-acetylmuramyl tripeptide synthase [Cytophaga hutchinsonii] | Anopheles gambiae ENSANGP00000000 0138 (ENSANGG0000000 00136) mRNA, partial cds | 81 | 1.00E-29 | 2.5.1.6 | 6.3.2.13 |
| 21915, 21916 21921, 21922 | 29348444 47 10956606 60 | 2.00E-59 2.00E-66 | Bacteroides thetaitaomicron VPI-5482 Riemerella anatipestifer | carboxy-terminal processing protease precursor [Bacteroides thetaitaomicron VPI-5482] gb AAO78141.1 carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] transposase [Riemerella anatipestifer] gb AAD33096.1 transposase [Riemerella anatipestifer] | | | | 3.4.21.- | |
| 21923, 21924 21925, 21926 | 15615497 32 48855386 28 | 1.00E-10 1.00E-07 | Bacillus halodurans C-125 Cytophaga hutchinsonii | aryldialkylphosphatase [Bacillus halodurans C-125] dbj BAB06654.1 aryldialkylphosphatase [Bacillus halodurans C-125] pir G84016 aryldialkylphosphatase BH2935 [Imported] - Bacillus halodurans (strain C- 125) COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | | | |
| 21927, 21928 21929, 21930 | 48766082 29 48853984 43 | 7.00E-15 4.00E-37 | Rhodospirillum rubrum Cytophaga hutchinsonii | COG0520: Selenocysteine lyase [Rhodospirillum rubrum] COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | | | |
| 2193, 2194 | 48864533 38 | 2.00E-10 | Microbulbifer degradans 2-40 | COG3291: FOG: PKD repeat [Microbulbifer degradans 2-40] | | | | | |
| 21931, 21932 | 48854966 75 | 6.00E-93 | Cytophaga hutchinsonii | COG0013: Alanyl-tRNA synthetase [Cytophaga hutchinsonii] | S.pombe chromosome I cosmid c23C11 | 88 | 2.00E-09 | 6.1.1.7 | |
| 21935, 21936 21939, 21940 | 53714728 67 48862079 50 | 3.00E-45 6.00E-47 | Bacteroides fragilis YCH46 Microbulbifer degradans 2-40 | dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] dbj BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] COG3738: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] | | | | 2.4.1.83 | |

| | | | | | | | | | |
|--------|----------|----|----------|--|--|--|--|--|---------|
| 21941, | 48856049 | 56 | 7.00E-59 | Cytophaga hutchinsonii | hypothetical protein Chui02001282 [Cytophaga hutchinsonii] | | | | |
| 21942 | | | | Dechloromonas aromatica RCB | COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB] | | | | 2.7.3.- |
| 21943, | 41723898 | 31 | 1.00E-24 | | similar to formate hydrogen-lyase transcriptional activator for fdhF, hyc and hyp operons [Shigella flexneri 2a str. 301] gb AAN44037.1 similar to formate hydrogen-lyase transcriptional activator for fdhF, hyc and hyp operons [Shigella flexneri 2a str. 301] | | | | |
| 21945, | 24113820 | 56 | 3.00E-63 | Shigella flexneri 2a str. 301 | | | | | |
| 21946 | | | | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS71873.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | 2.7.3.- |
| 21947, | 45659150 | 32 | 3.00E-18 | Candida glabrata | unnamed protein product [Candida glabrata] emb CAG61479.1 unnamed protein product [Candida glabrata CBS138] | | | | 6.4.1.1 |
| 21948 | 50292171 | 38 | 3.00E-14 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] db BAD51034.1 two-component system response regulator [Bacteroides fragilis YCH46] | | | | |
| 21949, | 53715576 | 37 | 9.00E-48 | uncultured archaeon | capsular polysaccharide biosynthesis protein [uncultured archaeon GZfos18F2] | | | | |
| 21950 | 52548765 | 28 | 2.00E-18 | Bacteroides fragilis YCH46 | endopeptidase Clp ATP-binding chain B [Bacteroides fragilis YCH46] db BAD47955.1 endopeptidase Clp ATP-binding chain B [Bacteroides fragilis YCH46] | | | | |
| 21951, | 53712497 | 46 | 8.00E-29 | Pseudomonas syringae pv. tomato str. DC3000 | ISPys11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794264.1 ISPys11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000] | | | | |
| 21952, | 28854897 | 53 | 3.00E-28 | Petunia integrifolia subsp. inflata | putative fructokinase 2; S2 self-incompatibility locus-linked 3.16 protein [Petunia integrifolia subsp. inflata] | | | | 2.7.1.4 |
| 21953, | 33329200 | 32 | 2.00E-14 | Streptococcus suis 89/1591 | COG0366: Glycosidases [Streptococcus suis 89/1591] | | | | 2.4.1.5 |
| 21954 | 50590978 | 33 | 2.00E-27 | Pseudomonas syringae | replication protein - Pseudomonas syringae plasmid pPS10 emb CAA41700.1 replication protein [Pseudomonas syringae] | | | | |
| 21955, | 95009 | 31 | 1.00E-20 | Porphyromonas gingivalis W83 | trigger factor, putative [Porphyromonas gingivalis W83] ref NP_905027.1 trigger factor, putative [Porphyromonas gingivalis W83] | | | | |
| 21956 | 34398861 | 48 | 2.00E-27 | Bdellovibrio bacteriovorus HD100 | predicted exonuclease of the beta-lactamase family [Bdellovibrio bacteriovorus HD100] emb CAE79883.1 predicted exonuclease of the beta-lactamase family [Bdellovibrio bacteriovorus HD100] | | | | |
| 21957, | 42523510 | 64 | 2.00E-42 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|--|----------|
| 21969, 21970 | 16332154 | 53 | 2.00E-44 | Synechocystis sp. PCC 6803 | 2-hydroxyaciddehydrogenase [Synechocystis sp. PCC 6803] dbj BAA18694.1 2-hydroxyaciddehydrogenase [Synechocystis sp. PCC 6803] pir S76782 D-2-hydroxy-acid dehydrogenase (EC 1.1.99.6) - Synechocystis sp. (strain PCC 6803) | | | 1.1.1.28 |
| 2197, 2198 | 53715576 | 37 | 2.00E-40 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD51034.1 two-component system response regulator [Bacteroides fragilis YCH46] | | | |
| 21971, 21972 | 25010929 | 38 | 5.00E-28 | Streptococcus agalactiae NEM316 | hypothetical protein gbs0874 [Streptococcus agalactiae NEM316] emb CAD46518.1 Unknown [Streptococcus agalactiae NEM316] sp Q8E5V5 GLGA_STRA3 Glycogen synthase (Starch [bacterial glycogen] synthase) | | | 2.4.1.21 |
| 21973, 21974 | 53734963 | 27 | 1.00E-17 | Crocospaera watsonii WH 8501 | COG0500: SAM-dependent methyltransferases [Crocospaera watsonii WH 8501] | | | 2.1.1.48 |
| 21977, 21978 | 29349340 | 57 | 1.00E-100 | Bacteroides thetataoamicon VPI-5482 | DNA primase [Bacteroides thetataoamicon VPI-5482] gb AAO79037.1 DNA primase [Bacteroides thetataoamicon VPI-5482] | | | 2.7.7.- |
| 21981, 21982 | 48854644 | 47 | 4.00E-42 | Cytophaga hutchinsonii | COG2003: DNA repair proteins [Cytophaga hutchinsonii] | | | |
| 21983, 21984 | 53713311 | 40 | 2.00E-21 | Bacteroides fragilis YCH46 | hypothetical protein BF2022 [Bacteroides fragilis YCH46] dbj BAD48769.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | 3.4.13.9 |
| 21985, 21986 | 53715627 | 38 | 1.00E-24 | Bacteroides fragilis YCH46 | putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46] dbj BAD51085.1 putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46] | | | |
| 21987, 21988 | 48854286 | 36 | 4.00E-12 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |

| | | | | | | |
|-----------------|----------|----|----------|--|---|----------|
| 21889, 21990 | 29144603 | 54 | 8.00E-53 | Salmonella enterica subsp. enterica serovar Typhi Ty2 | Vi polysaccharide biosynthesis protein, UDP-glucose/GDP-mannose dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi ref NP_458740.1 Vi polysaccharide biosynthesis protein, UDP-glucose/GDP- mannose dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi str. CT18] gb AAO71805.1 Vi polysaccharide biosynthesis protein, UDP- glucose/GDP-mannose dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD06781.1 Vi polysaccharide biosynthesis protein, UDP-glucose/GDP-mannose dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi] emb CAA47991.1 unnamed protein product [Salmonella typhi] pit AH1041 Vi polysaccharide biosynthesis protein, UDP- glucose/ GDP-mannose dehydrogenase (EC 1.1.1.-) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) pit B36892 Vi polysaccharide biosynthetic protein VlpA - Salmonella typhi sp Q04972 VIPA_SALT1 Vi polysaccharide biosynthesis protein vipA/viB dbj BAA03192.1 WcdA protein [Salmonella typhi] | 1.1.1.- |
| 2199, 2200 | 48892769 | 31 | 2.00E-08 | Trichodesmium erythraeum IMS101 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] two-component system response regulator [Bacteroides fragilis YCH46] | |
| 21991, 21992 | 53715398 | 49 | 4.00E-58 | Bacteroides fragilis YCH46 | dbj BAD50856.1 two-component system response regulator [Bacteroides fragilis YCH46] | 2.7.3.- |
| 21993, 21994 | 13183744 | 47 | 7.00E-23 | Pseudomonas aeruginosa | unknown [Pseudomonas aeruginosa] putative nucleotide-diphosphate sugar epimerase [Bacteroides fragilis YCH46] dbj BAD49720.1 putative nucleotide-diphosphate sugar epimerase [Bacteroides fragilis YCH46] | 2.7.7.38 |
| 21995, 21996 | 53714262 | 29 | 1.00E-15 | Bacteroides fragilis YCH46 | topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] | |
| 21997, 21998 | 29348988 | 36 | 9.00E-48 | Bacteroides thetaitaomicron VPI-5482 | hypothetical protein AGR_pAT_692 [Agrobacterium tumefaciens str. C58] gb AAK90844.1 AGR_pAT_692p [Agrobacterium tumefaciens str. C58] sp Q8UUK7 DP42_AGR15 DNA polymerase IV 2 (Pol IV 2) | 2.7.7.7 |
| 21999, 22000 | 16119697 | 40 | 4.00E-25 | Agrobacterium tumefaciens str. C58 | tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] dbj BAD48805.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | |
| 22001, 22002 | 53713347 | 45 | 2.00E-42 | Bacteroides fragilis YCH46 | helicase [Shewanella oneidensis MR-1] gb AAN53453.1 helicase [Shewanella oneidensis MR-1] | |
| 22005, 22006 | 24371966 | 40 | 3.00E-38 | Shewanella oneidensis MR-1 | COG1475: Predicted transcriptional regulators [Burkholderia fungorum LB400] | |
| 22009, 22010 | 48782956 | 37 | 9.00E-32 | Burkholderia fungorum LB400 | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------|---|--|--|--|---------|
| 22013, | 45505171 | 41 | 4.00E-17 | Homo sapiens | kyphoscoliosis peptidase [Homo sapiens] | | | | |
| 22014 | | | | | hypothetical protein NMA1791 [Neisseria meningitidis Z2491] | | | | |
| 22019, | | | | Neisseria | emb CAB85017.1 hypothetical protein [Neisseria meningitidis Z2491] | | | | |
| 22020 | 15794682 | 42 | 4.00E-66 | meningitidis Z2491 | pir E81804 hypothetical protein NMA1791 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) | | | | |
| 22021, | | | | Oryza sativa | phosphodiesterase/alkaline phosphatase D-like protein [Oryza sativa (japonica cultivar-group)] dbj BAD34083.1 phosphodiesterase/alkaline phosphatase D-like protein [Oryza sativa (japonica cultivar-group)] | | | | |
| 22022 | 50910003 | 37 | 9.00E-28 | (japonica cultivar-group) | | | | | |
| 22023, | | | | Wollinella | | | | | |
| 22024 | 34556505 | 36 | 7.00E-28 | succinogenes DSM 1740 | WLAC PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09220.1 | | | | 2.4.1.- |
| 22025, | | | | Chloroflexus | WLAC PROTEIN [Wollinella succinogenes] | | | | |
| 22026 | 53794823 | 41 | 5.00E-29 | aurantiacus | COG1131: ABC-type multidrug transport system, ATPase component [Chloroflexus aurantiacus] | | | | 1.8.-.- |
| 22027, | | | | Cytophaga | | | | | |
| 22028 | 48854853 | 36 | 2.00E-32 | hutchinsonii | COG0345: Pyrroline-5-carboxylate reductase [Cytophaga hutchinsonii] | | | | 1.5.1.2 |
| 22029, | | | | Chlorobium | UDP-glucose/GDP-mannose dehydrogenase family protein [Chlorobium tepidum TLS] gb AAM71474.1 UDP-glucose/GDP-mannose dehydrogenase family protein [Chlorobium tepidum TLS] | | | | |
| 22030 | 21673067 | 44 | 1.00E-27 | tepidum TLS | | | | | 1.1.1.- |
| 22031, | | | | Photobacterium | hypothetical protein PBPR1316 [Photobacterium profundum SS9] | | | | |
| 22032 | 54308509 | 48 | 7.00E-70 | profundum SS9 | emb CAG19727.1 hypothetical protein [Photobacterium profundum] | | | | |
| 22033, | | | | Cytophaga | | | | | |
| 22034 | 48855611 | 24 | 4.00E-08 | hutchinsonii | COG3696: Putative silver efflux pump [Cytophaga hutchinsonii] | | | | |
| 22035, | | | | Chromobacterium | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] | | | | |
| 22036 | 34101691 | 52 | 2.00E-51 | violaceum ATCC 12472 | ref NP_900051.1 hypothetical protein CV0381 [Chromobacterium violaceum ATCC 12472] | | | | |
| 22037, | | | | | phosphoenolpyruvate synthase [Aquifex aeolicus VF5] gb AAC07865.1 | | | | |
| 22038 | 15607086 | 52 | 6.00E-78 | Aquifex aeolicus VF5 | phosphoenolpyruvate synthase [Aquifex aeolicus VF5] pir G70483 pyruvate, water dikinase (EC 2.7.9.2) - Aquifex aeolicus sp D67899 PPSA_AQUAE | | | | 2.7.9.2 |
| 22039, | | | | Nostoc sp. PCC 7120 | Phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase) | | | | |
| 22040 | 17230890 | 29 | 4.00E-09 | 7120 | hypothetical protein ali3398 [Nostoc sp. PCC 7120] pir AG2230 hypothetical protein ali3398 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75097.1 ali3398 [Nostoc sp. PCC 7120] | | | | |
| 22041, | | | | Cytophaga | | | | | |
| 22042 | 48853745 | 33 | 1.00E-22 | hutchinsonii | hypothetical protein Chut02003380 [Cytophaga hutchinsonii] | | | | |
| 22047, | | | | Methanococcus | COG0668: Small-conductance mechanosensitive channel | | | | |
| 22048 | 53731688 | 35 | 6.00E-32 | burtonii DSM 6242 | [Methanococcus burtonii DSM 6242] | | | | |
| 22049, | | | | Cytophaga | | | | | |
| 22050 | 48853718 | 31 | 1.00E-35 | hutchinsonii | COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|------------------|----------|----|----------|--|--|--|--|--|----------|
| 2205, 2206 | 34762878 | 30 | 7.00E-07 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | Transcription antitermination protein nusG [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24529.1 Transcription antitermination protein nusG [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | | |
| 22051, 22052 | 15607112 | 42 | 1.00E-25 | Aquifex aeolicus VF5 | shikimate kinase [Aquifex aeolicus VF5] gb AAC07875.1 shikimate kinase [Aquifex aeolicus VF5] pir A70487 shikimate kinase - Aquifex aeolicus sp O67925 AROK_AQUAE Shikimate kinase (SK) | | | | 2.7.1.71 |
| 22053, 22054 | 29348444 | 50 | 5.00E-72 | Bacteroides thetaiotaomicron VPI-5482 | carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO78141.1 carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.4.21.- |
| 22057, 22058 | 48853721 | 38 | 1.00E-11 | Cytophaga hutchinsonii | hypothetical protein Chut02003580 [Cytophaga hutchinsonii] | | | | |
| 22059, 22060 | 48856113 | 45 | 4.00E-23 | Cytophaga hutchinsonii | COG0212: 5-formyltetrahydrofolate cyclo-ligase [Cytophaga hutchinsonii] | | | | 6.3.3.2 |
| 22061, 22062 | 29345572 | 47 | 3.00E-32 | Bacteroides thetaiotaomicron VPI-5482 | penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI- 5482] gb AAO75269.1 penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.4.2.- |
| 22063, 22064 | 48854895 | 59 | 2.00E-35 | Cytophaga hutchinsonii | COG0491: Zn-dependent hydrolases, including glyoxylases (Cytophaga hutchinsonii) | | | | |
| 22065, 22066 | 48855782 | 26 | 9.00E-08 | Cytophaga hutchinsonii | hypothetical protein Chut02000991 [Cytophaga hutchinsonii] | | | | |
| 22067, 22068 | 48856069 | 71 | 2.00E-32 | Cytophaga hutchinsonii | COG3093: Plasmid maintenance system antidote protein [Cytophaga hutchinsonii] | | | | |
| 2207, 22071, | 48856416 | 40 | 7.00E-51 | Cytophaga hutchinsonii | hypothetical protein Chut02000134 [Cytophaga hutchinsonii] | | | | |
| 22072, 22073, | 48856308 | 54 | 2.00E-58 | Cytophaga hutchinsonii | COG0602: Organic radical activating enzymes [Cytophaga hutchinsonii] | | | | |
| 22074, 22075, | 2281663 | 60 | 8.00E-30 | Flavobacterium johnsoniae | gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [Imported] - Flavobacterium johnsoniae | | | | |
| 22076 | AAU3497 | 46 | 5.00E-53 | | Desc:Enterococcus faecalis cellular proliferation protein #265. Org:Enterococcus faecalis | | | | 2.1.1.61 |
| 22077, 22078 | 52007397 | 52 | 2.00E-42 | Thiobacillus denitrificans ATCC 25259 | COG1752: Predicted esterase of the alpha-beta hydrolase superfamily [Thiobacillus denitrificans ATCC 25259] | | | | 3.4.21.- |
| 22079, 22080 | 31194819 | 54 | 3.00E-62 | Anopheles gambiae | ENSANGP00000002020 [Anopheles gambiae] | | | | |
| 22085, 22086 | 26370741 | 32 | 5.00E-10 | Mus musculus | unnamed protein product [Mus musculus] | | | | |
| 22087, 22088 | 21233748 | 46 | 2.00E-58 | Proteus vulgaris | transposase [Proteus vulgaris] db BAB93648.1 transposase [Proteus vulgaris] | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|----|------------|
| 22089, 22090 | 53714594 | 44 | 1.00E-37 | Bacteroides fragilis YCH46 | LacI family transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD5052.1 LacI family transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 2209, 2210 | 48856118 | 50 | 2.00E-47 | Cytophaga hutchinsonii | COG0242: N-formylmethionyl-tRNA deformylase [Cytophaga hutchinsonii] hypothetical protein PBPRB0095 [Photobacterium profundum SS9] | | | 3.5.1.88 |
| 22091, 22092 | 54301775 | 45 | 3.00E-07 | Photobacterium profundum SS9 | emb CAG21968.1 hypothetical protein [Photobacterium profundum] Nin 221 (pept unknown;221) [Bacteriophage lambda] pir Q1BP1.L multiple specificity phosphoprotein phosphatase (EC 3.1.3.-) - phage lambda ref NP_040641.1 Nin protein [Bacteriophage lambda] sp P03772 PP_LAMB Serine/threonine protein phosphatase transcription anti-termination protein [Bacteroides fragilis YCH46] | Bacteriophage lambda, complete genome | 99 | 0 3.1.3.16 |
| 22093, 22094 | 215160 | 98 | 1.00E-108 | bacteriophage lambda | dbj BAD50940.1 transcription anti-termination protein [Bacteroides fragilis YCH46] | | | |
| 22095, 22096 | 53715482 | 36 | 1.00E-23 | Bacteroides fragilis YCH46 | putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46] | | | 3.5.1.- |
| 22099, 22100 | 53712055 | 46 | 1.00E-55 | Bacteroides fragilis YCH46 | two-component system sensor histidine kinase [Bacteroides thetataoimicron VPI-5482] gb AAO76096.1 two-component system sensor histidine kinase [Bacteroides thetataoimicron VPI-5482] | | | 2.7.3.- |
| 22101, 22102 | 20088950 | 37 | 1.00E-21 | Methanosarcina acetivorans C2A | hypothetical protein MA0051 [Methanosarcina acetivorans C2A] gb AAM03505.1 predicted protein [Methanosarcina acetivorans str. C2A] | | | |
| 22103, 22104 | 11499143 | 39 | 3.00E-24 | Archaeoglobus fulgidus DSM 4304 | hypothetical protein AF1548 [Archaeoglobus fulgidus DSM 4304] gb AAB89701.1 A. fulgidus predicted coding region AF1548 [Archaeoglobus fulgidus DSM 4304] pir C69443 hypothetical protein AF1548 - Archaeoglobus fulgidus sp O28724 YF48_ARCFU Hypothetical protein AF1548 | | | |
| 22105, 22106 | 45657858 | 35 | 4.00E-15 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC12005 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_712075.1 hypothetical protein LA1894 [Leptospira interrogans serovar Lai str. 56601] gb AAN49093.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS70581.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 22109, 22110 | 32476521 | 44 | 6.00E-27 | Rhodopirellula baltica SH 1 | iduronate-2-sulfatase [Rhodopirellula baltica SH 1] emb CAD78972.1 iduronate-2-sulfatase [Pirellula sp.] | | | 3.1.6.6 |
| 22111, 22112 | 3093287 | 31 | 3.00E-18 | Bacillus sphaericus | heat shock protein [Bacillus sphaericus] sp O69268 DNAK_BACSH Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) | | | 3.6.1.3 |
| 22117, 22118 | 48854288 | 42 | 6.00E-32 | Cytophaga hutchinsonii | COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|--|----|----------|----------|
| 22123, | AAV3440 | 35 | 8.00E-43 | | Desc: Porphyromonas gingivalis protein PG67. Org: Porphyromonas gingivalis | | | | |
| 22124 | 3 | | | | RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO77291.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22125, | | | | | | | | | |
| 22126 | 29347594 | 44 | 1.00E-29 | Bacteroides thetaiotaomicron VPI-5482 | | | | | |
| 22127, | | | | | | | | | |
| 22128 | 41690073 | 93 | 2.00E-89 | Psychrobacter sp. 273-4 | COG0388: Predicted amidohydrolase [Psychrobacter sp. 273-4] | | | | |
| 22129, | | | | | | | | | |
| 22130 | 53711667 | 59 | 4.00E-30 | Bacteroides fragilis YCH46 | hypothetical protein BF0376 [Bacteroides fragilis YCH46] db BAD47125.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 2213, | | | | | | | | | |
| 2214 | 21674468 | 74 | 4.00E-43 | Chlorobium tepidum TLS | leucyl-tRNA synthetase [Chlorobium tepidum TLS] gb AAM72875.1 leucyl-tRNA synthetase [Chlorobium tepidum TLS] sp Q8KBY2 SYL_CHLTE Leucyl-tRNA synthetase (Leucine-tRNA ligase) (LeuRS) | | | | 6.1.1.4 |
| 22131, | | | | | | | | | |
| 22132 | 48854958 | 69 | 6.00E-52 | Cytophaga hutchinsonii | COG1432: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 22135, | | | | | | | | | |
| 22136 | 48868353 | 54 | 7.00E-36 | Haemophilus influenzae 86-028NP | COG2865: Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen [Haemophilus influenzae 86-028NP] | | | | |
| 22137, | | | | | | | | | |
| 22138 | 53712434 | 58 | 3.00E-71 | Bacteroides fragilis YCH46 | type III restriction-modification system restriction subunit [Bacteroides fragilis YCH46] db BAD47892.1 type III restriction-modification system restriction subunit [Bacteroides fragilis YCH46] | Haemophilus ducreyi strain 35000HP section 5 of 6 of the complete genome | 89 | 4.00E-11 | 3.1.21.5 |
| 22139, | | | | | | | | | |
| 22140 | 48853613 | 27 | 7.00E-16 | Cytophaga hutchinsonii | COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii] | | | | |
| 22141, | | | | | | | | | |
| 22142 | 48856398 | 53 | 1.00E-39 | Cytophaga hutchinsonii | COG0147: Anthranilate/para-aminobenzoate synthetases component I [Cytophaga hutchinsonii] | | | | 4.1.3.- |
| 22143, | | | | | | | | | |
| 22144 | 13474394 | 47 | 6.00E-16 | Mesorhizobium loti MAFF303099 | hypothetical protein ml15269 [Mesorhizobium loti MAFF303099] db BAB51748.1 ml15269 [Mesorhizobium loti MAFF303099] | | | | |
| 22145, | | | | | | | | | |
| 22146 | 29350005 | 51 | 2.00E-41 | Bacteroides thetaiotaomicron VPI-5482 | endopeptidase Clp ATP-binding chain B [Bacteroides thetaiotaomicron VPI-5482] sp Q89YY3 CLPB_BACTN Chaperone clpB gb AAO79702.1 endopeptidase Clp ATP-binding chain B [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22147, | | | | | | | | | |
| 22148 | 29348628 | 66 | 2.00E-73 | Bacteroides thetaiotaomicron VPI-5482 | S-adenosylmethionine synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78325.1 S-adenosylmethionine synthetase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A2T6 METK_BACTN S-adenosylmethionine synthetase (Methionine adenosyltransferase) (AdoMet synthetase) (MAT) | Bacteroides thetaiotaomicron VPI-5482, section 14 of 21 of the complete genome | 86 | 5.00E-07 | 2.5.1.6 |
| 22149, | | | | | | | | | |
| 22150 | 48853782 | 57 | 3.00E-57 | Cytophaga hutchinsonii | COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Cytophaga hutchinsonii] | | | | 2.7.7.7 |

| | | | | | | | | |
|--------|----------|----|-----------|-------------------------------------|--|--|--|---------|
| 2215, | 23098114 | 64 | 4.00E-42 | Oceanobacillus ihayensis HTE831 | hypothetical protein OB0659 [Oceanobacillus ihayensis HTE831] dbj BAC12615.1 hypothetical protein [Oceanobacillus ihayensis HTE831] | | | |
| 2216 | | | | | putative outer membrane protein [Bacteroides fragilis YCH46] dbj BAD48633.1 putative outer membrane protein [Bacteroides fragilis YCH46] | | | |
| 22151, | 53713175 | 31 | 2.00E-18 | Bacteroides fragilis YCH46 | | | | |
| 22152 | | | | | | | | |
| 22153, | 52853887 | 87 | 1.00E-122 | Psychrobacter sp. 273-4 | COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Psychrobacter sp. 273-4] | | | |
| 22154 | | | | | | | | |
| 22155, | | | | Geobacter sulfurreducens | nucleoside diphosphate kinase regulator protein, putative [Geobacter sulfurreducens PCA] gb AAR34062.1 nucleoside diphosphate kinase regulator protein, putative [Geobacter sulfurreducens PCA] | | | |
| 22156 | 39995838 | 34 | 2.00E-13 | PCA | | | | |
| 22157, | | | | Geobacter metallireducens GS | COG3863: Uncharacterized distant relative of cell wall-associated hydrolases [Geobacter metallireducens GS-15] | | | |
| 22158 | 48846570 | 26 | 1.00E-17 | 15 | | | | |
| 22159, | | | | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | |
| 22160 | 48855258 | 36 | 8.00E-17 | | | | | |
| 22161, | | | | Bacteroides thetataoamicron | hypothetical protein BT0909 [Bacteroides thetataoamicron VPI-5482] gb AAO76016.1 conserved hypothetical protein [Bacteroides thetataoamicron VPI-5482] | | | |
| 22162 | 29346319 | 50 | 2.00E-45 | VPI-5482 | | | | |
| 22167, | | | | Cytophaga hutchinsonii | | | | |
| 22168 | 48855120 | 48 | 5.00E-22 | | COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii] | | | 6.1.1.4 |
| 22169, | | | | Plasmodium yoelii | | | | |
| 22170 | 23479863 | 25 | 7.00E-07 | yoelii | CCAT-box DNA binding protein subunit B [Plasmodium yoelii yoelii] putative DNA mismatch repair protein [Streptomyces avermitilis MA-4680] dbj BAC75377.1 putative DNA mismatch repair protein [Streptomyces avermitilis] | | | |
| 2217, | | | | Streptomyces avermitilis MA-4680 | | | | |
| 2218 | 29826536 | 25 | 3.00E-13 | | | | | |
| 22171, | | | | Anopheles | | | | |
| 22172 | 31195649 | 48 | 5.00E-12 | gambiae | ENSANGP00000000282 [Anopheles gambiae] | | | |
| 22175, | | | | Cytophaga hutchinsonii | COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Cytophaga hutchinsonii] | | | |
| 22176 | 48855752 | 25 | 2.00E-17 | | | | | |
| 22177, | | | | Bacteroides fragilis YCH46 | valyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD47800.1 valyl-tRNA synthetase [Bacteroides fragilis YCH46] | | | 6.1.1.9 |
| 22178 | 53712342 | 65 | 1.00E-111 | | | | | |
| 22179, | | | | Cytophaga hutchinsonii | COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 22180 | 48855703 | 31 | 2.00E-29 | | | | | |
| 22183, | | | | Bacteroides thetataoamicron | hypothetical protein BT2211 [Bacteroides thetataoamicron VPI-5482] gb AAO77318.1 conserved hypothetical protein [Bacteroides thetataoamicron VPI-5482] | | | |
| 22184 | 29347621 | 52 | 2.00E-62 | VPI-5482 | | | | |
| 22185, | | | | Bdellovibrio bacteriovorus | transcriptional regulator, LysR family [Bdellovibrio bacteriovorus HD100] emb CAE80411.1 transcriptional regulator, LysR family [Bdellovibrio bacteriovorus HD100] | | | |
| 22186 | 42524039 | 41 | 7.00E-34 | HD100 | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|------------------------|--|--|--|--|----------|
| 22187, | 48853606 | 39 | 2.00E-32 | Cytophaga hutchinsonii | COG0497: ATPase involved in DNA repair [Cytophaga hutchinsonii] | | | | |
| 22188 | | | | | muchin-desulfating sulfatase (N-acetylglucosamine-6-sulfatase) | | | | |
| 22189, | | | | Rhodopirellula | (Rhodopirellula baltica SH 1) emb[CAD71852.1] muchin-desulfating sulfatase | | | | |
| 22190 | 32471182 | 63 | 3.00E-40 | baltica SH 1 | (N-acetylglucosamine-6-sulfatase) [Pirellula sp.] | | | | 3.1.6.4 |
| 22191, | | | | Thermococcus | geranylgeranyl hydrogenase [Thermococcus kodakaraensis] | | | | |
| 22192 | 57159347 | 38 | 3.00E-12 | kodakaraensis | ref YP_183501.1 geranylgeranyl hydrogenase [Thermococcus kodakaraensis] | | | | |
| 22193, | | | | Microbulbifer | | | | | |
| 22194 | 48863666 | 32 | 4.00E-07 | degradans 2-40 | COG3428: Predicted membrane protein [Microbulbifer degradans 2-40] | | | | |
| 22199, | | | | Bacteroides fragilis | adenylosuccinate lyase [Bacteroides fragilis YCH46] | | | | |
| 22200 | 53715302 | 66 | 3.00E-72 | YCH46 | adenylosuccinate lyase [Bacteroides fragilis YCH46] | | | | 4.3.2.2 |
| 22201, | | | | Bacteroides fragilis | putative chloride channel protein [Bacteroides fragilis YCH46] | | | | |
| 22202 | 53715188 | 49 | 3.00E-37 | YCH46 | dbj BAD50846.1 putative chloride channel protein [Bacteroides fragilis YCH46] | | | | |
| 22203, | | | | Cytophaga | COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair | | | | |
| 22204 | 48853782 | 52 | 3.00E-59 | hutchinsonii | [Cytophaga hutchinsonii] | | | | 2.7.7.7 |
| 22207, | | | | Porphyromonas | type I restriction-modification system, M subunit, putative [Porphyromonas | | | | |
| 22208 | 34397452 | 32 | 4.00E-22 | gingivalis W83 | gingivalis W83] ref NP_905615.1 type I restriction-modification system, M | | | | 2.1.1.72 |
| 22209, | | | | Bacteroides | subunit, putative [Porphyromonas gingivalis W83] | | | | |
| 22210 | 29349518 | 60 | 1.00E-33 | thetataoamicon | putative pectinesterase precursor [Bacteroides thetaiotaomicon VPI-5482] | | | | |
| 22211, | | | | Porphyromonas | thetataoamicon VPI-5482] | | | | |
| 22212 | 34396714 | 40 | 1.00E-38 | gingivalis W83 | htrA protein [Porphyromonas gingivalis W83] ref NP_904880.1 htrA protein | | | | 3.4.21.- |
| 22215, | | | | Desulfotalea | related to 5' to 3' DNA helicase [Desulfotalea psychrophila LSV54] | | | | |
| 22216 | 51245839 | 37 | 3.00E-26 | psychrophila LSV54 | emb CAG36716.1 related to 5' to 3' DNA helicase [Desulfotalea psychrophila LSV54] | | | | 3.6.1.- |
| 22217, | | | | Bacteroides | DNA repair and recombination protein, putative helicase [Bacteroides | | | | |
| 22218 | 29346131 | 52 | 1.00E-76 | thetataoamicon | thetataoamicon VPI-5482] gb AAO75828.1 DNA repair and recombination | | | | |
| 22219, | | | | Cytophaga | protein, putative helicase [Bacteroides thetaiotaomicon VPI-5482] | | | | |
| 22220 | 48856044 | 58 | 2.00E-48 | hutchinsonii | COG2908: Uncharacterized protein conserved in bacteria [Cytophaga | | | | 3.6.1.- |
| 22221, | | | | Bacteroides | hutchinsonii] | | | | |
| 22222 | 29346304 | 55 | 5.00E-48 | thetataoamicon | DNA ligase [Bacteroides thetaiotaomicon VPI-5482] gb AAO76001.1 DNA | | | | 6.5.1.2 |
| 22223, | | | | Bacteroides | ligase [Bacteroides thetaiotaomicon VPI-5482] | | | | |
| 22224 | 29348248 | 46 | 7.00E-18 | thetataoamicon | ribosome-binding factor A [Bacteroides thetaiotaomicon VPI-5482] | | | | |
| | | | | | gb AAO77945.1 ribosome-binding factor A [Bacteroides thetaiotaomicon | | | | |
| | | | | | VPI-5482] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|--|--|--|-----------|
| 22225, | 53715757 | 32 | 1.00E-14 | Bacteroides fragilis YCH46 | hypothetical protein BF4478 [Bacteroides fragilis YCH46] dbj BAD51215.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 22226 | 42630866 | 27 | 1.00E-09 | Haemophilus influenzae R2866 | COG0457: FOG: TPR repeat [Haemophilus influenzae R2866] | | | | |
| 22227, | 42630866 | 27 | 1.00E-09 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd3537 [Bdellovibrio bacteriovorus HD100] | | | | |
| 22228 | 42524889 | 54 | 4.00E-28 | Bdellovibrio bacteriovorus HD100 | emb CAE78328.1 unnamed protein product [Bdellovibrio bacteriovorus HD100] | | | | 1.14.16.1 |
| 22231, | 48854664 | 44 | 1.00E-58 | Cytophaga hutchinsonii | COG2217: Cation transport ATPase [Cytophaga hutchinsonii] | | | | 3.6.3.4 |
| 22232, | 48854664 | 44 | 1.00E-58 | Cytophaga hutchinsonii | hypothetical protein Chut02001333 [Cytophaga hutchinsonii] | | | | 6.4.--- |
| 22233, | 48854664 | 44 | 1.00E-58 | Cytophaga hutchinsonii | COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii] | | | | |
| 22234, | 48854664 | 44 | 1.00E-58 | Cytophaga hutchinsonii | Na+-translocating NADH-quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.--- |
| 22235, | 48854664 | 44 | 1.00E-58 | Cytophaga hutchinsonii | COG4258: Predicted exporter [Cytophaga hutchinsonii] | | | | |
| 22236, | 48854664 | 44 | 1.00E-58 | Cytophaga hutchinsonii | putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis YCH46] gb AAD56746.1 putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis] dbj BAD47860.1 putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis YCH46] | | | | |
| 22237, | 48854664 | 44 | 1.00E-58 | Cytophaga hutchinsonii | putative phosphoenolpyruvate carboxylase [Streptococcus mutans UA159] gb AAN58441.1 putative phosphoenolpyruvate carboxylase [Streptococcus mutans UA159] sp Q8DV10 CAPP_STRMU Phosphoenolpyruvate carboxylase (PEPC) | | | | 4.1.1.31 |
| 22238, | 48854664 | 44 | 1.00E-58 | Cytophaga hutchinsonii | COG0060: Isoleucyl-tRNA synthetase [Cytophaga hutchinsonii] | | | | 6.1.1.5 |
| 22241, | 29346568 | 33 | 4.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | fic family protein [Geobacter sulfurreducens PCA] gb AAR35559.1 fic family protein [Geobacter sulfurreducens PCA] | | | | |
| 22242, | 29346568 | 33 | 4.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | mannan endo-1,4-beta-mannosidase [Bacteroides fragilis YCH46] dbj BAD47597.1 mannan endo-1,4-beta-mannosidase [Bacteroides fragilis YCH46] | | | | |
| 22243, | 48854664 | 44 | 1.00E-58 | Cytophaga hutchinsonii | exonuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46] | | | | |
| 22244, | 48854664 | 29 | 1.00E-22 | Cytophaga hutchinsonii | | | | | |
| 22245, | 53712402 | 57 | 3.00E-59 | Bacteroides fragilis YCH46 | | | | | |
| 22246 | 53712402 | 57 | 3.00E-59 | Bacteroides fragilis YCH46 | | | | | |
| 22247, | 24379180 | 27 | 6.00E-15 | Streptococcus mutans UA159 | | | | | |
| 22248 | 24379180 | 27 | 6.00E-15 | Streptococcus mutans UA159 | | | | | |
| 22249, | 48854361 | 61 | 1.00E-93 | Cytophaga hutchinsonii | | | | | |
| 22250 | 48854361 | 61 | 1.00E-93 | Cytophaga hutchinsonii | | | | | |
| 22251, | 39997281 | 43 | 1.00E-65 | Geobacter sulfurreducens PCA | | | | | |
| 22252 | 39997281 | 43 | 1.00E-65 | Geobacter sulfurreducens PCA | | | | | |
| 22253, | 53712139 | 40 | 1.00E-23 | Bacteroides fragilis YCH46 | | | | | |
| 22254 | 53712139 | 40 | 1.00E-23 | Bacteroides fragilis YCH46 | | | | | |
| 22255, | 53713904 | 72 | 7.00E-98 | Bacteroides fragilis YCH46 | | | | | |
| 22256 | 53713904 | 72 | 7.00E-98 | Bacteroides fragilis YCH46 | | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|----------|----------|---------|
| 22261, 22262 | 56460133 | 47 | 3.00E-49 | Idiomarina loihiensis L2TR | Predicted extracellular metal-dependent peptidase [Idiomarina loihiensis L2TR] gb AAV81865.1 Predicted extracellular metal-dependent peptidase | | | | | |
| 22263, 22264 | 9929259 | 43 | 3.00E-39 | Lactobacillus reuteri | cystathionine beta-lyase [Lactobacillus reuteri] putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718] | Desc:Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1078. Org:Staphylococcus epidermidis | 86 | 4.00E-07 | 4.2.99.9 | |
| 22269, 22270 | 30249527 | 50 | 1.00E-27 | Nitrosomonas europaea ATCC 19718 | rRNA methylases [Vibrio vulnificus CMCP6] gb AAO08221.1 rRNA methylases [Vibrio vulnificus CMCP6] | | | | | |
| 22273, 22274 | 27367704 | 44 | 1.00E-33 | Vibrio vulnificus CMCP6 | COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii] | | | | 2.1.1.- | |
| 22275, 22276 | 48854545 | 53 | 3.00E-62 | Cytophaga hutchinsonii | Mismatch repair protein MutS-like ATPase [Clostridium acetobutylicum ATCC 824] gb AAK81487.1 Mismatch repair protein MutS-like ATPase [Clostridium acetobutylicum ATCC 824] pir D97337 mismatch repair protein MutS-like ATPase [imported] - Clostridium acetobutylicum | | | | 2.1.1.- | |
| 22277, 22278 | 15896798 | 45 | 5.00E-48 | Clostridium acetobutylicum ATCC 824 | hypothetical protein VPA0559 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61902.1 conserved hypothetical protein [Vibrio parahaemolyticus] COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii] | | | | | |
| 22279, 22280 | 28900414 | 33 | 3.00E-36 | Vibrio parahaemolyticus RIMD 2210633 | [SOLEUCYL-TRNA SYNTHETASE [Wolinnella succinogenes DSM 1740] emb CAE09339.1 ISOLEUCYL-TRNA SYNTHETASE [Wolinnella succinogenes] | | | | 6.1.1.5 | |
| 22281, 22282 | 48853718 | 30 | 3.00E-25 | Cytophaga hutchinsonii | hypothetical protein WS1689 [Wolinnella succinogenes DSM 1740] emb CAE10716.1 conserved hypothetical protein [Wolinnella succinogenes] | | | | | |
| 22285, 22286 | 34556624 | 50 | 2.00E-48 | Wolinnella succinogenes DSM 1740 | hypothetical protein VV20658 [Vibrio vulnificus CMCP6] gb AAO07600.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins [Cytophaga hutchinsonii] | | | | | |
| 22287, 22288 | 34558001 | 41 | 4.00E-17 | Wolinnella succinogenes DSM 1740 | hypothetical protein CNBJ2030 [Cryptococcus neoformans var. neoformans B-3501A] | | | | | 4.1.3.6 |
| 22289, 22290 | 27367083 | 20 | 2.00E-07 | Vibrio vulnificus CMCP6 | | | | | | |
| 22295, 22296 | 48854535 | 53 | 5.00E-53 | Cytophaga hutchinsonii | | | | | | |
| 22297, 22298 | 50255830 | 28 | 8.00E-16 | Cryptococcus neoformans var. neoformans B-3501A | | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|--|--|--|--|---------|
| 22299, 22300 | 34913154 | 25 | 1.00E-10 | Onyza sativa (japonica cultivar- group) | putative oxidoreductase, FAD-binding [Onyza sativa (japonica cultivar- group)] dbj BAC07074.1 putative oxidoreductase, FAD-binding [Onyza sativa (japonica cultivar-group)] | | | | |
| 22301, 22302 | 54302756 | 39 | 4.00E-13 | Photobacterium profundum SS9 | hypothetical protein PBPRB1077 [Photobacterium profundum SS9] emb CAG22949.1 conserved hypothetical protein [Photobacterium profundum] | | | | |
| 22303, 22304 | 33469585 | 43 | 3.00E-24 | Alcaligenes faecalis | hypothetical protein [Alcaligenes faecalis] | | | | |
| 22305, 22306 | 54308287 | 46 | 4.00E-51 | Photobacterium profundum SS9 | putative signal transduction protein containing EAL and modified HD-GYP domains [Photobacterium profundum SS9] emb CAG19505.1 putative signal transduction protein containing EAL and modified HD-GYP domains [Photobacterium profundum] | | | | |
| 22307, 22308 | 53714565 | 28 | 4.00E-18 | Bacteroides fragilis YCH46 | hypothetical protein BF3279 [Bacteroides fragilis YCH46] dbj BAD50023.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 22309, 22310 | 17231272 | 25 | 2.00E-10 | Nostoc sp. PCC 7120 | hypothetical protein all3780 [Nostoc sp. PCC 7120] pir AE2278 hypothetical protein all3780 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75479.1 all3780 [Nostoc sp. PCC 7120] | | | | |
| 22311, 22312 | 53712193 | 39 | 4.00E-15 | Bacteroides fragilis YCH46 | hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | 2.7.3.- |
| 22313, 22314 | 39935801 | 32 | 2.00E-11 | Rhodopseudomonas palustris CGA009 | possible epoxide hydrolase-related protein [Rhodopseudomonas palustris CGA009] emb CAE28176.1 possible epoxide hydrolase-related protein [Rhodopseudomonas palustris CGA009] | | | | |
| 22317, 22318 | 44004406 | 34 | 5.00E-36 | Bacillus cereus ATCC 10987 | transposase, IS605 OrfB family [Bacillus cereus ATCC 10987] gb AAAS44917.1 transposase, IS605 OrfB family [Bacillus cereus ATCC 10987] | | | | |
| 22319, 22320 | 53714063 | 34 | 2.00E-10 | Bacteroides fragilis YCH46 | hypothetical protein BF2771 [Bacteroides fragilis YCH46] dbj BAD49521.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 22321, 22322 | ABP6083 8 | 36 | 1.00E-16 | | Desc:Treponema pallidum thioredoxin-like protein SEQ ID NO:187. Org: Treponema pallidum | | | | |
| 22323, 22324 | 31790565 | 59 | 8.00E-70 | marine bacterium P99-3 | phytoene desaturase [marine bacterium P99-3] | | | | |
| 22325, 22326 | 29346223 | 27 | 6.00E-18 | Bacteroides thetaiotaomicron VPI-5482 | TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO75920.1 TonB [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22327, 22328 | 48854785 | 40 | 4.00E-46 | Cytophaga hutchinsonii | COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii] | | | | 2.7.7.- |
| 22329, 22330 | 49081478 | 31 | 1.00E-16 | synthetic construct | PA1776 [synthetic construct] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|----|----------|----------|
| 2233, 2234 | 18977094 | 57 | 3.00E-56 | Pyrococcus furius DSM 3638 | alkyl hydroperoxide reductase subunit c [Pyrococcus furiosus DSM 3638] gb AAL80846.1 alkyl hydroperoxide reductase subunit c [Pyrococcus furiosus DSM 3638] | | | | 1,6,4,- |
| 22331, 22332 | 37528152 | 77 | 1.00E-111 | Photobacterium luminescens subsp. laumondii TTO1 | Type I site-specific deoxyribonuclease HsdR [Photobacterium luminescens subsp. laumondii TTO1] emb CAE16694.1 Type I site-specific deoxyribonuclease HsdR [Photobacterium luminescens subsp. laumondii TTO1] | Escherichia coli prfB, prfC and prfD genes | 80 | 2.00E-40 | 3.1.21.3 |
| 22333, 22334 | 29347621 | 47 | 1.00E-25 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2211 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77318.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22337, 22338 | 48856102 | 39 | 1.00E-28 | Cytophaga hutchinsonii | COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 22341, 22342 | 29349390 | 50 | 4.00E-45 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Bacteroides thetaiotaomicron VPI-5482] gb AAO79087.1 ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.1.11.5 |
| 22343, 22344 | 54308172 | 52 | 1.00E-59 | Photobacterium profundum SS9 | putative transposase [Photobacterium profundum SS9] emb CAG19390.1 putative transposase [Photobacterium profundum] | | | | |
| 22345, 22346 | 53715189 | 47 | 5.00E-45 | Bacteroides fragilis YCH46 | putative translation factor [Bacteroides fragilis YCH46] dbj BAD50647.1 putative translation factor [Bacteroides fragilis YCH46] | | | | |
| 22349, 22350 | 14252939 | 40 | 3.00E-23 | Escherichia coli | hypothetical protein [Escherichia coli] | | | | |
| 2235, 2236 | 15669750 | 44 | 1.00E-56 | Methanocaldococcus jannaschii DSM 2661 | aspartyl-tRNA synthetase (aspS) [Methanocaldococcus jannaschii DSM 2661] gb AAB99575.1 aspartyl-tRNA synthetase (aspS) [Methanocaldococcus jannaschii DSM 2661] pir B64494 aspartate-tRNA ligase (EC 6.1.1.12) - Methanocaldococcus jannaschii sp Q58950 SYD_METJA Aspartyl-tRNA synthetase (Aspartate-tRNA ligase) (AspRS) | | | | 6.1.1.12 |
| 22351, 22352 | 52549170 | 42 | 2.00E-48 | uncultured archaeon GZfos26B2 | two-component sensor histidine kinase [uncultured archaeon GZfos26B2] putative N-acyl-D-glucosamine 2-epimerase [Bacteroides fragilis YCH46] dbj BAD47600.1 putative N-acyl-D-glucosamine 2-epimerase [Bacteroides fragilis YCH46] | | | | 2.7.3.- |
| 22353, 22354 | 53712142 | 42 | 3.00E-38 | Bacteroides fragilis YCH46 | peptide ABC transporter, peptide-binding protein, putative [Campylobacter lari RM2100] gb EAL54465.1 peptide ABC transporter, peptide-binding protein, putative [Campylobacter lari RM2100] | | | | 2.7.7.22 |
| 22357, 22358 | 57241353 | 36 | 3.00E-14 | Campylobacter lari RM2100 | putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79592.1 putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22359, 22360 | 29349895 | 43 | 6.00E-16 | Bacteroides thetaiotaomicron VPI-5482 | | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|--|-----------------------|
| 22361, | 34397312 | 28 | 2.00E-10 | Porphyromonas gingivalis W83 | hypothetical protein PG1302 [Porphyromonas gingivalis W83] | | | | |
| 22362, | | | | Porphyromonas gingivalis W83 | ref NP_905476.1 hypothetical protein PG1302 [Porphyromonas gingivalis W83] | | | | |
| 22365, | | | | Cytophaga hutchinsonii | COG0451: Nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii] | | | | 1.1.1.21 ₉ |
| 22366 | 48854193 | 37 | 1.00E-26 | Cytophaga hutchinsonii | putative UDP-galactose 4-epimerase [Bacteroides fragilis YCH46] | | | | |
| 22367, | | | | Bacteroides fragilis | dbj BAD48300.1 putative UDP-galactose 4-epimerase [Bacteroides fragilis YCH46] | | | | 5.1.3.- |
| 22368 | 53712842 | 47 | 1.00E-57 | Bacteroides fragilis YCH46 | DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] | | | | |
| 22369, | | | | Bacteroides fragilis YCH46 | dbj BAD50897.1 DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] | | | | 2.7.7.6 |
| 22370 | 53715439 | 59 | 3.00E-43 | Bacteroides fragilis YCH46 | cysteine synthase/cystathionine beta-synthase family protein [Chlorobium tepidum TLS] gb AAM73140.1 cysteine synthase/cystathionine beta-synthase family protein [Chlorobium tepidum TLS] | | | | 4.2.1.22 |
| 2237, | | | | Chlorobium tepidum TLS | COG0764: 3-hydroxymyristoyl-3-hydroxydecanoyl-(acyl carrier protein) dehydratases [Cytophaga hutchinsonii] | | | | |
| 22373, | 21674733 | 33 | 4.00E-18 | Cytophaga hutchinsonii | hypothetical protein Chut2002377 [Cytophaga hutchinsonii] | | | | |
| 22374 | 48853960 | 26 | 4.00E-17 | Cytophaga hutchinsonii | COG0330: Membrane protease subunits, stomatin/prohibitin homologs [Nostoc punctiforme PCC 73102] | | | | |
| 22375, | | | | Cytophaga hutchinsonii | | | | | |
| 22376 | 48854708 | 23 | 8.00E-15 | Cytophaga hutchinsonii | | | | | |
| 22377, | | | | Nostoc punctiforme PCC 73102 | | | | | |
| 22378 | 53688447 | 27 | 7.00E-19 | Nostoc punctiforme PCC 73102 | | | | | |
| 22379, | | | | Leptospira interrogans serovar Copenhageni str. | hypothetical protein LIC10638 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS69259.1 conserved hypothetical protein | | | | |
| 22380 | 45656536 | 33 | 1.00E-24 | Fiocruz L1-130 | [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] Likely secreted protein containing plastocyanin domain [Idiomarina loihiensis L2TR] gb AAV82057.1 Likely secreted protein containing plastocyanin domain [Idiomarina loihiensis L2TR] | | | | |
| 22381, | | | | Idiomarina loihiensis L2TR | ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78914.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22382 | 56460325 | 52 | 2.00E-30 | Bacteroides thetaiotaomicron VPI-5482 | deoxyribodipyrimidine photolyase, putative [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231036.1 deoxyribodipyrimidine photolyase, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir A82205 probable deoxyribodipyrimidine photolyase VC1392 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | 4.1.99.3 |
| 22385, | | | | Vibrio cholerae O1 biovar eltor str. | hypothetical protein VPA1268 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62611.1 hypothetical protein [Vibrio parahaemolyticus] | | | | |
| 22386 | 29349217 | 49 | 9.00E-44 | Vibrio cholerae O1 biovar eltor str. N16961 | | | | | |
| 22387, | | | | Vibrio cholerae O1 biovar eltor str. | | | | | |
| 22388 | 9655888 | 48 | 7.00E-60 | N16961 | | | | | |
| 22389, | | | | Vibrio parahaemolyticus RIMD 2210633 | | | | | |
| 22390 | 28901123 | 45 | 9.00E-38 | Vibrio parahaemolyticus RIMD 2210633 | | | | | |

| | | | | | | | | |
|--------|----------|----|-----------|--------------------------------------|---|--|--|----------|
| 2239, | 48856049 | 45 | 1.00E-31 | Cytophaga hutchinsonii | hypothetical protein Chut02001282 [Cytophaga hutchinsonii] | | | |
| 2240 | | | | Cytophaga hutchinsonii | | | | |
| 22391, | 48855674 | 44 | 3.00E-45 | Cytophaga hutchinsonii | hypothetical protein Chut02000868 [Cytophaga hutchinsonii] | | | |
| 22392 | | | | Cytophaga hutchinsonii | COG2804: Type II secretory pathway, ATPase PufE/Tfp pilus assembly pathway, ATPase PilB [Cytophaga hutchinsonii] | | | |
| 22393, | 48855356 | 66 | 7.00E-13 | Cytophaga hutchinsonii | | | | |
| 22394 | | | | Cytophaga hutchinsonii | hypothetical protein Chut02001689 [Cytophaga hutchinsonii] | | | |
| 22395, | 48855358 | 57 | 4.00E-38 | Cytophaga hutchinsonii | COG1280: Putative threonine efflux protein [Pseudomonas fluorescens PfO-1] | | | |
| 22396 | | | | Pseudomonas fluorescens PfO-1 | | | | |
| 22403, | 48730285 | 54 | 7.00E-59 | fluorescens PfO-1 | | | | |
| 22404 | | | | fluorescens PfO-1 | | | | |
| 22407, | 45516274 | 31 | 5.00E-11 | Ralstonia eutropha JMP134 | COG1335: Amidases related to nicotinamidase [Ralstonia eutropha JMP134] | | | |
| 22408 | | | | Ralstonia eutropha JMP134 | COG3228: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 22409, | 48855515 | 35 | 2.00E-11 | Cytophaga hutchinsonii | | | | |
| 22410 | | | | Cytophaga hutchinsonii | hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] | | | |
| 22411, | | | | Vibrio cholerae O1 biovar eltor str. | ref NP_229888.1 hypothetical protein VC0231 [Vibrio cholerae O1 biovar eltor str. N16961] pir J82349 hypothetical protein VC0231 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | |
| 22412 | 9654639 | 45 | 2.00E-53 | N16961 | | | | |
| 22413, | | | | Cytophaga hutchinsonii | | | | |
| 22414 | 48853635 | 57 | 5.00E-30 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 22415, | 31194159 | 48 | 4.00E-18 | Anopheles gambiae | | | | |
| 22416 | | | | Anopheles gambiae | ENSANGP0000000346 [Anopheles gambiae] | | | |
| 22417, | | | | Bacteroides thetaiotaomicron | topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 22418 | 29348988 | 46 | 1.00E-57 | VPI-5482 | gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 22421, | | | | Chlorobium tepidum TLS | hydrolase, alpha/beta hydrolase fold family [Chlorobium tepidum TLS] | | | |
| 22422 | 21674076 | 60 | 6.00E-62 | Chlorobium tepidum TLS | gb AAAM72483.1 hydrolase, alpha/beta hydrolase fold family [Chlorobium tepidum TLS] | | | 3.1.1.1 |
| 22423, | | | | Bacteroides fragilis YCH46 | seryl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD47757.1 seryl-tRNA synthetase [Bacteroides fragilis YCH46] | | | 6.1.1.11 |
| 22424 | 53712289 | 38 | 8.00E-16 | YCH46 | | | | |
| 22425, | | | | Pseudomonas aeruginosa | unknown [Pseudomonas aeruginosa] | | | 2.7.7.38 |
| 22426 | 13183744 | 54 | 1.00E-44 | aeruginosa | | | | |
| 22427, | | | | Cytophaga hutchinsonii | | | | |
| 22428 | 48855949 | 47 | 2.00E-07 | Cytophaga hutchinsonii | hypothetical protein Chut02001173 [Cytophaga hutchinsonii] | | | |
| 2243, | | | | Bacteroides thetaiotaomicron | 30S ribosomal protein S1 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2244 | 29349753 | 69 | 1.00E-125 | VPI-5482 | gb AAO79450.1 30S ribosomal protein S1 [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.7.8 |
| 22435, | | | | Bacteroides fragilis | hypothetical protein BF2134 [Bacteroides fragilis YCH46] dbj BAD48861.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22436 | 53713423 | 30 | 2.00E-07 | YCH46 | | | | |

| | | | | | | | | | |
|-------------------------------------|----------------------|----------|----------------------|---|---|--|--|--|---------|
| 22437, 22438, 22441, 22442 | 45655699 19879251 | 31 55 | 1.00E-17 4.00E-57 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 Flavobacterium johnsoniae | hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714691.1 conserved hypothetical protein [Leptospira interrogans serovar Lai str. 56601] gb AA051706.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 22443, 22444 | 28897347 | 42 | 1.00E-32 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical primosomal replication factor Y [Flavobacterium johnsoniae] polyposphate kinase [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58836.1 polyposphate kinase [Vibrio parahaemolyticus] sp Q87S51 PPK_VIBPA Polyposphate kinase (Polyposphate kinase) (ATP-polyposphate phosphotransferase) | | | | 2.7.4.1 |
| 22445, 22446 | 54307921 | 47 | 6.00E-37 | Photobacterium profundum SS9 | putative polyposphate kinase [Photobacterium profundum SS9] emb CAG19139.1 putative polyposphate kinase [Photobacterium profundum] | | | | 2.7.4.1 |
| 22447, 22448 | 48854784 | 61 | 5.00E-42 | Cytophaga hutchinsonii | COG0044: Dihydroorotase and related cyclic amidohydrolases [Cytophaga hutchinsonii] | | | | 3.5.2.3 |
| 22457, 22458 | 54031509 | 38 | 5.00E-18 | Polaromonas sp. JS666 | hypothetical protein PJS6w01001889 [Polaromonas sp. JS666] | | | | |
| 22459, 22460 | 48855208 | 36 | 2.00E-26 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | | |
| 22461, 22462 | 53713904 | 56 | 4.00E-56 | Bacteroides fragilis YCH46 | excinuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46] | | | | |
| 22463, 22464 | 51246763 | 35 | 3.00E-15 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb CAG37640.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | | |
| 22465, 22466 | 12024595 | 62 | 6.00E-78 | Flavobacterium johnsoniae | GldE [Flavobacterium johnsoniae] | | | | |
| 22467, 22468 | 53715357 | 27 | 3.00E-27 | Bacteroides fragilis YCH46 | hypothetical protein BF4073 [Bacteroides fragilis YCH46] dbj BAD50815.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 22469, 22470 | 53715356 | 30 | 6.00E-29 | Bacteroides fragilis YCH46 | peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] dbj BAD50814.1 peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] | | | | 5.2.1.8 |
| 22473, 22474 | 48891870 | 42 | 1.00E-44 | Trichodesmium erythraeum IMS101 | COG0566: rRNA methylases [Trichodesmium erythraeum IMS101] | | | | 2.1.1.- |
| 22475, 22476 | 56677793 | 42 | 7.00E-33 | Silicibacter pomeroiyi DSS-3 | conserved domain protein [Silicibacter pomeroiyi DSS-3] ref YP_166410.1 hypothetical protein SPO1160 [Silicibacter pomeroiyi DSS-3] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|--|---------|
| 22477, | 16119697 | 43 | 2.00E-39 | Agrobacterium tumefaciens str. C58 | hypothetical protein AGR_pAT_692 [Agrobacterium tumefaciens str. C58] gb AAK90844.1 AGR_pAT_692p [Agrobacterium tumefaciens str. C58] sp Q8JJK7 DP42_AGR15 DNA polymerase IV 2 (Pol IV 2) | | | | 2.7.7.7 |
| 22478 | | | | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0909 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76016.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22479, | 29346319 | 59 | 7.00E-94 | Monitella marina | ORF5 [Monitella marina] | | | | |
| 22480 | 6691651 | 40 | 2.00E-16 | Photobacterium profundum SS9 | hypothetical protein PBPRB1714 [Photobacterium profundum SS9] emb CAG3574.1 hypothetical protein [Photobacterium profundum] | | | | |
| 22483, | 54303381 | 36 | 1.00E-42 | Photobacterium profundum SS9 | hypothetical protein PBPRB0445 [Photobacterium profundum SS9] emb CAG18876.1 conserved hypothetical protein [Photobacterium profundum] | | | | 1.14.- |
| 22484 | 54307658 | 30 | 4.00E-28 | Microcystis aeruginosa | McyA [Microcystis aeruginosa] | | | | |
| 22485, | 18920646 | 27 | 2.00E-15 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0909 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76016.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | 6.3.2.- |
| 22486 | 29346319 | 62 | 8.00E-56 | Bacteroides fragilis YCH46 | putative transcription regulator [Bacteroides fragilis YCH46] db BAD48047.1 putative transcription regulator [Bacteroides fragilis YCH46] | | | | |
| 22489, | 53712589 | 36 | 5.00E-13 | Methanococcus maripaludis S2 | cation transport ATPase [Methanococcus maripaludis S2] emb CAF30076.1 cation transport ATPase [Methanococcus maripaludis S2] | | | | 3.6.1.- |
| 22490 | 45358083 | 38 | 5.00E-37 | Thiobacillus denitrificans ATCC 25259 | COG0543: 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases [Thiobacillus denitrificans ATCC 25259] | | | | 1.6.5.- |
| 22491, | 52006884 | 41 | 4.00E-31 | Dehalococcoides ethenogenes 195 | ABC transporter, ATP-binding protein [Dehalococcoides ethenogenes 195] gb AAW39901.1 ABC transporter, ATP-binding protein [Dehalococcoides ethenogenes 195] | | | | 1.8.- |
| 22492, | 57234396 | 46 | 8.00E-19 | Cytophaga hutchinsonii | hypothetical protein Chut02001830 [Cytophaga hutchinsonii] | | | | |
| 22493, | 48855491 | 42 | 1.00E-43 | Staphylococcus aureus subsp. aureus MRSA252 | hypothetical protein SAR2531 [Staphylococcus aureus subsp. aureus MRSA252] emb CAG41512.1 putative exported protein [Staphylococcus aureus subsp. aureus MRSA252] | | | | 3.5.2.6 |
| 22494, | 49484658 | 36 | 1.00E-10 | Tetrahymena thermophila | endonuclease [Tetrahymena thermophila] | | | | |
| 22495, | 18481487 | 25 | 3.00E-08 | Xanthomonas axonopodis pv. citri | phage-related protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM36364.1 phage-related protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 22496 | 21242246 | 36 | 1.00E-08 | str. 306 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|----------|
| 22509, 22510 | 17229899 | 38 | 8.00E-15 | Nostoc sp. PCC 7120 | hypothetical protein alr2407 [Nostoc sp. PCC 7120] pir AH2106 hypothetical protein alr2407 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB74106.1 alr2407 [Nostoc sp. PCC 7120] | | | | 3.1.2.6 |
| 2251, 2252 | 48854244 | 47 | 2.00E-31 | Cytophaga hutchinsonii | COG0644: Dehydrogenases (flavoproteins) [Cytophaga hutchinsonii] | | | | |
| 22511, 22512 | 9655831 | 46 | 2.00E-25 | Vibrio cholerae O1 biovar eltor str. N16961 | prpE protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230984.1 prpE protein [Vibrio cholerae O1 biovar eltor str. N16961] pir DB2213 prpE protein VC1340 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | 6.2.1.17 |
| 22515, 22516 | 23128539 | 31 | 7.00E-20 | Nostoc punctiforme PCC 73102 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 22517, 22518 | 15079944 | 30 | 4.00E-13 | Bacillus subtilis subsp. subtilis str. 168 | two-component response regulator [Bacillus subtilis subsp. subtilis str. 168] emb CAA9961.1 autolysin response regulator [Bacillus subtilis] | | | | |
| 22521, 22522 | 18309198 | 26 | 2.00E-08 | Clostridium perfringens str. 13 | emb CAB14852.1 two-component response regulator [Bacillus subtilis subsp. subtilis str. 168] pir B69655 two-component response regulator lyt-involved - Bacillus subtilis sp P94514 LYTT_BACSU Sensory transduction protein lytT | | | | 2.7.3.- |
| 22523, 22524 | 48854404 | 44 | 2.00E-38 | Cytophaga hutchinsonii | COG0881: Signal peptidase I [Cytophaga hutchinsonii] | | | | 3.1.11.- |
| 22525, 22526 | 30248800 | 30 | 3.00E-15 | Nitrosomonas europaea ATCC 19718 | possible capK protein [Nitrosomonas europaea ATCC 19718] emb CAD84707.1 possible capK protein [Nitrosomonas europaea ATCC 19718] | | | | 3.4.21.8 |
| 22527, 22528 | 29170611 | 53 | 2.00E-52 | Brevibacillus agri | b-alanine synthase [Brevibacillus agri] | | | | 3.5.1.6 |
| 22529, 22530 | 48855760 | 66 | 2.00E-80 | Cytophaga hutchinsonii | COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii] | | | | 3.2.1.4 |
| 22531, 22532 | 33864192 | 35 | 4.00E-37 | Prochlorococcus marinus str. MIT 9313 | Glycosyl transferase, group 1 [Prochlorococcus marinus str. MIT 9313] emb CAE22101.1 Glycosyl transferase, group 1 [Prochlorococcus marinus str. MIT 9313] | | | | 2.-.-.- |
| 22533, 22534 | 29347385 | 63 | 4.00E-79 | Bacteroides thetaiotaomicron VPI-5482 | tRNA nucleotidyltransferase [Bacteroides thetaiotaomicron VPI-5482] gbl AAO77082.1 tRNA nucleotidyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.7.19 |
| 22535, 22536 | 37786088 | 40 | 2.00E-23 | Escherichia coli | putative fucosyltransferase [Escherichia coli] | | | | |
| 22537, 22538 | 54309130 | 66 | 1.00E-24 | Photobacterium profundum SS9 | hypothetical protein PBPRA1944 [Photobacterium profundum SS9] emb CAG20348.1 Conserved hypothetical protein [Photobacterium profundum] | | | | |

| | | | | | | | | |
|--------|----------|----|-----------|---|--|---|----|-------------------|
| 22541, | 53797086 | 39 | 4.00E-41 | Chloroflexus aurantiacus | COG0614: ABC-type Fe ³⁺ -hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus] | | | |
| 22542, | | | | | | | | |
| 22543, | 48854815 | 51 | 2.00E-40 | Cytophaga hutchinsonii | COG0719: ABC-type transport system involved in Fe-S cluster assembly, peremease component [Cytophaga hutchinsonii] | | | |
| 22544, | | | | | | | | |
| 22545, | 52143874 | 33 | 1.00E-06 | Bacillus cereus ZK | thiol-disulfide oxidoreductase [Bacillus cereus ZK] gb AAU18893.1 thiol-disulfide oxidoreductase [Bacillus cereus ZK] | | | |
| 22546, | | | | | | | | |
| 22547, | | | | | | | | |
| 22548, | 48856312 | 29 | 3.00E-10 | Cytophaga hutchinsonii | hypothetical protein Chut02000024 [Cytophaga hutchinsonii] | | | |
| 22549, | | | | | | | | |
| 22550, | 52853441 | 77 | 5.00E-65 | Psychrobacter sp. 273-4 | COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] | | | |
| 22551, | ABP7788 | 8 | | | Desc.N. gonorrhoeae amino acid sequence SEQ ID 2306. Org:Neisseria gonorrhoeae | | | |
| 22552, | | 39 | 2.00E-33 | | | | | |
| 22553, | | | | | | | | |
| 22554, | 53714262 | 35 | 9.00E-50 | Bacteroides fragilis YCH46 | putative nucleotide-diphosphate sugar epimerase [Bacteroides fragilis YCH46] dbj BAD49720.1 putative nucleotide-diphosphate sugar epimerase [Bacteroides fragilis YCH46] | | | 4.2.1.- |
| 22555, | | | | | | | | |
| 22556, | 56459508 | 76 | 2.00E-74 | Idiomarina loihiensis L2TR | Unclassified ABC-type transport system, ATPase component [Idiomarina loihiensis L2TR] gb AAV81240.1 Unclassified ABC-type transport system, ATPase component [Idiomarina loihiensis L2TR] | Photobacterium profundum SS9; segment 11/12 | 81 | 1.00E-10 1.8.- |
| 22559, | | | | | | | | |
| 22560, | 46580119 | 72 | 1.00E-113 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | type I restriction-modification system, M subunit [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96186.1 type I restriction-modification system, M subunit [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | Yersinia pseudotuberculosis IP32953 genome, complete sequence | 79 | 5.00E-20 2.1.1.72 |
| 22563, | | | | | | | | |
| 22564, | 29349972 | 55 | 2.00E-38 | Bacteroides thetaiotaomicron VPI-5482 | putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.4.1.83 |
| 22569, | | | | | | | | |
| 22570, | 29347621 | 50 | 3.00E-58 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2211 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77318.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2257, | | | | | | | | |
| 2258, | 27377973 | 51 | 2.00E-67 | Bradyrhizobium japonicum USDA 110 | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] | | | 2.7.3.- |
| 22571, | | | | | | | | |
| 22572, | 48856381 | 47 | 1.00E-46 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | |
| 22573, | | | | | | | | |
| 22574, | 18391088 | 62 | 8.00E-45 | Shigella dysenteriae | RfbB [Shigella dysenteriae] | | | 2.4.1.- |
| 22577, | | | | | | | | |
| 22578, | 48855214 | 39 | 1.00E-35 | Cytophaga hutchinsonii | hypothetical protein Chut02002288 [Cytophaga hutchinsonii] | | | |

| | | | | | | | | | | |
|-----------------|----------|----|-----------|--|---|---|---|----|----------|----------|
| 22583, 22584 | 16077689 | 29 | 1.00E-06 | 168 | Bacillus subtilis subsp. subtilis str. | hypothetical protein BSU06220 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12441.1 ydJ [Bacillus subtilis subsp. subtilis str. 168] pir F69789 hypothetical protein ydJ - Bacillus subtilis dbj BAA22765.1 function unknown [Bacillus subtilis] | | | | |
| 22585, 22586 | 29349251 | 74 | 1.00E-101 | VPI-5482 | Bacteroides thetataoiaomicon | ATP-dependent Cip protease ATP-binding subunit [Bacteroides thetataoiaomicon VPI-5482] gb AAO78948.1 ATP-dependent Cip protease ATP-binding subunit [Bacteroides thetataoiaomicon VPI-5482] sp Q8A128 CLPX_BACTN ATP-dependent Cip protease ATP-binding subunit clpX | Buchnera aphidicola str. Bp (Baizongia pistaciae), section 2 of 2 of the complete genome | 83 | 6.00E-16 | |
| 22587, 22588 | 48853912 | 60 | 8.00E-30 | Cytophaga hutchinsonii | | COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii] | | | | |
| 22589, 22590 | 52853571 | 91 | 6.00E-97 | Psychrobacter sp. | | COG0784: FOG: CheY-like receiver [Psychrobacter sp. 273-4] | | | | 2.7.3.- |
| 22591, 22592 | 38174845 | 36 | 5.00E-09 | Melittangium lichenicola | | hypothetical protein [Melittangium lichenicola] | | | | |
| 22593, 22594 | 42523322 | 36 | 3.00E-11 | Bdellovibrio bacteriovorus HD100 | | oxidoreductase [Bdellovibrio bacteriovorus HD100] emb CAE79695.1 oxidoreductase [Bdellovibrio bacteriovorus HD100] | | | | |
| 22595, 22596 | 31194343 | 65 | 2.00E-51 | Anopheles gambiae | | ENSANGP00000000181 [Anopheles gambiae] GTP-binding elongation factor family protein TypA/BipA [Bacteroides fragilis YCH46] dbj BAD51200.1 GTP-binding elongation factor family protein TypA/BipA [Bacteroides fragilis YCH46] phosphoenolpyruvate carboxylase [Haloarcula marismortui ATCC 43049] gb AAV45577.1 phosphoenolpyruvate carboxylase [Haloarcula marismortui ATCC 43049] | Anopheles gambiae ENSANGP000000000 0181 (ENSANGG0000000 00177) mRNA, partial cds | 87 | 1.00E-06 | |
| 22597, 22598 | 53715742 | 62 | 7.00E-55 | Bacteroides fragilis YCH46 | | | | | | |
| 22599, 22600 | 55377433 | 28 | 2.00E-14 | Haloarcula marismortui ATCC 43049 | | | | | | 4.1.1.31 |
| 22601, 22602 | 50122772 | 46 | 1.00E-37 | Erwinia carotovora subsp. atroseptica SCRI1043 | | hypothetical protein ECA3851 [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76749.1 putative exported protein [Erwinia carotovora subsp. atroseptica SCRI1043] | | | | 2.7.3.- |
| 22603, 22604 | 48854352 | 50 | 3.00E-26 | Cytophaga hutchinsonii | | COG0629: Single-stranded DNA-binding protein [Cytophaga hutchinsonii] | | | | |
| 22605, 22606 | 29348417 | 36 | 9.00E-31 | Bacteroides thetataoiaomicon VPI-5482 | | hypothetical protein BT3008 [Bacteroides thetataoiaomicon VPI-5482] gb AAO78114.1 conserved hypothetical protein [Bacteroides thetataoiaomicon VPI-5482] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|------------------------------|--|--|--|--|----------|
| 22607, | 3329480 | 35 | 1.00E-18 | Trichinella pseudospiralis | unknown [Trichinella pseudospiralis] | | | | |
| 22608 | | | | pseudospiralis | | | | | |
| 22609, | 5360168 | 53 | 2.00E-36 | Flavobacterium johnsoniae | GidB [Flavobacterium johnsoniae] | | | | |
| 22610 | | | | johnsoniae | | | | | |
| 2261, | 48855091 | 41 | 6.00E-35 | Cytophaga hutchinsonii | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii] | | | | 3.1.1.61 |
| 2262 | | | | hutchinsonii | | | | | |
| 22611, | 48853408 | 51 | 3.00E-40 | Cytophaga hutchinsonii | COG0567: 2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes [Cytophaga hutchinsonii] | | | | 1.2.4.2 |
| 22612 | | | | hutchinsonii | | | | | |
| 22613, | 48853408 | 42 | 1.00E-56 | Cytophaga hutchinsonii | COG0567: 2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes [Cytophaga hutchinsonii] | | | | 1.2.4.2 |
| 22614 | | | | hutchinsonii | | | | | |
| 22615, | | | | Bacteroides thetaiotaomicron | putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22616 | 29347582 | 24 | 4.00E-07 | VPI-5482 | | | | | |
| 22617, | | | | Bacteroides thetaiotaomicron | topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22618 | 29348988 | 33 | 6.00E-38 | VPI-5482 | gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22619, | 53797086 | 38 | 1.00E-40 | Chloroflexus aurantiacus | COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus] | | | | |
| 22620 | | | | aurantiacus | | | | | |
| 22623, | | | | Synechococcus sp. | | | | | |
| 22624 | 22652003 | 43 | 2.00E-15 | PCC 7002 | hypothetical protein [Synechococcus sp. PCC 7002] | | | | |
| 22629, | | | | Bacillus thuringiensis | conserved hypothetical protein, possible penicillin-binding protein [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT59973.1 conserved | | | | |
| 22630 | 49477771 | 31 | 2.00E-17 | serovar konkukian str. 97-27 | hypothetical protein, possible penicillin-binding protein [Bacillus thuringiensis serovar konkukian str. 97-27] | | | | 3.4.16.4 |
| 2263, | | | | Dechloromonas aromatica RCB | COG4585: Signal transduction histidine kinase [Dechloromonas aromatica RCB] | | | | 2.7.3.- |
| 2264 | 53730927 | 41 | 3.00E-30 | aromatica RCB | | | | | |
| 22631, | | | | Bacteroides thetaiotaomicron | riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22632 | 29349136 | 44 | 1.00E-11 | VPI-5482 | gb AAO78833.1 riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22633, | | | | Neisseria meningitidis Z2491 | hypothetical protein NMA0240 [Neisseria meningitidis Z2491] | | | | |
| 22634 | 15793258 | 52 | 9.00E-42 | meningitidis Z2491 | emb CAB83548.1 hypothetical protein NMA0240 [Neisseria meningitidis Z2491] pir D82018 hypothetical protein NMA0240 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) | | | | 3.4.13.9 |
| 22635, | 48863717 | 24 | 7.00E-07 | degradans 2-40 | COG2308: Uncharacterized conserved protein [Microbulbifer degradans 2-40] | | | | |
| 22636 | | | | Rhodospirillum rubrum | COG1664: Integral membrane protein CcmA involved in cell shape determination [Rhodospirillum rubrum] | | | | |
| 22637, | | | | | | | | | |
| 22638 | 48764291 | 43 | 6.00E-19 | rubrum | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|--|----------|
| 22639, 22640 | 15794870 | 51 | 1.00E-24 | Neisseria meningitidis Z2491 | integral membrane protein [Neisseria meningitidis Z2491] emb CAB85208.1 putative integral membrane protein [Neisseria meningitidis Z2491] gb AAAF42077.1 transporter, putative [Neisseria meningitidis MC58] pir C81049 transporter, probable NMB1732 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain Z2491 serogroup A) ref NP_274735.1 transporter, putative [Neisseria meningitidis MC58] | | | | |
| 22641, 22642 | 48859645 | 41 | 2.00E-17 | Clostridium thermocellum ATCC 27405 | COG3587: Restriction endonuclease [Clostridium thermocellum ATCC 27405] | | | | 3.1.21.5 |
| 22643, 22644 | 48854463 | 56 | 4.00E-46 | Cytophaga hutchinsonii | COG0193: Peptidyl-tRNA hydrolase [Cytophaga hutchinsonii] | | | | 3.1.1.29 |
| 22647, 22648 | 53713159 | 31 | 7.00E-21 | Bacteroides fragilis YCH46 | putative two-component system sensor protein without kinase domain [Bacteroides fragilis YCH46] db BAD48617.1 putative two-component system sensor protein without kinase domain [Bacteroides fragilis YCH46] two-component system response regulator [Bacteroides fragilis YCH46] db BAD50109.1 two-component system response regulator [Bacteroides fragilis YCH46] | | | | 3.1.1.61 |
| 22649, 22650 | 53714651 | 45 | 4.00E-56 | Bacteroides fragilis YCH46 | SAM-dependent methyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK76829.1 SAM-dependent methyltransferase [Clostridium acetobutylicum ATCC 824] | | | | |
| 2265, 2266 | 15004787 | 33 | 7.00E-08 | Clostridium acetobutylicum ATCC 824 | TETRA TRICOPEPTIDE REPEAT FAMILY PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24695.1 TETRA TRICOPEPTIDE REPEAT FAMILY PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | | |
| 22653, 22654 | 34762717 | 26 | 2.00E-09 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | COG0451: Nucleoside-diphosphate-sugar epimerases [Anabaena variabilis ATCC 29413] | | | | 5.1.3.- |
| 22659, 22660 | 45509650 | 39 | 7.00E-32 | Anabaena variabilis ATCC 29413 | 50S ribosomal protein L31 type B [Bacteroides fragilis YCH46] db BAD50045.1 50S ribosomal protein L31 type B [Bacteroides fragilis YCH46] | | | | |
| 22661, 22662 | 53714587 | 69 | 3.00E-28 | Bacteroides fragilis YCH46 | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | | |
| 22663, 22664 | 48855208 | 33 | 6.00E-23 | Cytophaga hutchinsonii | ENSANGP00000000352 [Anopheles gambiae] | | | | |
| 22667, 22668 | 31195671 | 51 | 1.00E-32 | Anopheles gambiae | hypothetical protein aq_268 [Aquifex aeolicus VF5] gb AAC06590.1 hypothetical protein [Aquifex aeolicus VF5] pir E70324 conserved hypothetical protein aq_268 - Aquifex aeolicus | | | | |
| 2267, 2268 | 15605808 | 37 | 3.00E-18 | Aquifex aeolicus VF5 | COG2148: Sugar transferases involved in lipopolysaccharide synthesis [Rhodospirillum rubrum] | | | | 2.7.8.6 |
| 22677, 22678 | 48766144 | 37 | 2.00E-32 | Rhodospirillum rubrum | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|--|--|--|----|----------|
| 22681, 22682 | 29345574 | 24 | 2.00E-16 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0164 [Bacteroides thetaiotaomicron VPI-5482] gb AA075271.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22685, 22686 | 53714651 | 45 | 2.00E-39 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD50109.1 two-component system response regulator [Bacteroides fragilis YCH46] | | | | |
| 22687, 22688 | 48855309 | 67 | 5.00E-62 | Cytophaga hutchinsonii | COG0094: Ribosomal protein L5 [Cytophaga hutchinsonii] hypothetical protein BF3562 [Bacteroides fragilis YCH46] dbj BAD50305.1 hypothetical protein [Bacteroides fragilis YCH46] | | | 88 | 3.00E-08 |
| 22689, 22690 | 53714847 | 29 | 2.00E-17 | Bacteroides fragilis YCH46 | COG0131: Imidazolglycerol-phosphate dehydratase [Cytophaga hutchinsonii] | | | | |
| 22691, 22692 | 48855137 | 57 | 1.00E-87 | Cytophaga hutchinsonii | COG0365: Acyl-coenzyme A synthetases/AMP- (fatty) acid ligases [Cytophaga hutchinsonii] | | | | 3.1.3.15 |
| 22693, 22694 | 48855752 | 26 | 7.00E-17 | Cytophaga hutchinsonii | hypothetical protein PG0517 [Porphyromonas gingivalis W83] ref NP_904812.1 hypothetical protein PG0517 [Porphyromonas gingivalis W83] | | | | |
| 22695, 22696 | 34396645 | 31 | 3.00E-08 | Porphyromonas gingivalis W83 | COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga hutchinsonii] | | | | 3.4.21.5 |
| 22697, 22698 | 48853586 | 52 | 5.00E-22 | Cytophaga hutchinsonii | possible capK protein [Nitrosomonas europaea ATCC 19718] emb CAD84707.1 possible capK protein [Nitrosomonas europaea ATCC 19718] | | | | 3 |
| 22699, 22700 | 30248800 | 36 | 2.00E-26 | Nitrosomonas europaea ATCC 19718 | hypothetical protein Chut02001282 [Cytophaga hutchinsonii] | | | | |
| 22705, 22706 | 48856049 | 49 | 2.00E-48 | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | | |
| 22707, 22708 | 48855612 | 33 | 9.00E-33 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | | |
| 22709, 22710 | 48856940 | 33 | 8.00E-15 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Anabaena variabilis ATCC 29413] | | | | 2.4.-.- |
| 22711, 22712 | 45509997 | 50 | 1.00E-23 | Anabaena variabilis ATCC 29413 | Desc:S. pneumoniae type 4 strain protein from coding region #1256. Org:Streptococcus pneumoniae type 4 strain | | | | |
| 22713, 22714 | ABU0168 0 | 46 | 1.00E-53 | | | | | | |
| 22715, 22716 | 4559150 | 34 | 1.00E-35 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AA571873.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | 2.7.3.- |

| | | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|--|----------|
| 22717, | 48854506 | 36 | 2.00E-15 | Cytophaga hutchinsonii | hypothetical protein Chut02002705 [Cytophaga hutchinsonii] | | | | 3.6.1.- |
| 22718 | | | | Cytophaga hutchinsonii | COG0719: ABC-type transport system involved in Fe-S cluster assembly, permease component [Cytophaga hutchinsonii] | | | | |
| 22719, | 48854815 | 47 | 1.00E-54 | Cytophaga hutchinsonii | DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22720 | | | | Bacteroides thetaiotaomicron | gb AAO78227.1 DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482] sp Q8A334 MUTS_BACTN DNA mismatch repair protein mutS | | | | |
| 22721, | 29348530 | 48 | 3.00E-73 | VPI-5482 | tRNA/rRNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22722 | | | | Bacteroides thetaiotaomicron | gb AAO7827.1 tRNA/rRNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.1.1.- |
| 22723, | 29348574 | 65 | 2.00E-60 | VPI-5482 | type I restriction-modification system R subunit (endonuclease) [Geobacillus kaustophilus HTA426] db BAD74631.1 type I restriction-modification system R subunit (endonuclease) [Geobacillus kaustophilus HTA426] | | | | 3.1.21.3 |
| 22727, | 56418881 | 30 | 6.00E-28 | HTA426 | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | | |
| 22728 | | | | Cytophaga hutchinsonii | COG0242: N-formylmethionyl-tRNA deformylase [Cytophaga hutchinsonii] | | | | 3.5.1.88 |
| 22729, | 48853984 | 38 | 7.00E-63 | Cytophaga hutchinsonii | glucose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi Ty2] ref NP_458519.1 glucose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. CT18] | | | | |
| 22730 | | | | Salmonella enterica subsp. enterica serovar Typhi Ty2 | gb AAO71591.1 glucose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD09205.1 glucose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi] pir AD1013 | | | | 5.3.1.9 |
| 22731, | 29144389 | 55 | 6.00E-57 | VPI-5482 | glucose-6-phosphate isomerase (EC 5.3.1.9) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) | | | | |
| 22732, | | | | Porphyromonas gingivalis W83 | spiQ8Z1U7 G6PI_SALTI Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) | | | | 1.17.4.1 |
| 22733, | 34397173 | 44 | 2.00E-77 | VPI-5482 | ribonucleotide reductase [Porphyromonas gingivalis W83] ref NP_905338.1 ribonucleotide reductase [Porphyromonas gingivalis W83] | | | | |
| 22734 | | | | Bacteroides thetaiotaomicron | ribonucleoside-diphosphate reductase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO77252.1 ribonucleoside-diphosphate reductase alpha chain [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22735, | 29347555 | 56 | 1.00E-55 | VPI-5482 | hypothetical protein BT1767 [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22736 | | | | Bacteroides thetaiotaomicron | gb AAO76874.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22737, | 29347177 | 31 | 2.00E-34 | VPI-5482 | | | | | |
| 22738 | | | | | | | | | |
| 22739, | | | | | | | | | |
| 22740 | | | | | | | | | |
| 22741, | | | | | | | | | |
| 22742 | | | | | | | | | |

| | | | | | | | | |
|--------|----------|----|----------|---|--|--|---------|---------|
| 22743, | 29349728 | 24 | 5.00E-09 | Bacteroides [thetataoamlicron VPI-5482] | putative zinc protease [Bacteroides thetataoamlicron VPI-5482] gb AAO79425.1] putative zinc protease [Bacteroides thetataoamlicron VPI- 5482] | | | |
| 22744 | | | | | | | | |
| 22747, | | | | | | | | |
| 22748 | 48856327 | 55 | 6.00E-36 | Cytophaga hutchinsonii | COG3968: Uncharacterized protein related to glutamine synthetase [Cytophaga hutchinsonii] | | | 6.3.1.2 |
| 22749, | | | | | | | | |
| 22750 | 48856043 | 27 | 8.00E-10 | Cytophaga hutchinsonii | COG1556: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 2275, | | | | | | | | |
| 2276 | 28211428 | 54 | 5.00E-37 | Clostridium tetani E88 | D-hydantoinase [Clostridium tetani E88] [Clostridium tetani E88] | | | 3.5.2.2 |
| 22751, | | | | | | | | |
| 22752 | 24373122 | 38 | 1.00E-35 | Shewanella oneidensis MR-1 | GGDEF domain protein [Shewanella oneidensis MR-1] gb AAN54608.1] | | | 2.7.3.- |
| 22753, | | | | | | | | |
| 22754 | 48854312 | 38 | 1.00E-42 | Cytophaga hutchinsonii | COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii] | | | |
| 22755, | | | | | | | | |
| 22756 | 48856925 | 32 | 2.00E-17 | Cytophaga hutchinsonii | COG1309: Transcriptional regulator [Cytophaga hutchinsonii] | | | |
| 22757, | | | | | | | | |
| 22758 | 48844296 | 32 | 7.00E-07 | Geobacter metallireducens GS 15 | COG1858: Cytochrome c peroxidase [Geobacter metallireducens GS-15] hypothetical protein RB12645 [Rhodopirellula baltica SH 1] emb CAD77701.1] hypothetical protein [Pirellula sp.] | | | |
| 22761, | | | | | | | | |
| 22762 | 32477630 | 36 | 3.00E-13 | Rhodopirellula baltica SH 1 | | | | |
| 22765, | | | | | | | | |
| 22766 | 29346648 | 63 | 1.00E-62 | Bacteroides thetataoamlicron VPI-5482 | putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetataoamlicron VPI-5482] gb AAO76345.1] putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetataoamlicron VPI-5482] hypothetical protein Bd3477 [Bdellovibrio bacteriovorus HD100] emb CAE78269.1] conserved hypothetical protein [Bdellovibrio bacteriovorus HD100] | | 2.7.7.8 | |
| 22767, | | | | | | | | |
| 22768 | 42524830 | 26 | 5.00E-08 | Bdellovibrio bacteriovorus HD100 | | | | |
| 2277, | | | | | | | | |
| 2278 | 56675038 | 48 | 6.00E-20 | uncultured bacterium | cellulase [uncultured bacterium] | | | |
| 22771, | | | | | | | | |
| 22772 | 48855958 | 37 | 2.00E-10 | Cytophaga hutchinsonii | hypothetical protein Chu02001184 [Cytophaga hutchinsonii] | | | |
| 22773, | | | | | | | | |
| 22774 | 34557509 | 44 | 3.00E-31 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] emb CAE10224.1] hypothetical protein [Wolinella succinogenes] COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus] | | | |
| 22775, | | | | | | | | |
| 22776 | 53797086 | 39 | 4.00E-41 | Chloroflexus aurantiacus | | | | |
| 22777, | | | | | | | | |
| 22778 | 28901123 | 46 | 5.00E-44 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA1268 [Vibrio parahaemolyticus RIMD 2210633] db BAC62611.1] hypothetical protein [Vibrio parahaemolyticus] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|---------|
| 22779, 22780 | 15668711 | 29 | 8.00E-09 | Methanocaldococcus jannaschii DSM 2661 | hypothetical protein MJ0531 [Methanocaldococcus jannaschii DSM 2661] gb AAB98522.1 conserved hypothetical protein [Methanocaldococcus jannaschii DSM 2661] sp Q57951 Y531_METJA Hypothetical protein MJ0531 pir C64366 hypothetical protein homolog MJ0531 - Methanococcus jannaschii | | | | |
| 22781, 22782 | 32477622 | 41 | 4.00E-52 | Rhodopirellula baltica SH 1 | hypothetical protein-signal peptide and transmembrane prediction [Rhodopirellula baltica SH 1] emb CAD7693.1 hypothetical protein-signal peptide and transmembrane prediction [Pirellula sp.] | | | | |
| 22785, 22786 | 29349423 | 41 | 1.00E-14 | Bacteroides thetaiotaomicron VPI-5482 | transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79120.1 transposase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22787, 22788 | 53712707 | 49 | 3.00E-26 | Bacteroides fragilis YCH46 | penicillin-binding protein 1C [Bacteroides fragilis YCH46] dbj BAD48165.1 penicillin-binding protein 1C [Bacteroides fragilis YCH46] | | | | 2.4.2.- |
| 2279, 2280 | 48854863 | 55 | 3.00E-88 | Cytophaga hutchinsonii | COG0358: DNA primase (bacterial type) [Cytophaga hutchinsonii] hypothetical protein PG0517 [Porphyromonas gingivalis W83] ref NP_904812.1 hypothetical protein PG0517 [Porphyromonas gingivalis W83] | | | | 2.7.7.- |
| 22791, 22792 | 34396645 | 27 | 1.00E-25 | Porphyromonas gingivalis W83 | 5'-nucleotidase precursor [Bacteroides fragilis YCH46] dbj BAD47314.1 5'- nucleotidase precursor [Bacteroides fragilis YCH46] | | | | 3.1.3.5 |
| 22793, 22794 | 53711856 | 40 | 5.00E-11 | Bacteroides fragilis YCH46 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | 2.7.3.- |
| 22799, 22800 | 45657883 | 51 | 2.00E-34 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | COG0096: Ribosomal protein S8 [Cytophaga hutchinsonii] | | | | |
| 22801, 22802 | 48855307 | 72 | 1.00E-49 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | | |
| 22805, 22806 | 48856903 | 35 | 2.00E-37 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | | |
| 22807, 22808 | 48856903 | 38 | 2.00E-39 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | | |
| 22809, 22810 | 48854156 | 37 | 6.00E-32 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] cell division protein FisQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO78552.1 cell division protein FisQ [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |
| 22811, 22812 | 29348855 | 30 | 7.00E-20 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein lpp0444 [Legionella pneumophila str. Paris] emb CAH11592.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | |
| 22813, 22814 | 54296414 | 44 | 4.00E-48 | Legionella pneumophila str. Paris | | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|----------|----------|
| 22819, 22820 | 15643161 | 32 | 6.00E-26 | Thermotoga maritima MSB8 | NADH oxidase, putative [Thermotoga maritima MSB8] gb AAD35480.1 NADH oxidase, putative [Thermotoga maritima MSB8] pir D72382 hypothetical protein TM0395 - Thermotoga maritima (strain MSB8) | | | | | 1.6.- |
| 22821, 22822 | 19705016 | 31 | 1.00E-26 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Probable quinovosaminephosphotransferase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93810.1 Probable quinovosaminephosphotransferase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | | 2.7.8.6 |
| 22825, 22826 | 53729687 | 35 | 2.00E-37 | Dechloromonas aromatica RCB | COG0591: Na ⁺ /proline symporter [Dechloromonas aromatica RCB] | | | | | 2.7.3.- |
| 22827, 22828 | 29346156 | 35 | 1.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | putative zinc protease [Bacteroides thetaiotaomicron VPI-5482] gb AAO75853.1 putative zinc protease [Bacteroides thetaiotaomicron VPI- 5482] | | | | | 3.4.99.- |
| 22829, 22830 | 28897010 | 76 | 3.00E-80 | Vibrio parahaemolyticus RIMD 2210633 | nucleotide sugar dehydrogenase [Vibrio parahaemolyticus RIMD 2210633] db BAC58499.1 nucleotide sugar dehydrogenase [Vibrio parahaemolyticus] | Vibrio vulnificus CMCP6 chromosome I section 3 of 11 of the complete sequence | 87 | 3.00E-17 | 1.1.1.22 | |
| 2283, 2284 | 48853339 | 40 | 7.00E-16 | Cytophaga hutchinsonii | hypothetical protein Chut02003926 [Cytophaga hutchinsonii] | | | | | |
| 22831, 22832 | 48864178 | 31 | 1.00E-33 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02000551 [Microbulbifer degradans 2-40] | | | | | |
| 22833, 22834 | 52842769 | 41 | 1.00E-17 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | hypothetical protein lpg2561 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28621.1 hypothetical protein lpg2561 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | | |
| 22837, 22838 | 45916344 | 52 | 3.00E-35 | Mesorhizobium sp. BNC1 | COG2220: Predicted Zn-dependent hydrolases of the beta-lactamase fold [Mesorhizobium sp. BNC1] | | | | | |
| 22839, 22840 | 48856049 | 50 | 5.00E-72 | Cytophaga hutchinsonii | hypothetical protein Chut02001282 [Cytophaga hutchinsonii] | | | | | |
| 22843, 22844 | 48891870 | 43 | 3.00E-45 | Trichodesmium erythraeum IMS101 | COG0566: rRNA methylases [Trichodesmium erythraeum IMS101] | | | | | 2.1.1.- |
| 22845, 22846 | 26246782 | 43 | 2.00E-56 | Escherichia coli CFT073 | Hypothetical protein ybIN [Escherichia coli CFT073] gb JAN79365.1 Hypothetical protein ybIN [Escherichia coli CFT073] | | | | | |
| 22847, 22848 | 47566806 | 51 | 1.00E-41 | Bacillus cereus G9241 | O6-methylguanine-DNA methyltransferase [Bacillus cereus G9241] gb JAL14768.1 O6-methylguanine-DNA methyltransferase [Bacillus cereus G9241] | | | | | 2.1.1.63 |

| | | | | | | | | | | |
|-----------------|----------|----|-----------|---------------------|---------------------------------------|---|---|----|----------|----------|
| 22849, 22850 | 53713280 | 72 | 1.00E-123 | YCH46 | Bacteroides fragilis | ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD48738.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] | Pasteurella multocida subsp. multocida str. Pm70 section 45 of 204 of the complete genome | 84 | 3.00E-09 | 1.8.- |
| 2285, 2286 | 48853339 | 40 | 7.00E-16 | hutchinsonii | Cytophaga | hypothetical protein Chut02003926 [Cytophaga hutchinsonii] | | | | |
| 22851, 22852 | 18310442 | 33 | 6.00E-11 | perfringens str. 13 | Clostridium | hypothetical protein CPE1460 [Clostridium perfringens str. 13] dbj BAB81166.1 hypothetical protein [Clostridium perfringens str. 13] | | | | |
| 22853, 22854 | 27117221 | 33 | 2.00E-33 | megaterium | Bacillus | glutaryl-tRNA reductase [Bacillus megaterium] sp Q8GCB0 HEM1_BACME | | | | 1.2.1.- |
| 22855, 22856 | 33149015 | 30 | 5.00E-09 | ducreyi 35000HP | Haemophilus | cytochrome D ubiquinol oxidase, subunit II [Haemophilus ducreyi 35000HP] ref NP_874144.1 cytochrome D ubiquinol oxidase, subunit II [Haemophilus ducreyi 35000HP] | | | | 1.10.3.- |
| 22859, 22860 | 22298886 | 62 | 5.00E-37 | cus elongatus BP-1 | Thermosynechococcus | hypothetical protein tlr1343 [Thermosynechococcus elongatus BP-1] dbj BAC08895.1 tlr1343 [Thermosynechococcus elongatus BP-1] | | | | |
| 22861, 22862 | 48856939 | 55 | 5.00E-24 | hutchinsonii | Cytophaga | COG2884: Predicted ATPase involved in cell division [Cytophaga hutchinsonii] | | | | 1.8.- |
| 22865, 22866 | 51893010 | 30 | 2.00E-22 | 14863 | Symbiobacterium thermophilum IAM | 8-amino-7-oxononanoate synthetase [Symbiobacterium thermophilum IAM 14863] dbj BAD40857.1 8-amino-7-oxononanoate synthetase [Symbiobacterium thermophilum IAM 14863] | | | | 2.3.1.47 |
| 22867, 22868 | 48853807 | 50 | 5.00E-57 | hutchinsonii | Cytophaga | COG0793: Periplasmic protease [Cytophaga hutchinsonii] | | | | 3.4.21.- |
| 22869, 22870 | 56416952 | 32 | 6.00E-07 | Maries | Anaplasma marginale str. St. Marie | hypothetical protein AM854 [Anaplasma marginale str. St. Marie] gb AAV86771.1 hypothetical protein AM854 [Anaplasma marginale str. St. Marie] | | | | |
| 2287, 2288 | 50122086 | 55 | 6.00E-89 | SCRI1043 | Erwinia carotovora subsp. atroseptica | polyphosphate kinase [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76062.1 polyphosphate kinase [Erwinia carotovora subsp. atroseptica SCRI1043] | | | | 2.7.4.1 |
| 22873, 22874 | AAO2094 | 9 | 4.00E-33 | | | Desc:Protein of the Bpmi endonuclease gene (BpmiRM). Org:Bacillus pumilus | | | | 2.1.1.72 |
| 22877, 22878 | 48855820 | 50 | 3.00E-37 | hutchinsonii | Cytophaga | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | | |
| 22881, 22882 | 56498315 | 26 | 1.00E-09 | berghei | Plasmodium | hypothetical protein PB000201.03.0 [Plasmodium berghei] | | | | |
| 22885, 22886 | 54302404 | 35 | 3.00E-30 | profundum SS9 | Photobacterium | hypothetical protein PBPRB0725 [Photobacterium profundum SS9] emb CAG22597.1 hypothetical protein [Photobacterium profundum] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|----------|
| 22887, 22888 | 55377565 | 28 | 7.00E-09 | Haloarcula marismortui ATCC 43049 | universal stress protein [Haloarcula marismortui ATCC 43049] gb AAV45709.1 universal stress protein [Haloarcula marismortui ATCC 43049] | | | |
| 22891, 22892 | 57241727 | 31 | 5.00E-29 | Campylobacter lari RM2100 | iron(III) ABC transporter, ATP-binding protein [Campylobacter lari RM2100] gb EAL54397.1 iron(III) ABC transporter, ATP-binding protein [Campylobacter lari RM2100] | | | 1.8.- |
| 22893, 22894 | 23129686 | 26 | 1.00E-13 | Nostoc punctiforme PCC 73102 | COG2207: AraC-type DNA-binding domain-containing proteins [Nostoc punctiforme PCC 73102] | | | |
| 22897, 22898 | 29347921 | 49 | 3.00E-29 | Bacteroides thetataoamicron VPI-5482 | putative transcription regulator [Bacteroides thetataoamicron VPI-5482] gb AAO77618.1 putative transcription regulator [Bacteroides thetataoamicron VPI-5482] | | | |
| 22899, 22900 | 48856956 | 42 | 3.00E-42 | Cytophaga hutchinsonii | COG0135: Phosphoribosylanthranilate isomerase [Cytophaga hutchinsonii] | | | 5.3.1.24 |
| 22901, 22902 | 28211485 | 30 | 1.00E-13 | Clostridium tetani E88 | two-component sensor kinase yesM [Clostridium tetani E88] gb AAO36366.1 two-component sensor kinase yesM [Clostridium tetani E88] | | | 2.7.3.- |
| 22905, 22906 | 56477234 | 30 | 6.00E-16 | Azoarcus sp. Ebn1 Ralstonia | hypothetical protein ebA3194 [Azoarcus sp. Ebn1] emb CAI07922.1 conserved hypothetical protein [Azoarcus sp. Ebn1] | | | |
| 22907, 22908 | 48770184 | 25 | 5.00E-11 | metallidurans CH34 | COG369: Sulfite reductase, alpha subunit (flavoprotein) [Ralstonia metallidurans CH34] | | | 1.8.1.2 |
| 22909, 22910 | 9946545 | 41 | 2.00E-39 | Pseudomonas aeruginosa PAO1 | conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir B83563 conserved hypothetical protein PA0667 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_249358.1 hypothetical protein PA0667 [Pseudomonas aeruginosa PAO1] | | | 3.5.1.- |
| 2291, 2292 | 2947297 | 40 | 2.00E-26 | Myxococcus xanthus | putative ECF sigma factor RpoE1 [Myxococcus xanthus] | | | |
| 22917, 22918 | 53712491 | 35 | 1.00E-44 | Bacteroides fragilis YCH46 | putative nitrogen utilization substance protein [Bacteroides fragilis YCH46] db BAD47949.1 putative nitrogen utilization substance protein [Bacteroides fragilis YCH46] | | | |
| 22919, 22920 | 15614651 | 39 | 1.00E-20 | Bacillus halodurans C-125 | hypothetical protein BH2088 [Bacillus halodurans C-125] db BAB05807.1 BH2088 [Bacillus halodurans C-125] pir H83910 hypothetical protein BH2088 [imported] - Bacillus halodurans (strain C-125) db BAA75367.1 Ydel [Bacillus halodurans] | | | |
| 22923, 22924 | 19879252 | 72 | 4.00E-71 | Flavobacterium johnsoniae | hypothetical pseudouridine synthase [Flavobacterium johnsoniae] | | | 4.2.1.70 |
| 22929, 22930 | 32473830 | 55 | 3.00E-28 | Rhodopirellula baltica SH 1 | hypothetical protein RB5657 [Rhodopirellula baltica SH 1] emb CAD74364.1 conserved hypothetical protein [Pirellula sp.] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|----|----------|---------|
| 22931, 22932 | 46141353 | 91 | 7.00E-73 | Psychrobacter sp. 273-4 | COG0086: DNA-directed RNA polymerase, beta' subunit/160 kD subunit [Psychrobacter sp. 273-4] | Acinetobacter sp. ADP1 complete genome | 92 | 1.00E-15 | 2.7.7.6 |
| 22933, 22934 | 29349121 | 38 | 1.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | D-alanine-D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78818.1 D-alanine-D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine-D-alanine ligase (D- alanine synthetase) (D-Ala-D-Ala ligase) | | | 6.3.2.4 | |
| 22937, 22938 | 54308287 | 46 | 1.00E-59 | Photobacterium profundum SS9 | putative signal transduction protein containing EAL and modified HD-GYP domains [Photobacterium profundum SS9] emb CAG19505.1 putative signal transduction protein containing EAL and modified HD-GYP domains [Photobacterium profundum] | | | | |
| 22939, 22940 | 48856613 | 43 | 1.00E-31 | Cytophaga hutchinsonii | COG0486: Predicted GTPase [Cytophaga hutchinsonii] | | | | |
| 22941, 22942 | 57158781 | 33 | 2.00E-23 | Thermococcus kodakaraensis | carbohydrate esterase, family 1 [Thermococcus kodakaraensis] ref YP_182935.1 carbohydrate esterase, family 1 [Thermococcus kodakaraensis] | | | 3.2.1.41 | |
| 22945, 22946 | 56416308 | 42 | 3.00E-35 | Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150 | subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV80071.1 subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] ref NP_808151.1 subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Typhi Ty2] ref NP_458948.1 subunit S of type I restriction- modification system [Salmonella enterica subsp. enterica serovar Typhi str. CT18] gb AAO72011.1 subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD03369.1 subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Typhi] pir AB1069 chain S of type I restriction- modification system [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) | | | 3.1.21.3 | |
| 22947, 22948 | 29349306 | 35 | 9.00E-10 | Bacteroides thetaiotaomicron VPI-5482 | TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO79003.1 TonB [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 22949, 22950 | 42522703 | 47 | 5.00E-28 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd1162 [Bdellovibrio bacteriovorus HD100] emb CAE79076.1 unnamed protein product [Bdellovibrio bacteriovorus HD100] | | | 1.--- | |
| 22951, 22952 | 16127050 | 40 | 4.00E-22 | Caulobacter crescentus CB15 | TPR domain protein [Caulobacter crescentus CB15] gb AAK24782.1 TPR domain protein [Caulobacter crescentus CB15] pir B87598 TPR domain protein [imported] - Caulobacter crescentus | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|---------|----------|
| 22953, 22954 | 17936552 | 45 | 1.00E-29 | Agrobacterium tumefaciens str. C58 | protein tyrosine phosphatase [Agrobacterium tumefaciens str. C58] gb AAL43658.1 protein tyrosine phosphatase [Agrobacterium tumefaciens str. C58] pir AD2905 protein tyrosine phosphatase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) | | | | 3.1.3.48 |
| 22955, 22956 | 20808235 | 33 | 2.00E-41 | Thermoanaerobact er tengcongensis MB4 | DNA polymerase III alpha subunit [Thermoanaerobacter tengcongensis MB4] gb AAM25010.1 DNA polymerase III alpha subunit [Thermoanaerobacter tengcongensis MB4] | | | | 2.7.7.7 |
| 22957, 22958 | 48854578 | 36 | 5.00E-38 | Cytophaga hutchinsonii | COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii] | | | | |
| 22959, 22960 | 22094882 | 58 | 2.00E-46 | Flavobacterium johnsoniae | GldH [Flavobacterium johnsoniae] | | | | |
| 22961, 22962 | 13357977 | 38 | 4.00E-09 | Ureaplasma parvum serovar 3 str. ATCC 700970 | DNA polymerase III alpha chain 2 [Ureaplasma parvum serovar 3 str. ATCC 700970] gb AAF30826.1 DNA polymerase III alpha chain 2 [Ureaplasma parvum serovar 3 str. ATCC 700970] sp Q9PQ74 DP3A_UREPA DNA polymerase III alpha subunit pir D82895 DNA polymerase III alpha chain 2 UU415 [imported] - Ureaplasma urealyticum | | | 2.7.7.7 | |
| 22963, 22964 | 23099733 | 46 | 1.00E-17 | Oceanobacillus lheyensis HTE831 | hypothetical protein OB2278 [Oceanobacillus lheyensis HTE831] dbj BAC14234.1 hypothetical conserved protein [Oceanobacillus lheyensis HTE831] | | | | |
| 22965, 22966 | 29350071 | 37 | 2.00E-16 | Bacteroides thetalaotomicron VPI-5482 | two-component system sensor histidine kinase/response [Bacteroides thetalaotomicron VPI-5482] gb AAO79768.1 two-component system sensor histidine kinase/response [Bacteroides thetalaotomicron VPI-5482] | | | | |
| 22967, 22968 | 46199940 | 36 | 4.00E-12 | Thermus thermophilus HB27 | porphobilinogen deaminase [Thermus thermophilus HB27] ref YP_143611.1 porphobilinogen deaminase [Thermus thermophilus HB8] gb AAS81980.1 porphobilinogen deaminase [Thermus thermophilus HB27] dbj BAD70168.1 porphobilinogen deaminase [Thermus thermophilus HB8] sp Q72H57 HEM3_THET2 Porphobilinogen deaminase (PBG) (Hydroxymethylbilane synthase) (HMB) (Pre-uroporphyrinogen synthase) | | | 4.3.1.8 | |
| 22969, 22970 | 53711360 | 49 | 2.00E-72 | Bacteroides fragilis YCH46 | putative Tricorn-like protease [Bacteroides fragilis YCH46] dbj BAD46818.1 putative Tricorn-like protease [Bacteroides fragilis YCH46] | | | | 3.4.21.- |
| 22971, 22972 | 57234507 | 48 | 2.00E-28 | Fe | [Fe] hydrogenase, HymA subunit, putative [Dehalococcoides ethenogenes 195] gb AAW40012.1 [Fe] hydrogenase, HymA subunit, putative [Dehalococcoides ethenogenes 195] | | | | 1.6.5.3 |
| 22973, 22974 | 29346842 | 53 | 2.00E-97 | Bacteroides thetalaotomicron VPI-5482 | mannonate dehydratase [Bacteroides thetalaotomicron VPI-5482] gb AAO76539.1 mannonate dehydratase [Bacteroides thetalaotomicron VPI- 5482] sp Q8A7U2 UXUA_BACTN Mannonate dehydratase (D-mannonate hydrolase) | | | | 4.2.1.8 |

| | | | | | | | | |
|--------|----------|----|----------|-------------------------------------|---|--|--|----------|
| 22975, | 53712512 | 31 | 2.00E-21 | Bacteroides fragilis YCH46 | iron(III) ABC transporter periplasmic iron-binding protein [Bacteroides fragilis YCH46] dbj BAD47970.1 iron(III) ABC transporter periplasmic iron-binding protein [Bacteroides fragilis YCH46] | | | |
| 22976 | 53713975 | 34 | 4.00E-10 | Bacteroides fragilis YCH46 | hypothetical protein BF2683 [Bacteroides fragilis YCH46] dbj BAD49433.1 | | | |
| 22979, | | | | Legionella pneumophila str. Lens | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22980 | 54295111 | 44 | 1.00E-31 | Chloroflexus aurantiacus | hypothetical protein [Bacteroides fragilis YCH46] | | | 2.3.1.51 |
| 22981, | 53796261 | 72 | 1.00E-37 | Haemophilus | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22982 | 48127605 | 22 | 1.00E-07 | Apis mellifera | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22983, | 48856243 | 37 | 4.00E-23 | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22984 | 48855792 | 33 | 1.00E-13 | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22985, | | | | Haemophilus | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22986 | 53728283 | 78 | 2.00E-38 | Haemophilus somnus 2336 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22989, | 53712209 | 52 | 2.00E-31 | Bacteroides fragilis YCH46 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22990 | 48855464 | 40 | 4.00E-22 | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22993, | 48853635 | 27 | 5.00E-07 | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22994 | | | | Clostridium thermocellum ATCC 27405 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22995, | | | | Xylella fastidiosa Temecula1 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22996 | 53712209 | 52 | 2.00E-31 | Bacteroides fragilis YCH46 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22997, | | | | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22998 | 48855464 | 40 | 4.00E-22 | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 22999, | 48853635 | 27 | 5.00E-07 | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23000 | | | | Clostridium thermocellum ATCC 27405 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23001, | | | | Xylella fastidiosa Temecula1 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23002 | 48853635 | 27 | 5.00E-07 | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23005, | | | | Clostridium thermocellum ATCC 27405 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23006 | 48859715 | 44 | 2.00E-31 | Xylella fastidiosa Temecula1 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 2301, | 28199942 | 31 | 2.00E-16 | Xylella fastidiosa Temecula1 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 2302 | | | | Acinetobacter sp. ADP1 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23011, | 50083970 | 48 | 1.00E-69 | Acinetobacter sp. ADP1 | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23012 | 48854107 | 29 | 3.00E-12 | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23013, | | | | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23014 | | | | Cytophaga hutchinsonii | hypothetical protein [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|--|---|----|-------------------|
| 23015, 23016 | 32473146 | 41 | 5.00E-23 | Rhodopirellula baltica SH 1 | conserved hypothetical protein-putative membrane protein [Rhodopirellula baltica SH 1] embiCAD73826.1] conserved hypothetical protein-putative membrane protein [Pirellula sp.] | | | |
| 23017, 23018 | 40643170 | 50 | 2.00E-76 | Leptospira biflexa temperate bacteriophage LE1 | unnamed protein product [Leptospira biflexa temperate bacteriophage LE1] | | | |
| 23019, 23020 | 53713904 | 77 | 3.00E-81 | Bacteroides fragilis YCH46 | exonuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46] | | | |
| 23021, 23022 | 31194849 | 33 | 2.00E-20 | Anopheles gambiae | ENSANGP0000001858 [Anopheles gambiae] | | | 1.1.99.5 |
| 23023, 23024 | 29027481 | 59 | 3.00E-89 | Aster yellows phytoplasma | threonine dehydratase [Aster yellows phytoplasma] | | | 4.2.1.16 |
| 23025, 23026 | 46142301 | 64 | 1.00E-125 | Methanococcoides burtonii DSM 6242 | COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Methanococcoides burtonii DSM 6242] | Synthetic construct Francisella tularensis clone FLH156713.01X NT02FT0491 gene, complete cds | 90 | 5.00E-17 3.1.21.3 |
| 23027, 23028 | 48862212 | 20 | 2.00E-09 | Microbulbifer degradans 2-40 | COG0419: ATPase involved in DNA repair [Microbulbifer degradans 2-40] conserved hypothetical protein [Silicibacter pomeroyi DSS-3] ref YP_168839.1 hypothetical protein SPO3644 [Silicibacter pomeroyi DSS- 3] | | | |
| 23029, 23030 | 56680201 | 29 | 2.00E-17 | Silicibacter pomeroyi DSS-3 | COG2755: Lysophospholipase L1 and related esterases [Enterococcus faecium] | | | |
| 2303, 2304 | 48824677 | 36 | 5.00E-29 | Enterococcus faecium | putative haloacid dehalogenase-like family hydrolase [Bacteroides fragilis YCH46] dbj BAD50300.1 putative haloacid dehalogenase-like family hydrolase [Bacteroides fragilis YCH46] | | | |
| 23031, 23032 | 53714842 | 47 | 1.00E-30 | Bacteroides fragilis YCH46 | shikimate 5-dehydrogenase [Bacteroides fragilis YCH46] dbj BAD47667.1 shikimate 5-dehydrogenase [Bacteroides fragilis YCH46] | | | 1.1.1.25 |
| 23035, 23036 | 53712209 | 50 | 1.00E-45 | Bacteroides fragilis YCH46 | hypothetical protein Chut02002554 [Cytophaga hutchinsonii] | | | |
| 23037, 23038 | 48854871 | 31 | 1.00E-13 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|----------|
| 23041, 23042 | 16330995 | 56 | 2.00E-41 | Synechocystis sp. PCC 6803 | fructose-bisphosphate aldolase [Synechocystis sp. PCC 6803] sp P74309 ALF1_SYNY3 Fructose-bisphosphate aldolase class I (FBP aldolase) dbj BAA18403.1 fructose-bisphosphate aldolase [Synechocystis sp. PCC 6803] pir S76144 hypothetical protein - Synechocystis sp. (strain PCC 6803) | | | | 4.1.2.13 |
| 23045, 23046 | 9955888 | 52 | 5.00E-55 | Vibrio cholerae O1 biovar eltor str. N16961 | deoxyribodipyrimidine photolyase, putative [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231036.1 deoxyribodipyrimidine photolyase, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir A82205 probable deoxyribodipyrimidine photolyase VC1392 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | 4.1.99.3 |
| 23047, 23048 | 18309705 | 41 | 8.00E-24 | Clostridium perfringens str. 13 | hypothetical protein CPE0723 [Clostridium perfringens str. 13] dbj BAB80429.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | | |
| 23049, 23050 | 48854027 | 30 | 5.00E-18 | Cytophaga hutchinsonii | COG0747: ABC-type dipeptide transport system, periplasmic component [Cytophaga hutchinsonii] | | | | |
| 23051, 23052 | 48853539 | 38 | 2.00E-12 | Cytophaga hutchinsonii | COG3021: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 23053, 23054 | 37519590 | 36 | 2.00E-38 | Gloeobacter violaceus PCC 7421 | Hyb/MsBA family ABC transporter [Gloeobacter violaceus PCC 7421] dbj BAC87962.1 Hyb/MsBA family ABC transporter [Gloeobacter violaceus PCC 7421] | | | | 1.8.-.- |
| 23055, 23056 | 48854085 | 36 | 1.00E-17 | Cytophaga hutchinsonii | COG0607: Rhodanese-related sulfurtransferase [Cytophaga hutchinsonii] | | | | 3.1.2.6 |
| 23057, 23058 | 48855702 | 38 | 6.00E-42 | Cytophaga hutchinsonii | COG3279: Response regulator of the LytR/AIGR family [Cytophaga hutchinsonii] | | | | 3.1.4.17 |
| 23059, 23060 | 56543155 | 33 | 1.00E-14 | Zymomonas mobilis subsp. mobilis ZM4 | conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_162420.1 hypothetical protein ZMO0685 [Zymomonas mobilis subsp. mobilis ZM4] | | | | |
| 23061, 23062 | 6691651 | 41 | 6.00E-25 | Moritella marina | ORF5 [Moritella marina] | | | | 3.4.21.- |
| 23063, 23064 | 42524257 | 43 | 1.00E-15 | Bdellovibrio bacteriovorus HD100 | sensor histidine kinase/response regulator [Bdellovibrio bacteriovorus HD100] emb CAE80630.1 sensor histidine kinase/response regulator [Bdellovibrio bacteriovorus HD100] | | | | 2.7.3.- |
| 23067, 23068 | 48855243 | 41 | 3.00E-15 | Cytophaga hutchinsonii | hypothetical protein Chut02001571 [Cytophaga hutchinsonii] | | | | |
| 23069, 23070 | 32473409 | 30 | 2.00E-22 | Rhodopirellula baltica SH 1 | probable aminopeptidase [Rhodopirellula baltica SH 1] emb CAD78184.1 probable aminopeptidase [Pirellula sp.] | | | | 3.4.21.- |
| 23073, 23074 | 48854978 | 72 | 8.00E-98 | Cytophaga hutchinsonii | COG1410: Methionine synthase I, cobalamin-binding domain [Cytophaga hutchinsonii] | Acinetobacter sp. ADP1 complete genome | 89 | 1.00E-10 | 2.1.1.13 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|---|----|----------|----------|
| 23077, 23078 | 53714415 | 64 | 3.00E-74 | Bacteroides fragilis YCH46 | dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] | | | | 2.4.1.83 |
| 23079, 23080 | 21674237 | 41 | 5.00E-35 | Chlorobium tepidum TLS | glycosyl transferase [Chlorobium tepidum TLS] gb AAM72644.1 glycosyl transferase [Chlorobium tepidum TLS] | | | | 2.4.-.- |
| 23081, 23082 | 48853820 | 76 | 4.00E-94 | Cytophaga hutchinsonii | COG0540: Aspartate carbamoyltransferase, catalytic chain [Cytophaga hutchinsonii] | Bartonella henselae strain Houston-1, complete genome | 92 | 3.00E-08 | 2.1.3.2 |
| 23083, 23084 | 48855014 | 37 | 2.00E-24 | Cytophaga hutchinsonii | COG0571: dsRNA-specific ribonuclease [Cytophaga hutchinsonii] | | | | 3.1.26.3 |
| 23087, 23088 | 48854175 | 56 | 1.00E-68 | Cytophaga hutchinsonii | COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] | | | | 2.7.7.24 |
| 23089, 23090 | 48856121 | 40 | 1.00E-57 | Cytophaga hutchinsonii | COG3781: Predicted membrane protein [Cytophaga hutchinsonii] | | | | |
| 2309, 2310 | 46187901 | 34 | 4.00E-23 | Pseudomonas syringae pv. syringae B728a | COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a] ref ZP_00205512.1 COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a] | | | | |
| 23093, 23094 | 48863739 | 39 | 7.00E-20 | Microbulbifer degradans 2-40 | COG2202: FOG: PAS/PAC domain [Microbulbifer degradans 2-40] | | | | 2.7.3.- |
| 23095, 23096 | 34397012 | 60 | 3.00E-35 | Porphyromonas gingivalis W83 | ABC transporter, ATP-binding protein [Porphyromonas gingivalis W83] ref NP_905177.1 ABC transporter, ATP-binding protein [Porphyromonas gingivalis W83] | | | | 1.8.-.- |
| 23099, 23100 | 54302756 | 38 | 1.00E-11 | Photobacterium profundum SS9 | hypothetical protein PBPRB1077 [Photobacterium profundum SS9] emb CAG22949.1 conserved hypothetical protein [Photobacterium profundum] | | | | |
| 23101, 23102 | 79387 | 41 | 2.00E-13 | | clindamycin resistance transfer factor btgB - Bacteroides fragilis plasmid pBFTM10 gb AAA22903.1 putative | | | | |
| 23103, 23104 | 38637754 | 46 | 7.00E-57 | Cupriavidus necator | NAD-reducing hydrogenase diaphorase moiety small subunit [Cupriavidus necator] gb AAP85842.1 NAD-reducing hydrogenase diaphorase moiety small subunit [Ralstonia eutropha] pir B35385 hydrogen dehydrogenase (EC 1.12.1.2) gamma chain - Alcaligenes eutrophus gb AAC0614.1 NAD-reducing hydrogenase [Ralstonia eutropha] sp P22318 HOXU_ALCEU NAD-reducing hydrogenase hoxS gamma subunit | | | | 1.6.5.3 |
| 23105, 23106 | 48839250 | 32 | 1.00E-20 | Methanosarcina barkeri str. fusaro | COG2202: FOG: PAS/PAC domain [Methanosarcina barkeri str. fusaro] conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_904419.1 hypothetical protein PG0069 [Porphyromonas gingivalis W83] | | | | 2.7.3.- |
| 23109, 23110 | 34396251 | 41 | 1.00E-46 | Porphyromonas gingivalis W83 | | | | | |

| | | | | | | | | | |
|--------|---------|----------|----|----------|---|--|--|--|----------|
| 2311, | 2311, | 46187901 | 34 | 4.00E-23 | Pseudomonas syringae pv. syringae B728a | COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a] ref JP_00205512.1 COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a] | | | |
| 2312, | 2311, | 48854716 | 46 | 8.00E-27 | Cytophaga hutchinsonii | COG0009: Putative translation factor (SUA5) [Cytophaga hutchinsonii] | | | |
| 2313, | 2311, | 58543618 | 28 | 6.00E-08 | Zymomonas mobilis subsp. mobilis ZM4 | outer membrane protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_162883.1 outer membrane protein [Zymomonas mobilis subsp. mobilis ZM4] | | | |
| 2315, | AA1168 | 58543618 | 28 | 6.00E-08 | Zymomonas mobilis subsp. mobilis ZM4 | outer membrane protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_162883.1 outer membrane protein [Zymomonas mobilis subsp. mobilis ZM4] | | | |
| 2316 | 3 | 58543618 | 25 | 2.00E-08 | uncultured archaeon | Desc:Sulfated fucose-containing polysaccharide degrading polypeptide. Org:Flavobacterium sp | | | |
| 23119, | | 52549170 | 34 | 6.00E-16 | GZfos26B2 | two-component sensor histidine kinase [uncultured archaeon GZfos26B2] | | | 2.7.3.- |
| 23121, | | 48856974 | 54 | 2.00E-43 | Cytophaga hutchinsonii | COG1778: Low specificity phosphatase (HAD superfamily) [Cytophaga hutchinsonii] | | | 3.1.3.29 |
| 23123, | | 46141620 | 58 | 8.00E-28 | Psychrobacter sp. 273-4 | COG3335: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] | | | |
| 23125, | | 54302404 | 35 | 1.00E-16 | Photobacterium profundum SS9 | hypothetical protein PBPB0725 [Photobacterium profundum SS9] | | | |
| 23126 | | 54302404 | 35 | 1.00E-16 | Photobacterium profundum SS9 | emb CAG22597.1 hypothetical protein [Photobacterium profundum] | | | |
| 23127, | | 21674236 | 37 | 3.00E-29 | Chlorobium tepidum TLS | hypothetical protein CT1415 [Chlorobium tepidum TLS] gb AAM72643.1 conserved hypothetical protein [Chlorobium tepidum TLS] | | | |
| 23128 | | 21674236 | 37 | 3.00E-29 | Chlorobium tepidum TLS | hypothetical protein CT1415 [Chlorobium tepidum TLS] gb AAM72643.1 conserved hypothetical protein [Chlorobium tepidum TLS] | | | |
| 23129, | | 48854514 | 49 | 4.00E-68 | Cytophaga hutchinsonii | COG1216: Predicted glycosyltransferases [Cytophaga hutchinsonii] | | | 2.4.1.- |
| 23130 | | 48854514 | 49 | 4.00E-68 | Cytophaga hutchinsonii | COG1216: Predicted glycosyltransferases [Cytophaga hutchinsonii] | | | |
| 2313, | | 48855191 | 48 | 4.00E-53 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 2314, | | 48855191 | 48 | 4.00E-53 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | |
| 23131, | | 53713687 | 43 | 1.00E-31 | Bacteroides fragilis YCH46 | hypothetical protein BF2396 [Bacteroides fragilis YCH46] dbj BAD49145.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23132 | | 53713687 | 43 | 1.00E-31 | Bacteroides fragilis YCH46 | hypothetical protein BF2396 [Bacteroides fragilis YCH46] dbj BAD49145.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23133, | | 20092576 | 55 | 5.00E-55 | Methanosarcina acetivorans C2A | dTDP-4-dehydrothiamine 3,5-epimerase [Methanosarcina acetivorans C2A] gb AAM07131.1 dTDP-4-dehydrothiamine 3,5-epimerase [Methanosarcina acetivorans str. C2A] | | | 5.1.3.13 |
| 23134 | | 20092576 | 55 | 5.00E-55 | Methanosarcina acetivorans C2A | dTDP-4-dehydrothiamine 3,5-epimerase [Methanosarcina acetivorans C2A] gb AAM07131.1 dTDP-4-dehydrothiamine 3,5-epimerase [Methanosarcina acetivorans str. C2A] | | | |
| 23135, | | 48854901 | 29 | 1.00E-08 | Cytophaga hutchinsonii | COG3696: Putative silver efflux pump [Cytophaga hutchinsonii] | | | |
| 23136 | | 48854901 | 29 | 1.00E-08 | Cytophaga hutchinsonii | ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] dbj BAD50703.1 ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] | | | |
| 23137, | | 53715245 | 48 | 3.00E-73 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] dbj BAD50703.1 ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] | | | 3.6.1.- |
| 23138 | | 53715245 | 48 | 3.00E-73 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] dbj BAD50703.1 ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] | | | 1.1.1.15 |
| 23139, | AAB4698 | 53715245 | 48 | 3.00E-73 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] dbj BAD50703.1 ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] | | | 8 |
| 23140 | 1 | 53715245 | 48 | 2.00E-29 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] dbj BAD50703.1 ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|--|--|--|----------|--|
| 23141, | 48854182 | 36 | 4.00E-38 | Cytophaga hutchinsonii | COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii] | | | | |
| 23142 | | | | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0820 [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23147, | 29346230 | 54 | 1.00E-29 | Anopheles gambiae | gb AAO75927.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23148 | 31195713 | 63 | 2.00E-94 | Cytophaga hutchinsonii | ENSANGP00000000218 [Anopheles gambiae] | | | 6.3.2.- | |
| 23149, | 48855186 | 36 | 8.00E-11 | Anopheles gambiae | COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii] | | | | |
| 23150 | | | | Anopheles gambiae str. PEST | ENSANGP00000000095 [Anopheles gambiae str. PEST] ref XP_561483.1 | | | | |
| 23151, | 55247361 | 48 | 3.00E-36 | Bacillus thuringiensis serovar konkukian str. 97-27 | ENSANGP00000000095 [Anopheles gambiae str. PEST] | | | | |
| 23152 | | | | Cytophaga hutchinsonii | uroporphyrinogen-III synthase [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA160847.1 uroporphyrinogen-III synthase [Bacillus thuringiensis serovar konkukian str. 97-27] | | | | |
| 23157, | 49478645 | 32 | 3.00E-08 | Cytophaga hutchinsonii | COG0373: Glutaryl-tRNA reductase [Cytophaga hutchinsonii] | | | 1.2.1.- | |
| 23158 | 48855777 | 33 | 5.00E-31 | Acinetobacter sp. ADP1 | putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] | | | | |
| 23159, | 50083970 | 49 | 1.00E-48 | Geobacter sulfurreducens PCA | emb CAG67658.1 putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] | | | 4.1.99.4 | |
| 23160 | | | | Geobacter sulfurreducens PCA | thioredoxin family protein [Geobacter sulfurreducens PCA] gb AAR34697.1 | | | | |
| 23161, | 39986423 | 32 | 2.00E-17 | Bdellovibrio bacteriovorus HD100 | thioredoxin family protein [Geobacter sulfurreducens PCA] | | | | |
| 23162 | 42524028 | 43 | 7.00E-19 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | major anaerobically induced transmembrane protein [Bdellovibrio bacteriovorus HD100] emb CAE80401.1 major anaerobically induced transmembrane protein [Bdellovibrio bacteriovorus HD100] | | | 1.7.99.3 | |
| 23165, | | | | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_710808.1 Putative glycosyl transferase [Leptospira interrogans serovar Lai str. 56601] gb AAN47826.1 Putative glycosyl transferase [Leptospira interrogans serovar lai str. 56601] gb AAS71510.1 | | | | |
| 23166 | 45658787 | 32 | 4.00E-37 | Cytophaga hutchinsonii | glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | |
| 23167, | 48856470 | 35 | 2.00E-16 | Bacteroides thetaiotaomicron VPI-5482 | COG2932: Predicted transcriptional regulator [Cytophaga hutchinsonii] | | | | |
| 23168 | | | | Bacteroides thetaiotaomicron VPI-5482 | putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79825.1 putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23169, | | | | | | | | | |
| 23170 | | | | | | | | | |
| 23171, | | | | | | | | | |
| 23172 | | | | | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|--|----|------------------|
| 23177, 23178 | 48856945 | 48 | 1.00E-43 | Cytophaga hutchinsonii | COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309595.1 COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308310.1 COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308305.1 COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | | |
| 23183, 23184 | 29349785 | 29 | 8.00E-09 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT4377 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79482.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482] | | | | |
| 23187, 23188 | 27364673 | 28 | 4.00E-09 | Vibrio vulnificus CMCP6 | Transcriptional regulator [Vibrio vulnificus CMCP6] ref NP_935886.1 transcriptional regulator [Vibrio vulnificus YJ016] gb AAO09728.1 Transcriptional regulator [Vibrio vulnificus CMCP6] dbj BAC95857.1 transcriptional regulator [Vibrio vulnificus YJ016] | | | | |
| 2319, 2320 | 48856489 | 45 | 5.00E-61 | Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 23193, 23194 | 12024595 | 56 | 6.00E-87 | Flavobacterium johnsoniae | GidE [Flavobacterium johnsoniae] | | | | |
| 23195, 23196 | 48855328 | 73 | 1.00E-65 | Cytophaga hutchinsonii | COG0085: DNA-directed RNA polymerase, beta subunit/140 kD subunit [Cytophaga hutchinsonii] | | | 92 | 1.00E-10 2.7.7.6 |
| 23197, 23198 | 48786803 | 36 | 2.00E-24 | Burkholderia fungorum LB400 | COG0438: Glycosyltransferase [Burkholderia fungorum LB400] related to MCBG protein (microcin resistance protein) [Desulfotalea psychrophila Lsv54] emb CAG35262.1 related to MCBG protein (microcin resistance protein) [Desulfotalea psychrophila Lsv54] | | | | |
| 23199, 23200 | 51244385 | 37 | 3.00E-30 | Desulfotalea psychrophila Lsv54 | ATP-independent RNA helicase [Bacteroides fragilis YCH46] dbj BAD48764.1 ATP-independent RNA helicase [Bacteroides fragilis YCH46] | | | | 2.7.7.- |
| 23203, 23204 | 53713306 | 48 | 1.00E-39 | Bacteroides fragilis YCH46 | similar to cell wall-associated protein precursor wapA [Bdellovibrio bacteriovorus HD100] emb CAE77783.1 similar to cell wall-associated protein precursor wapA [Bdellovibrio bacteriovorus HD100] | | | | |
| 23205, 23206 | 42521749 | 31 | 6.00E-10 | Bdellovibrio bacteriovorus HD100 | putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.4.1.83 |
| 23209, 23210 | 29349972 | 64 | 1.00E-106 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein Chut02003580 [Cytophaga hutchinsonii] phosphohydrolase [Bacteroides fragilis YCH46] dbj BAD47659.1 phosphohydrolase [Bacteroides fragilis YCH46] | | | | |
| 2321, 2322 | 48853721 | 51 | 3.00E-22 | Cytophaga hutchinsonii | | | | | |
| 23211, 23212 | 53712201 | 39 | 2.00E-19 | Bacteroides fragilis YCH46 | | | | | |

| | | | | | | | | | |
|--|----------------------------------|----------------|----------------------------------|---|--|---|----|----------|------------------------|
| 23213, 23214, 23215, 23216 23217, 23218 | 29349615 45524044 29347921 | 50 49 50 | 7.00E-41 8.00E-71 3.00E-31 | 3-hydroxymyristoyl Crocosphaera watsonii WH 8501 Bacteroides thetaitotaomicron VPI-5482 | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79312.1 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Bacteroides thetaiotaomicron VPI-5482] COG0280: Phosphotransacetylase [Crocosphaera watsonii WH 8501] putative transcription regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO77618.1 putative transcription regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.3.1.- 2.3.1.8 |
| 23219, 23220 23223, 23224 | 9947830 48856903 | 49 33 | 4.00E-64 2.00E-35 | Pseudomonas aeruginosa PAO1 Cytophaga hutchinsonii | methionine synthase [Pseudomonas aeruginosa PAO1] ref NP_250534.1 methionine synthase [Pseudomonas aeruginosa PAO1] pir E83415 methionine synthase PA1843 [Imported] - Pseudomonas aeruginosa (strain PAO1) COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | | 2.1.1.13 |
| 23227, 23228 | 48855349 | 58 | 8.00E-76 | Cytophaga hutchinsonii Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150 | COG0320: Lipote synthase [Cytophaga hutchinsonii] hypothetical protein SPA4314 [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV80042.1 orf, hypothetical protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO79565.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] | Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis DNA, complete genome | 93 | 5.00E-07 | |
| 23229, 23230 2323, 2324 | 56416279 29349868 | 27 36 | 9.00E-18 2.00E-11 | Bacteroides thetaitotaomicron VPI-5482 Vibrio parahaemolyticus RIMD 2210633 | | | | | |
| 23235, 23236 23237, 23238 | 28901124 48772259 | 61 30 | 6.00E-60 1.00E-10 | metallidurans CH34 | hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] db BAC62612.1 hypothetical protein [Vibrio parahaemolyticus] hypothetical protein Reut02001021 [Ralstonia metallidurans CH34] | | | | |
| 23239, 23240 23243, 23244 | 27366889 585368 | 56 40 | 6.00E-32 5.00E-22 | Vibrio vulnificus CMCP6 Vibrio vulnificus CMCP6 | hypothetical protein VV20452 [Vibrio vulnificus CMCP6] gb AAO07406.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Phosphoribulokinase (Phosphopentokinase) (PRK) gb AAA27293.1 phosphoribulokinase | | | | 2.7.1.19 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|----------|
| 23247, 23248 | 52842769 | 41 | 1.00E-17 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | hypothetical protein lpg2561 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gblAAU28621.1] hypothetical protein lpg2561 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | |
| 2325, 2326 | 52425394 | 53 | 5.00E-11 | Mannheimia succiniciproducens MBEL55E | hypothetical protein MS1339 [Mannheimia succiniciproducens MBEL55E] gblAAU37946.1] unknown [Mannheimia succiniciproducens MBEL55E] | | | | |
| 23255, 23256 | 53714706 | 56 | 7.00E-31 | Bacteroides fragilis YCH46 | adenylosuccinate synthetase [Bacteroides fragilis YCH46] dbj BAD50164.1] | | | | 6.3.4.4 |
| 23259, 23260 | 48854535 | 49 | 9.00E-53 | Cytophaga hutchinsonii | adenylosuccinate synthetase [Bacteroides fragilis YCH46] COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins [Cytophaga hutchinsonii] | | | | |
| 23261, 23262 | 48855642 | 28 | 4.00E-24 | Cytophaga hutchinsonii | COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gblAAO76947.1] histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A6N7 SYH_BACTN Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS) lycopene beta-monoxygenase [marine bacterium P99-3] | | | | 6.1.1.21 |
| 23263, 23264 | 29347250 | 63 | 3.00E-90 | Bacteroides thetaitaomicron VPI-5482 | | | | | |
| 23265, 23266 | 31790570 | 41 | 7.00E-32 | marine bacterium P99-3 | | | | | |
| 23269, 23270 | 23125566 | 27 | 1.00E-15 | Nostoc punctiforme PCC 73102 | COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102] | | | | |
| 2327, 2328 | 48854348 | 52 | 4.00E-68 | Cytophaga hutchinsonii | COG1530: Ribonucleases G and E [Cytophaga hutchinsonii] | | | | 3.1.4.- |
| 23271, 23272 | 53712308 | 47 | 1.00E-60 | Bacteroides fragilis YCH46 | ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD47766.1 ATP- binding protein [Bacteroides fragilis YCH46] | | | | 1.8.- |
| 23273, 23274 | 53715023 | 49 | 2.00E-32 | Bacteroides fragilis YCH46 | hypothetical protein BF3739 [Bacteroides fragilis YCH46] dbj BAD50481.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 23275, 23276 | 29348700 | 27 | 5.00E-23 | Bacteroides thetaitaomicron VPI-5482 | hypothetical protein BT3291 [Bacteroides thetaiotaomicron VPI-5482] gblAAO78397.1] hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23277, 23278 | 48863715 | 23 | 8.00E-08 | Microbulifer degradans 2-40 | COG0845: Membrane-fusion protein [Microbulifer degradans 2-40] | | | | |
| 23285, 23286 | 48854655 | 27 | 8.00E-10 | Cytophaga hutchinsonii | hypothetical protein Chui02002321 [Cytophaga hutchinsonii] | | | | |
| 23287, 23288 | 34396743 | 25 | 2.00E-07 | Porphyromonas gingivalis W83 | hypothetical protein PG0624 [Porphyromonas gingivalis W83] ref NP_904909.1] hypothetical protein PG0624 [Porphyromonas gingivalis W83] | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|---------------------------------------|--|--|--|----|----------|
| 23289, | 48853745 | 29 | 1.00E-14 | Cytophaga hutchinsonii | hypothetical protein Chut02003380 [Cytophaga hutchinsonii] | | | | |
| 23290 | | | | | Probable cysteine desulfurase (Nifs protein homolog) gb AAG01802.1 | | | | |
| 2329, | 13431585 | 48 | 3.00E-60 | Methanosarcina thermophila | cysteine desulfurase Nifs [Methanosarcina thermophila] | | | | 4.4.1.- |
| 23291, | | | | | Uncharacterized conserved secreted protein [Idiomarina loihiensis L2TR] | | | | |
| 23292 | 56459184 | 53 | 5.00E-42 | Idiomarina loihiensis L2TR | gb AAV80916.1 Uncharacterized conserved secreted protein [Idiomarina loihiensis L2TR] | | | | |
| 23295, | | | | | | | | | |
| 23296 | 31195677 | 62 | 1.00E-91 | Anopheles gambiae | ENSANGP00000000375 [Anopheles gambiae] | | | | 6.1.1.18 |
| 23297, | | | | | replication protein - Pseudomonas syringae plasmid pPS10 | | | | |
| 23298 | 95009 | 31 | 1.00E-23 | Pseudomonas syringae | emb CAA41700.1 replication protein [Pseudomonas syringae] | | | | |
| 23299, | | | | | | | | | |
| 23300 | 46321450 | 29 | 5.00E-17 | Burkholderia cepacia R1808 | COG5135: Uncharacterized conserved protein [Burkholderia cepacia R1808] | | | | |
| 233, | | | | | | | | | |
| 234 | 53731213 | 48 | 3.00E-44 | Methanococcoides burtonii DSM 6242 | hypothetical protein Mbur03001560 [Methanococcoides burtonii DSM 6242] | | | | |
| 23301, | | | | | | | | | |
| 23302 | 17548499 | 46 | 1.00E-13 | Ralstonia solanacearum GMI1000 | hypothetical protein RS03686 [Ralstonia solanacearum GMI1000] | | | | |
| 23303, | | | | | emb CAD17429.1 HYPOTHETICAL PROTEIN [Ralstonia solanacearum] | | | | |
| 23304 | 53715185 | 28 | 9.00E-17 | Bacteroides fragilis YCH46 | competence protein [Bacteroides fragilis YCH46] db BAD50643.1 | | | | |
| 23305, | | | | | competence protein [Bacteroides fragilis YCH46] | | | | |
| 23306 | 29346570 | 49 | 9.00E-62 | Bacteroides thetaiotaomicron VPI-5482 | Na ⁺ -translocating NADH-quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO76267.1 Na ⁺ -translocating NADH-quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.6.5.- |
| 23309, | | | | | probable ABC transporter (ATPase component). [Rhizobium etli] | | | | |
| 23310 | 21467398 | 56 | 9.00E-39 | Rhizobium etli | ref NP_660060.1 probable ABC transporter (ATPase component). [Rhizobium etli] | | | | 3.4.21.- |
| 2331, | | | | | | | | | |
| 2332 | 22298131 | 47 | 3.00E-24 | Thermosynechococcus elongatus BP-1 | hypothetical protein tir0588 [Thermosynechococcus elongatus BP-1] db BAC08140.1 tir0588 [Thermosynechococcus elongatus BP-1] | | | | |
| 23311, | | | | | | | | | |
| 23312 | 51245771 | 88 | 1.00E-122 | Desulfotalea psychrophila Lsv54 | hypothetical protein DP1919 [Desulfotalea psychrophila Lsv54] emb CAG36648.1 hypothetical protein [Desulfotalea psychrophila Lsv54] | | | | |
| 23313, | | | | | | | | 81 | 3.00E-80 |
| 23314 | 48728488 | 40 | 4.00E-34 | Pseudomonas fluorescens PfO-1 | hypothetical protein Pflu02005424 [Pseudomonas fluorescens PfO-1] | | | | |
| 23317, | | | | | | | | | |
| 23318 | 53714414 | 56 | 1.00E-102 | Bacteroides fragilis YCH46 | transcription-repair coupling factor [Bacteroides fragilis YCH46] db BAD49872.1 transcription-repair coupling factor [Bacteroides fragilis YCH46] | | | | 3.6.1.- |
| 23319, | | | | | | | | | |
| 23320 | 48854452 | 56 | 1.00E-67 | Cytophaga hutchinsonii | COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii] | | | | 2.4.2.14 |

| | | | | | | | | | |
|--------------|--------------|----|----------|--|--|--|--|--|---------------|
| 23321, 23322 | 48854240 | 62 | 1.00E-66 | Cytophaga hutchinsonii | COG3145: Alkylated DNA repair protein [Cytophaga hutchinsonii] | | | | |
| 23327, 23328 | 34396493 | 45 | 1.00E-73 | Porphyromonas gingivalis W83 | ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] ref NP_904660.1 ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] | | | | 3.6.1.- |
| 23329, 23330 | 48855778 | 26 | 6.00E-13 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | |
| 23331, 23332 | 48855778 | 47 | 9.00E-36 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 23333, 23334 | ABP2759 2 | 33 | 2.00E-28 | | Desc: Streptococcus polypeptide SEQ ID NO 4360. Org: Streptococcus agalactiae | | | | 2.4.1.21 |
| 23335, 23336 | 16126741 | 43 | 2.00E-45 | Caulobacter crescentus CB15 | peptidase M20/M25/M40 family protein [Caulobacter crescentus CB15] gb AAK24473.1 peptidase M20/M25/M40 family protein [Caulobacter crescentus CB15] pir E87559 peptidase M20/M25/M40 family protein [Imported] - Caulobacter crescentus | | | | 3.4.17.2 1 |
| 23337, 23338 | 48853326 | 42 | 1.00E-32 | Cytophaga hutchinsonii | COG1485: Predicted ATPase [Cytophaga hutchinsonii] | | | | |
| 23339, 23340 | 16078366 | 38 | 6.00E-27 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU13010 [Bacillus subtilis subsp. subtilis str. 168] emb CAA05581.1 YkgB [Bacillus subtilis] emb CAB13158.1 ykgB [Bacillus subtilis subsp. subtilis str. 168] pir D69856 conserved hypothetical protein ykgB - Bacillus subtilis sp O34499 YKGB_BACSU Hypothetical protein ykgB | | | | |
| 23341, 23342 | 46141524 | 59 | 8.00E-72 | Psychrobacter sp. 273-4 | hypothetical protein Psc03000453 [Psychrobacter sp. 273-4] | | | | 3.1.21.4 |
| 23343, 23344 | 9946150 | 36 | 2.00E-38 | Pseudomonas aeruginosa PAO1 | hypothetical protein PA0305 [Pseudomonas aeruginosa PAO1] pir B83608 hypothetical protein PA0305 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_248996.1 hypothetical protein PA0305 [Pseudomonas aeruginosa PAO1] | | | | 3.5.1.11 |
| 23345, 23346 | 48853805 | 51 | 1.00E-45 | Cytophaga hutchinsonii | COG0166: Glucose-6-phosphate isomerase [Cytophaga hutchinsonii] | | | | |
| 23347, 23348 | 56965532 | 31 | 5.00E-13 | Bacillus clausii KSM-K16 | hypothetical protein ABC3772 [Bacillus clausii KSM-K16] dbj BAD66304.1 conserved hypothetical protein [Bacillus clausii KSM-K16] | | | | 6.3.4.6 |
| 2335, 2336 | 53715357 | 26 | 1.00E-11 | Bacteroides fragilis YCH46 | hypothetical protein BF4073 [Bacteroides fragilis YCH46] dbj BAD50815.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 23353, 23354 | 28901124 | 44 | 2.00E-48 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62612.1 hypothetical protein [Vibrio parahaemolyticus] | | | | |

| | | | | | | | | | | |
|--------|----------|----|----------|-------|---|--|--|--|--|----------|
| 23355, | 30249527 | 48 | 2.00E-27 | 19718 | Nitrosomonas europaea ATCC 19718 | putative transposase [Nitrosomonas europaea ATCC 19718] | | | | |
| 23356 | | | | | Nitrosomonas europaea ATCC 19718 | emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718] | | | | |
| 23357, | | | | | Crocospaera watsonii WH 8501 | COG1252: NADH dehydrogenase, FAD-containing subunit [Crocospaera watsonii WH 8501] | | | | 1.6.99.3 |
| 23358 | 53735983 | 50 | 2.00E-57 | | Bacteroides fragilis YCH46 | hypothetical protein BF3562 [Bacteroides fragilis YCH46] dbj BAD50305.1 | | | | |
| 23359, | 53714847 | 25 | 9.00E-14 | | Bacteroides fragilis YCH46 | hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 23360 | | | | | Bacteroides fragilis YCH46 | putative glycosyltransferase [Bacteroides fragilis YCH46] | | | | 2.4.1.16 |
| 23361, | | | | | Cytophaga hutchinsonii | putative glycosyltransferase [Bacteroides fragilis YCH46] | | | | 6 |
| 23362 | 53711519 | 32 | 6.00E-30 | | Cytophaga hutchinsonii | COG0159: Tryptophan synthase alpha chain [Cytophaga hutchinsonii] | | | | |
| 23363, | 48856725 | 66 | 4.00E-47 | | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 23364 | 48856487 | 38 | 3.00E-39 | | Cytophaga hutchinsonii | lipopolysaccharide biosynthesis [Oceanobacillus theyensis HTE831] | | | | |
| 23367, | | | | | Oceanobacillus theyensis HTE831 | lipopolysaccharide biosynthesis [Oceanobacillus theyensis HTE831] | | | | 2.4.1.- |
| 23373, | 23099221 | 26 | 4.00E-16 | | Bacillus thuringiensis serovar konkukian str. 97-27 | phenylalanine 4-monooxygenase (phenylalanine-4-hydroxylase) [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA163620.1 phenylalanine 4-monooxygenase (phenylalanine-4-hydroxylase) [Bacillus thuringiensis serovar konkukian str. 97-27] | | | | |
| 23374 | 49481418 | 38 | 2.00E-35 | | Bacillus thuringiensis serovar konkukian str. 97-27 | phenylalanine 4-monooxygenase (phenylalanine-4-hydroxylase) [Bacillus thuringiensis serovar konkukian str. 97-27] | | | | |
| 23375, | | | | | Nostoc sp. PCC 7120 | transcriptional regulator [Nostoc sp. PCC 7120] dbj BAB74294.1 | | | | |
| 23376 | | | | | Nostoc sp. PCC 7120 | transcriptional regulator [Nostoc sp. PCC 7120] pir AD2130 transcription regulator alr2595 [imported] - Nostoc sp. (strain PCC 7120) | | | | |
| 23379, | 17230087 | 32 | 2.00E-19 | | Nostoc sp. PCC 7120 | transcriptional regulator [Nostoc sp. PCC 7120] dbj BAB74294.1 | | | | |
| 23380 | | | | | Nostoc sp. PCC 7120 | transcriptional regulator [Nostoc sp. PCC 7120] pir AD2130 transcription regulator alr2595 [imported] - Nostoc sp. (strain PCC 7120) | | | | |
| 23381, | | | | | Cytophaga hutchinsonii | COG0504: CTP synthase (UTP-ammonia lyase) [Cytophaga hutchinsonii] | | | | |
| 23382 | 48856944 | 64 | 8.00E-69 | | Cytophaga hutchinsonii | hypothetical protein BT3321 [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23385, | 29348730 | 43 | 3.00E-43 | | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23386 | | | | | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23387, | 48853613 | 45 | 3.00E-33 | | Cytophaga hutchinsonii | COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii] | | | | |
| 23388 | | | | | Cytophaga hutchinsonii | hydrogenase expression/formation protein HypD [Chlorobium tepidum TLS] | | | | |
| 23389, | | | | | Chlorobium tepidum TLS | hydrogenase expression/formation protein HypD [Chlorobium tepidum TLS] | | | | |
| 23390 | 21674608 | 55 | 3.00E-26 | | Chlorobium tepidum TLS | hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1 | | | | |
| 23393, | | | | | Bacteroides fragilis YCH46 | hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 23394 | 53712193 | 25 | 1.00E-19 | | Bacteroides fragilis YCH46 | hypothetical protein [Bacteroides fragilis YCH46] | | | | 2.7.3.- |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|--|--|--|----------|
| 23395, | 30248905 | 38 | 2.00E-12 | Nitrosomonas europaea ATCC 19718 | PDZ domain (also known as DHR or GLGF) [Nitrosomonas europaea ATCC 19718] emb CAD84812.1 PDZ domain (also known as DHR or GLGF) [Nitrosomonas europaea ATCC 19718] | | | | |
| 23396 | | | | Rhodopirellula baltica SH 1 | alpha-L-fucosidase [Rhodopirellula baltica SH 1] emb CAD74450.1 alpha-L-fucosidase [Pirellula sp.] | | | | 3.2.1.51 |
| 23397, | 32473915 | 30 | 9.00E-17 | Desulfotobacterium hafniense DCB-2 | COG3669: Alpha-L-fucosidase [Desulfotobacterium hafniense DCB-2] | | | | 3.2.1.51 |
| 23398, | 23119926 | 35 | 2.00E-18 | Lactobacillus gasseri | COG2755: Lysophospholipase L1 and related esterases [Lactobacillus gasseri] | | | | |
| 23399, | 23003108 | 27 | 3.00E-07 | Bacillus clausii KSM-K16 | transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16] | | | | |
| 23400, | 56962028 | 29 | 1.00E-14 | Bacteroides fragilis YCH46 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacteroides fragilis YCH46] dbj BAD50445.1 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacteroides fragilis YCH46] | | | | 2.5.1.7 |
| 23401, | 53714987 | 63 | 1.00E-62 | | COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00310901.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309724.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309596.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308324.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308306.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23402, | 48856946 | 31 | 4.00E-07 | Cytophaga hutchinsonii | outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23403, | 29345970 | 26 | 3.00E-19 | Burkholderia pseudomallei K96243 | putative helicase family protein [Burkholderia pseudomallei K96243] emb CAH34757.1 putative helicase family protein [Burkholderia pseudomallei K96243] | | | | |
| 23404, | 53718404 | 36 | 8.00E-29 | Shewanella oneidensis MR-1 | adenylate cyclase-related protein [Shewanella oneidensis MR-1] gb AA054394.1 adenylate cyclase-related protein [Shewanella oneidensis MR-1] | | | | 4.6.1.1 |
| 23405, | 24372907 | 31 | 4.00E-41 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0164 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75271.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23406, | 29345574 | 44 | 2.00E-68 | | | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|------------------------|--|--|--|--|----------|
| 23421, | 48853385 | 41 | 2.00E-12 | Cytophaga hutchinsonii | hypothetical protein Chut02003884 [Cytophaga hutchinsonii] | | | | |
| 23422, | | | | Shewanella | GGDEF domain protein [Shewanella oneidensis MR-1] gb AAN54609.1] | | | | |
| 23423, | 24373122 | 36 | 4.00E-52 | oneidensis MR-1 | GGDEF domain protein [Shewanella oneidensis MR-1] | | | | 2.7.3.- |
| 23425, | | | | Anopheles | | | | | |
| 23426, | 31194223 | 40 | 3.00E-47 | gambiae | ENSANGP0000015562 [Anopheles gambiae] | | | | 2.7.6.5 |
| 23433, | | | | Bacteroides fragilis | O-succinylbenzoic acid-CoA ligase [Bacteroides fragilis YCH46] | | | | |
| 23434, | 53712612 | 38 | 2.00E-23 | YCH46 | dbj BAD48070.1] O-succinylbenzoic acid-CoA ligase [Bacteroides fragilis YCH46] | | | | |
| 23435, | | | | Thermotoga | hypothetical protein TM0358 [Thermotoga maritima MSB8] gb AAD35445.1] | | | | |
| 23436 | 15643126 | 26 | 2.00E-21 | maritima MSB8 | conserved hypothetical protein [Thermotoga maritima MSB8] pir F72386 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | | |
| 23437, | | | | Nostoc sp. PCC | two-component response regulator [Nostoc sp. PCC 7120] dbj BAB75465.1] | | | | |
| 23438 | 17231258 | 35 | 4.00E-17 | 7120 | two-component response regulator [Nostoc sp. PCC 7120] pir AG2276 two-component response regulator all3766 [imported] - Nostoc sp. (strain PCC 7120) | | | | 2.7.3.- |
| 23441, | | | | Cytophaga | COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases | | | | |
| 23442 | 48856843 | 60 | 3.00E-47 | hutchinsonii | [Cytophaga hutchinsonii] | | | | 6.2.1.1 |
| 23443, | | | | Caulobacter | hypothetical protein CC0341 [Caulobacter crescentus CB15] | | | | |
| 23444 | 16124596 | 34 | 4.00E-30 | crescentus CB15 | gb AAK22328.1] hypothetical protein [Caulobacter crescentus CB15] pir D87291 hypothetical protein CC0341 [imported] - Caulobacter crescentus | | | | 3.2.1.41 |
| 23447, | | | | Synechocystis sp. | hybrid sensory kinase [Synechocystis sp. PCC 6803] dbj BAA17056.1] | | | | |
| 23448 | 16329648 | 45 | 3.00E-44 | PCC 6803 | hybrid sensory kinase [Synechocystis sp. PCC 6803] pir S75142 sensory transduction histidine kinase sir1759 - Synechocystis sp. (strain PCC 6803) | | | | 2.7.3.- |
| 23449, | | | | Bacteroides fragilis | adenylosuccinate synthetase [Bacteroides fragilis YCH46] dbj BAD50164.1] | | | | |
| 23450 | 53714706 | 56 | 7.00E-34 | YCH46 | adenylosuccinate synthetase [Bacteroides fragilis YCH46] | | | | 6.3.4.4 |
| 2345, | | | | uncultured | hypothetical protein [uncultured crenarchaeote] | | | | |
| 2346 | 42557719 | 60 | 3.00E-29 | crenarchaeote | | | | | |
| 23451, | | | | Pseudomonas | COG2808: Transcriptional regulator [Pseudomonas aeruginosa UCBPP-PA14] | | | | |
| 23452 | 32039397 | 35 | 6.00E-18 | PA14 | | | | | |
| 23455, | | | | Chlorobium | hypothetical protein CT2083 [Chlorobium tepidum TLS] gb AAM73300.1] | | | | |
| 23456 | 21674893 | 37 | 7.00E-20 | tepidum TLS | conserved hypothetical protein [Chlorobium tepidum TLS] | | | | |
| 23457, | | | | uncultured | polyposphate kinase [uncultured bacterium] | | | | |
| 23458 | 22596896 | 43 | 6.00E-51 | bacterium | | | | | 2.7.4.1 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 23459, 23460 | 45658362 | 51 | 3.00E-44 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | pyridoxamine 5'-phosphate oxidase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_711347.1 Pyridoxamine 5'-phosphate oxidase [Leptospira interrogans serovar Lai str. 56601] gb AA048365.1 Pyridoxamine 5'-phosphate oxidase [Leptospira interrogans serovar lai str. 56601] gb AA071085.1 pyridoxamine 5'-phosphate oxidase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | 1.4.3.5 |
| 23461, 23462 | 15678496 | 43 | 7.00E-16 | Methanothermobacter thermautotrophicus str. Delta H | sensory transduction histidine kinase [Methanothermobacter thermotrophicus str. Delta H] gb AAB84974.1 sensory transduction histidine kinase [Methanothermobacter thermotrophicus str. Delta H] pi C69161 sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Delta H) | | | | 2.7.3.- |
| 23463, 23464 | 48855925 | 40 | 6.00E-16 | Cytophaga hutchinsonii | COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family [Cytophaga hutchinsonii] | | | | 5.2.1.8 |
| 23465, 23466 | 53712193 | 30 | 5.00E-19 | Bacteroides fragilis YCH46 | hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | 2.7.3.- |
| 23467, 23468 | 48853591 | 50 | 6.00E-23 | Cytophaga hutchinsonii | COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii] | | | | |
| 23469, 23470 | 53714985 | 39 | 3.00E-46 | Bacteroides fragilis YCH46 | putative membrane peptidase [Bacteroides fragilis YCH46] dbj BAD50443.1 putative membrane peptidase [Bacteroides fragilis YCH46] | | | | 3.5.1.- |
| 2347, 2348 | ABJ18796 | 41 | 9.00E-12 | | Desc:Pseudomonas aeruginosa biofilm formation-related protein #60. Org:Pseudomonas aeruginosa | | | | |
| 23471, 23472 | 52548588 | 23 | 4.00E-16 | uncultured archaeon GZfos17F1 | FOG TPR repeat [uncultured archaeon GZfos17F1] | | | | |
| 23473, 23474 | 48854351 | 58 | 3.00E-32 | Cytophaga hutchinsonii | COG1194: A/G-specific DNA glycosylase [Cytophaga hutchinsonii] | | | | 3.2.2.- |
| 23475, 23476 | 48854348 | 54 | 2.00E-74 | Cytophaga hutchinsonii | COG1530: Ribonucleases G and E [Cytophaga hutchinsonii] | | | | 3.1.4.- |
| 23477, 23478 | 41725492 | 34 | 5.00E-14 | Dechloromonas aromatica RCB | COG0232: dGTP triphosphohydrolase [Dechloromonas aromatica RCB] | | | | 3.1.5.1 |
| 23479, 23480 | 48854329 | 39 | 4.00E-51 | Cytophaga hutchinsonii | COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii] | | | | |
| 23481, 23482 | 48856501 | 40 | 5.00E-42 | Cytophaga hutchinsonii | COG1234: Metal-dependent hydrolases of the beta-lactamase superfamily III [Cytophaga hutchinsonii] | | | | |
| 23483, 23484 | 53714728 | 67 | 3.00E-45 | Bacteroides fragilis YCH46 | dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] dbj BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] | | | | 2.4.1.83 |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 23487, 23488 | 29346648 | 62 | 1.00E-96 | Bacteroides thetaiotaomicron VPI-5482 | putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76345.1 putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.7.8 |
| 23489, 23490 | 53711885 | 42 | 5.00E-44 | Bacteroides fragilis YCH46 | GTP cyclohydrolase II [Bacteroides fragilis YCH46] dbj BAD47343.1 GTP cyclohydrolase II [Bacteroides fragilis YCH46] | | | | 3.5.4.25 |
| 2349, 2350 | 48854812 | 55 | 4.00E-44 | Cytophaga hutchinsonii | COG1522: Transcriptional regulators [Cytophaga hutchinsonii] | | | | |
| 23491, 23492 | | | | Porphyromonas gingivalis W83 | hypothetical protein PG0598 [Porphyromonas gingivalis W83] ref NP_904885.1 hypothetical protein PG0598 [Porphyromonas gingivalis W83] | | | | |
| 23493, 23494 | 34396719 | 38 | 4.00E-17 | Cytophaga hutchinsonii | COG0770: UDP-N-acetylmuramyl pentapeptide synthase [Cytophaga hutchinsonii] | | | | 5.1.1.1 |
| 23495, 23496 | 48854314 | 43 | 5.00E-61 | Cytophaga hutchinsonii | hypothetical protein Chut02001715 [Cytophaga hutchinsonii] | | | | |
| 23499, 23500 | 48855383 | 64 | 8.00E-61 | Dechloromonas aromatica RCB | COG0493: NADPH-dependent glutamate synthase beta chain and related oxidoreductases [Dechloromonas aromatica RCB] | | | | 1.4.1.13 |
| | 41726215 | 56 | 2.00E-86 | | type I restriction-modification system restriction subunit [Methanosarcina mazei Go1] gb AAM31357.1 type I restriction-modification system restriction subunit [Methanosarcina mazei Go1] | | | | |
| 235, 236 | 21227763 | 50 | 3.00E-57 | Methanosarcina mazei Go1 | conserved hypothetical protein [Bacillus cereus G9241] gb EAL16872.1 conserved hypothetical protein [Bacillus cereus G9241] | | | | 3.1.21.3 |
| 23501, 23502 | 47564397 | 39 | 1.00E-23 | Bacillus cereus G9241 | | | | | |
| | | | | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | transposase (resolvase, DNA invertase) [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28632.1 transposase (resolvase, DNA invertase) [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | |
| 23503, 23504 | 52842780 | 54 | 8.00E-22 | Philadelphia 1 | hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714691.1 conserved hypothetical protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51706.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS72145.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 23507, 23508 | 45655699 | 25 | 3.00E-09 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | | | | | |
| 23509, 23510 | 48854949 | 26 | 3.00E-28 | Cytophaga hutchinsonii | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | | | | |
| 2351, 2352 | 32472461 | 32 | 2.00E-18 | Rhodopirellula baltica SH 1 | conserved hypothetical protein-putative sodium:solute symporter [Rhodopirellula baltica SH 1] emb CAD73139.1 conserved hypothetical protein-putative sodium:solute symporter [Pirellula sp.] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|---------------|
| 23511, 23512 | 29349999 | 35 | 6.00E-47 | Bacteroides thetaiotaomicron VPI-5482 | putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 23513, 23514 | 23112449 | 52 | 6.00E-89 | Desulfitobacterium hafnense DCB-2 | COG1012: NAD-dependent aldehyde dehydrogenases [Desulfitobacterium hafnense DCB-2] | | | 1.2.1.3 |
| 23521, 23522 | 53715189 | 44 | 2.00E-38 | Bacteroides fragilis YCH46 | putative translation factor [Bacteroides fragilis YCH46] dbj BAD50647.1 putative translation factor [Bacteroides fragilis YCH46] | | | |
| 23525, 23526 | 48853966 | 58 | 4.00E-33 | Cytophaga hutchinsonii | COG0537: Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases [Cytophaga hutchinsonii] | | | 3.6.1.17 |
| 23527, 23528 | 53713063 | 32 | 1.00E-23 | Bacteroides fragilis YCH46 | IS110 family transposase [Bacteroides fragilis YCH46] dbj BAD48521.1 IS110 family transposase [Bacteroides fragilis YCH46] | | | |
| 23529, 23530 | 29349346 | 34 | 2.00E-44 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | 3.6.1.- |
| 2353, 2354 | 16125143 | 30 | 4.00E-13 | Caulobacter crescentus CB15 | hypothetical protein CC0890 [Caulobacter crescentus CB15] gb AAK22875.1 hypothetical protein [Caulobacter crescentus CB15] | | | |
| 23531, 23532 | 45681680 | 32 | 3.00E-14 | Mesorhizobium sp. BNC1 | pir G87359 hypothetical protein CC0890 [Imported] - Caulobacter crescentus | | | |
| 23533, 23534 | 48855358 | 57 | 4.00E-38 | Cytophaga hutchinsonii | COG3911: Predicted ATPase [Mesorhizobium sp. BNC1] | | | |
| 23535, 23536 | 48854812 | 44 | 3.00E-31 | Cytophaga hutchinsonii | hypothetical protein Chut02001689 [Cytophaga hutchinsonii] | | | |
| 23539, 23540 | 31195963 | 68 | 3.00E-83 | Anopheles gambiae | COG1522: Transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 23541, 23542 | 53764144 | 50 | 4.00E-41 | Anabaena variabilis ATCC 29413 | ENSANGP00000000454 [Anopheles gambiae] | | | 4.2.1.22 |
| 23543, 23544 | 58002517 | 42 | 5.00E-24 | Gluconobacter oxydans 621H | COG1770: Protease II [Anabaena variabilis ATCC 29413] | | | 3.4.21.8 3 |
| 23545, 23546 | 48854662 | 24 | 7.00E-12 | Cytophaga hutchinsonii | ApaG protein [Gluconobacter oxydans 621H] COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Cytophaga hutchinsonii] | | | |
| 2355, 2356 | 21233496 | 33 | 2.00E-30 | Xanthomonas campestris pv. campestris str. ATCC 33913 | hypothetical protein XCC4074 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM43295.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|---|----|----------|--|----------|
| 23555, | 53715557 | 29 | 3.00E-15 | Bacteroides fragilis YCH46 | tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | | |
| 23556 | | | | | | | | | |
| 23557, | 56609590 | 20 | 8.00E-10 | Cystobacter fuscus | hypothetical protein [Cystobacter fuscus] | | | | |
| 23558 | | | | | | | | | |
| 23559, | 34398043 | 27 | 1.00E-15 | Porphyromonas gingivalis W83 | LysM domain protein [Porphyromonas gingivalis W83] ref NP_906204.1 | | | | 3.2.1.- |
| 23560 | | | | | LysM domain protein [Porphyromonas gingivalis W83] | | | | |
| 23561, | | | | | | | | | |
| 23562 | 53712371 | 31 | 4.00E-37 | Bacteroides fragilis YCH46 | hypothetical protein BF1079 [Bacteroides fragilis YCH46] dbj BAD47829.1 | | | | |
| 23563, | | | | | conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 23564 | 29348968 | 49 | 1.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3559 [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23567, | | | | | gb AAO78665.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23568 | 48855142 | 32 | 1.00E-26 | Cytophaga hutchinsonii | COG4585: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| | | | | | | | | | |
| 23569, | | | | | hypothetical protein BH0710 [Bacillus halodurans C-125] dbj BAB04429.1 | | | | |
| 23570 | 15613273 | 37 | 3.00E-45 | Bacillus halodurans C-125 | BH0710 [Bacillus halodurans C-125] pir F83738 hypothetical protein | | | | 1.1.1.18 |
| 23575, | | | | | BH0710 [imported] - Bacillus halodurans (strain C-125) | | | | |
| 23576 | 48854288 | 36 | 2.00E-33 | Cytophaga hutchinsonii | COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii] | | | | |
| 23583, | | | | | homoserine O-acetyltransferase [Haloarcula marismortui ATCC 43049] | | | | |
| 23584 | 55379638 | 33 | 1.00E-08 | Haloarcula marismortui ATCC 43049 | gb AAV47782.1 homoserine O-acetyltransferase [Haloarcula marismortui ATCC 43049] | | | | 2.3.1.31 |
| | | | | | | | | | |
| 23585, | | | | | CYTA PROTEIN PRECURSOR [Wolinella succinogenes DSM 1740] | | | | |
| 23586 | 34556468 | 44 | 2.00E-39 | Wolinella succinogenes DSM 1740 | emb CAE09183.1 CYTA PROTEIN PRECURSOR [Wolinella succinogenes] emb CAC50081.1 Cyta protein [Wolinella succinogenes] | | | | |
| | | | | | Membrane-associated lipoprotein involved in thiamine biosynthesis | | | | |
| 23587, | | | | | [Thermoanaerobacter tengcongensis MB4] gb AAM25612.1 Membrane-associated lipoprotein involved in thiamine biosynthesis | | | | |
| 23588 | 20808837 | 37 | 1.00E-27 | Thermoanaerobacter tengcongensis MB4 | [Thermoanaerobacter tengcongensis MB4] | | | | |
| | | | | | | | | | |
| 23589, | | | | | COG3328: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] | | | | |
| 23590 | 46141805 | 52 | 2.00E-82 | Psychrobacter sp. 273-4 | | | | | |
| 23591, | | | | | | | | | |
| 23592 | 48856061 | 38 | 1.00E-12 | Cytophaga hutchinsonii | hypothetical protein Chut02001296 [Cytophaga hutchinsonii] | | | | |
| | | | | | | | | | |
| | | | | | Ornithobacterium rhinotracheale plasmid pOR1, complete sequence | 82 | 1.00E-29 | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|---------------|--|
| 23593, 23594 | 34396861 | 42 | 2.00E-35 | Porphyromonas gingivalis W83 | trigger factor, putative [Porphyromonas gingivalis W83] trigger factor, putative [Porphyromonas gingivalis W83] | | | |
| 23595, 23596 | 9657128 | 63 | 2.00E-25 | Vibrio cholerae O1 biovar eltor str. N16961 | fructose-1,6-bisphosphatase [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232172.1 fructose-1,6-bisphosphatase [Vibrio cholerae O1 biovar eltor str. N16961] pir B82064 fructose-1,6-bisphosphatase VC2544 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | 3.1.3.11 | |
| 23597, 23598 | 29346223 | 28 | 5.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO75920.1 TonB [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 23599, 23600 | 53711581 | 60 | 1.00E-33 | Bacteroides fragilis YCH46 | ribonuclease HII [Bacteroides fragilis YCH46] dbj BAD47039.1 ribonuclease HII [Bacteroides fragilis YCH46] | | 3.1.26.4 | |
| 23603, 23604 | 29347298 | 31 | 7.00E-11 | Bacteroides thetaiotaomicron VPI-5482 | transcriptional regulator, LuxR family [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76995.1 transcriptional regulator, LuxR family [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 23605, 23606 | 37520392 | 34 | 1.00E-37 | Gloeobacter violaceus PCC 7421 | hypothetical protein glr0823 [Gloeobacter violaceus PCC 7421] dbj BAC88764.1 glr0823 [Gloeobacter violaceus PCC 7421] | | | |
| 23607, 23608 | 41152672 | 37 | 1.00E-34 | Geobacter sulfurreducens PCA | glycosyl transferase, group 2 family protein [Geobacter sulfurreducens PCA] helicase [Shewanella oneidensis MR-1] gb AAN53453.1 helicase | | 2.4.-- | |
| 23611, 23612 | 24371966 | 44 | 8.00E-49 | Shewanella oneidensis MR-1 | [Shewanella oneidensis MR-1] | | | |
| 23613, 23614 | 42524558 | 41 | 4.00E-69 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd3175 [Bdellovibrio bacteriovorus HD100] emb CAE80931.1 ptrB [Bdellovibrio bacteriovorus HD100] | | 3.4.21.8 3 | |
| 23615, 23616 | 10956806 | 63 | 2.00E-78 | Riemerella anatipestifer | transposase [Riemerella anatipestifer] gb AAD33096.1 transposase [Riemerella anatipestifer] | | | |
| 23617, 23618 | 56460927 | 67 | 3.00E-92 | Idiomarina loihensis L2TR | Acyl-CoA synthetase [Idiomarina loihensis L2TR] gb AAV82659.1 Acyl-CoA synthetase [Idiomarina loihensis L2TR] | | 6.2.1.3 | |
| 23619, 23620 | 48854285 | 32 | 2.00E-26 | Cytophaga hutchinsonii | COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|-----------------|--------------------------------|--|--|--|--|----------|
| 23621, 23622 | 16129122 | 40 | 2.00E-12 | K12 | Escherichia coli | e14 prophage; restriction of DNA at 5-methylcytosine residues [Escherichia coli K12] emb CAA79520.1 methyl cytosine restriction enzyme [Escherichia coli] gb AAC74243.1 restriction of DNA at 5-methylcytosine residues; at locus of e14 element; e14 prophage; restriction of DNA at 5-methylcytosine residues [Escherichia coli K12] dbj BAA35995.1 Modified cytosine restriction protein a [Escherichia coli K12] pir A41424 5-methylcytosine-specific restriction enzyme A (EC 3.1.21.-) - Escherichia coli (strain K-12) sp P24200 MCRA_ECOLI 5-methylcytosine-specific restriction enzyme A (EcoKMcra) gb AAA68481.1 mcrA gene product | | | | 3.1.21.- |
| 23623, 23624 | 29348486 | 53 | 2.00E-36 | VPI-5482 | Bacteroides thetaiotaomicron | ribonuclease R [Bacteroides thetaiotaomicron VPI-5482] gb AAO78183.1 ribonuclease R [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.1.- |
| 23625, 23626 | 20093240 | 27 | 3.00E-11 | acetivorans C2A | Methanosarcina acetivorans C2A | hypothetical protein MA4454 [Methanosarcina acetivorans C2A] gb AAM07795.1 predicted protein [Methanosarcina acetivorans str. C2A] | | | | |
| 23627, 23628 | 48855337 | 57 | 8.00E-81 | hutchinsonii | Cytophaga hutchinsonii | COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii] | | | | |
| 23629, 23630 | 34397767 | 52 | 6.00E-61 | gingivalis W83 | Porphyromonas gingivalis W83 | glycogen synthase-related protein [Porphyromonas gingivalis W83] ref NP_905929.1 glycogen synthase-related protein [Porphyromonas gingivalis W83] | | | | 2.4.1.21 |
| 2363, 2364 | 15616225 | 23 | 1.00E-12 | C-125 | Bacillus halodurans C-125 | [lipopolysaccharide biosynthesis [Bacillus halodurans C-125] dbj BAB07382.1 lipopolysaccharide biosynthesis [Bacillus halodurans C-125] pir G84107 lipopolysaccharide biosynthesis BH3663 [imported] - Bacillus halodurans (strain C-125)] | | | | |
| 23631, 23632 | 53712371 | 33 | 2.00E-26 | YCH46 | Bacteroides fragilis YCH46 | hypothetical protein BF1079 [Bacteroides fragilis YCH46] dbj BAD47829.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 23633, 23634 | 54302415 | 49 | 5.00E-31 | profundum SS9 | Photobacterium profundum SS9 | hypothetical protein PBPRB0736 [Photobacterium profundum SS9] emb CAG22608.1 hypothetical protein [Photobacterium profundum] | | | | |
| 23635, 23636 | 48854645 | 36 | 3.00E-31 | hutchinsonii | Cytophaga hutchinsonii | COG3358: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 23637, 23638 | 52853520 | 94 | 4.00E-81 | 273-4 | Psychrobacter sp. 273-4 | COG0160: 4-aminobutyrate aminotransferase and related aminotransferases [Psychrobacter sp. 273-4] | | | | 2.6.1.19 |
| 23639, 23640 | 23485476 | 23 | 1.00E-11 | yoelii | Plasmodium yoelii | hypothetical protein [Plasmodium yoelii yoelii] | | | | 3.1.11.- |
| 23641, 23642 | 21228523 | 28 | 2.00E-17 | mazei Go1 | Methanosarcina mazei Go1 | Chaperone protein [Methanosarcina mazei Go1] gb AAM32117.1 Chaperone protein [Methanosarcina mazei Go1] | | | | |
| 23643, 23644 | 48856104 | 37 | 4.00E-25 | hutchinsonii | Cytophaga hutchinsonii | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|------------------------------|--|----|----------|----------|----------|
| 23645, | 30020660 | 54 | 3.00E-49 | Bacillus cereus ATCC 14579 | Methyltransferase [Bacillus cereus ATCC 14579] gb AAP09492.1 | | | | |
| 23646 | | | | | Methyltransferase [Bacillus cereus ATCC 14579] | | | | |
| 23647, | | | | | | | | | |
| 23648 | 48854412 | 46 | 9.00E-33 | Cytophaga hutchinsonii | COG0492: Thioredoxin reductase [Cytophaga hutchinsonii] | | | | 1.6.4.5 |
| 2365, | | | | | COG0610: Type I site-specific restriction-modification system, R (restriction) | | | | |
| 2366 | 22995174 | 50 | 2.00E-35 | Xylella fastidiosa Dixon | subunit and related helicases [Xylella fastidiosa Dixon] | | | | 3.1.21.3 |
| 23651, | | | | | | | | | |
| 23652 | 53714775 | 35 | 3.00E-31 | Bacteroides fragilis YCH46 | transcription regulator [Bacteroides fragilis YCH46] dbj BAD50233.1 | | | | |
| 23653, | | | | | transcription regulator [Bacteroides fragilis YCH46] | | | | |
| 23654 | 54307397 | 58 | 4.00E-29 | Photobacterium profundum SS9 | hypothetical protein PBPR0176 [Photobacterium profundum SS9] | | | | |
| | | | | Legionella | emb CAG18615.1 hypothetical protein [Photobacterium profundum] | | | | |
| | | | | pneumophila subsp. | | | | | |
| 23655, | | | | pneumophila str. | hypothetical protein lpg1074 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27160.1 hypothetical protein lpg1074 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | |
| 23656 | 52841308 | 42 | 1.00E-22 | Philadelphia 1 | | | | | |
| 23657, | | | | Bacteroides | | | | | |
| 23658 | 1066445 | 38 | 9.00E-13 | vulgatus | mobB [Bacteroides vulgatus] | | | | |
| | | | | | | | | | |
| 23659, | | | | Microbulbifer | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Microbulbifer degradans 2-40] | | | | |
| 23660 | 48864587 | 27 | 2.00E-20 | degradans 2-40 | | | | | |
| | | | | Bacteroides | hypothetical protein BT3291 [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23661, | | | | thetaitaomicron | gb AAO78397.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23662 | 29348700 | 26 | 2.00E-22 | VPI-5482 | | | | | |
| | | | | | | | | | |
| 23663, | | | | Methanococcoides | | | | | |
| 23664 | 46141914 | 65 | 4.00E-52 | burtonii DSM 6242 | COG0450: Peroxiredoxin [Methanococcoides burtonii DSM 6242] | | | | 1.6.4.- |
| 23667, | | | | Mesorhizobium sp. | COG1236: Predicted exonuclease of the beta-lactamase fold involved in RNA processing [Mesorhizobium sp. BNC1] | | | | |
| 23668 | 45915228 | 38 | 1.00E-55 | BNC1 | | | | | |
| | | | | Legionella | | | | | |
| 23669, | | | | pneumophila str. | hypothetical protein lpp2210 [Legionella pneumophila str. Paris] | | | | |
| 23670 | 54298153 | 52 | 3.00E-50 | Paris | emb CAH13362.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | |
| | | | | | Aminotransferase [Sulfolobus solfataricus P2] gb AAK42830.1 | | | | |
| 2367, | | | | Sulfolobus | Aminotransferase [Sulfolobus solfataricus P2] pir G90446 aminotransferase [Imported] - Sulfolobus solfataricus | | | | 2.6.1.- |
| 2368 | 15899435 | 38 | 1.00E-19 | solfataricus P2 | | | | | |
| | | | | | | | | | |
| | | | | | | | | | |
| 23671, | | | | Vibrio vulnificus | Type I restriction enzyme EcoEI R protein [Vibrio vulnificus CMCP6] | | | | |
| 23672 | 27365375 | 86 | 1.00E-138 | CMCP6 | gb AAO10430.1 Type I restriction enzyme EcoEI R protein [Vibrio vulnificus CMCP6] | | | | |
| | | | | | Desc:E. coli CFT073 genomic sequence #225. Org:Escherichia coli | 82 | 8.00E-22 | 3.1.21.3 | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----------|---|
| 23673, 23674 | 53714874 | 56 | 5.00E-59 | Bacteroides fragilis YCH46 | putative outer membrane protein [Bacteroides fragilis YCH46] dbj BAD50332.1 putative outer membrane protein [Bacteroides fragilis YCH46] | | | |
| 23675, 23676 | 48858283 | 57 | 2.00E-76 | Clostridium thermocellum ATCC 27405 | COG2304: Uncharacterized protein containing a von Willebrand factor type A (VWA) domain [Clostridium thermocellum ATCC 27405] | | | |
| 23677, 23678 | 48864000 | 34 | 2.00E-20 | Microbulbifer degradans 2-40 | COG1428: Deoxynucleoside kinases [Microbulbifer degradans 2-40] | | 2.7.1.11 | 3 |
| 23679, 23680 | 48854772 | 60 | 9.00E-62 | Cytophaga hutchinsonii | COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii] | | | |
| 23681, 23682 | 45656536 | 32 | 1.00E-16 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC10638 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69259.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 23683, 23684 | 20806551 | 57 | 5.00E-27 | Thermoanaerobact er tengcongensis MB4 | EMAP domain [Thermoanaerobacter tengcongensis MB4] gb AAM23326.1 EMAP domain [Thermoanaerobacter tengcongensis MB4] | | 6.1.1.10 | |
| 23685, 23686 | 56421039 | 35 | 1.00E-34 | Geobacillus kaustophilus HTA426 | chaperone protein (heat shock protein 70) (HSP70) [Geobacillus kaustophilus HTA426] dbj BAD76789.1 chaperone protein (heat shock protein 70) (HSP70) [Geobacillus kaustophilus HTA426] | | 3.6.1.3 | |
| 2369, 2370 | 45657908 | 30 | 4.00E-17 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70631.1 histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 23691, 23692 | 29349119 | 33 | 1.00E-13 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3711 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78816.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | 2.7.1.37 | |
| 23693, 23694 | 48854504 | 27 | 1.00E-25 | Cytophaga hutchinsonii | COG1072: Panthothenate kinase [Cytophaga hutchinsonii] | | | |
| 23695, 23696 | 29348158 | 30 | 1.00E-10 | Bacteroides thetaiotaomicron VPI-5482 | putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO7855.1 putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 23697, 23698 | 53715492 | 25 | 2.00E-16 | Bacteroides fragilis YCH46 | putative membrane-associated HD superfamily hydrolase [Bacteroides fragilis YCH46] dbj BAD50950.1 putative membrane-associated HD superfamily hydrolase [Bacteroides fragilis YCH46] | | | |
| 23699, 23700 | 48853783 | 26 | 7.00E-16 | Cytophaga hutchinsonii | COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 237, 238 | 23125015 | 54 | 2.00E-27 | Nostoc punctiforme PCC 73102 | COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | | | 2.7.3.- |
| 23701, 23702 | 29348771 | 44 | 8.00E-35 | Bacteroides thetaiotaomicron VPI-5482 | heptosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78468.1 heptosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 23703, 23704 | 53715600 | 56 | 3.00E-18 | Bacteroides fragilis YCH46 | hypothetical protein BF4320 [Bacteroides fragilis YCH46] db BAD51058.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 23705, 23706 | 34762436 | 43 | 6.00E-40 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | 3-deoxy-manno-octulosonate cytidylyltransferase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24972.1 3-deoxy-manno-octulosonate cytidylyltransferase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | 2.7.7.38 |
| 23707, 23708 | 16329450 | 36 | 2.00E-31 | Synechocystis sp. PCC 6803 | regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] db BAA16858.1 regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] pir S74707 nitrogen fixation positive activator protein - Synechocystis sp. (strain PCC 6803) | | | 2.7.3.- |
| 23709, 23710 | 29654894 | 42 | 8.00E-40 | Coxiella burnetii RSA 493 | hypothetical protein CBU1603 [Coxiella burnetii RSA 493] gb AAO91100.1 conserved hypothetical protein [Coxiella burnetii RSA 493] | | | |
| 2371, 2372 | 29349869 | 42 | 1.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79566.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 23711, 23712 | 23465361 | 44 | 2.00E-18 | Bifidobacterium longum NCC2705 | possible alpha beta hydrolase [Bifidobacterium longum NCC2705] gb AAN24600.1 possible alpha beta hydrolase [Bifidobacterium longum NCC2705] | | | 3.8.1.2 |
| 23713, 23714 | 48856184 | 34 | 3.00E-13 | Cytophaga hutchinsonii | hypothetical protein Chut02001428 [Cytophaga hutchinsonii] | | | |
| 23717, 23718 | 48856007 | 35 | 8.00E-34 | Cytophaga hutchinsonii | COG0308: Aminopeptidase N [Cytophaga hutchinsonii] | | | 3.4.11.- |
| 23719, 23720 | 57234123 | 58 | 4.00E-98 | Dehalococcoides ethenogenes 195 | helicase domain/SNF2 family domain protein [Dehalococcoides ethenogenes 195] gb AAW39628.1 helicase domain/SNF2 family domain protein [Dehalococcoides ethenogenes 195] | | | |
| 23721, 23722 | 48856110 | 61 | 1.00E-74 | Cytophaga hutchinsonii | COG0031: Cysteine synthase [Cytophaga hutchinsonii] | | | 4.2.99.8 |
| 23723, 23724 | 48856125 | 44 | 9.00E-31 | Cytophaga hutchinsonii | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|---------------|
| 23725, 23726 | 29349412 | 51 | 9.00E-50 | [Bacteroides thetaiotaomicron VPI-5482] | lipid-A-disaccharide synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79109.1 lipid-A-disaccharide synthase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.4.1.18 2 |
| 23727, 23728 | 29347827 | 25 | 3.00E-20 | [Bacteroides thetaiotaomicron VPI-5482] | hypothetical protein BT2417 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77524.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 23729, 23730 | 16127932 | 47 | 8.00E-19 | Caulobacter crescentus CB15 | peptidyl-dipeptidase Dcp [Caulobacter crescentus CB15] gb AAK25664.1 peptidyl-dipeptidase Dcp [Caulobacter crescentus CB15] pir D87708 peptidyl-dipeptidase Dcp [imported] - Caulobacter crescentus | | | 3.4.15.5 |
| 2373, 2374 | 48854680 | 25 | 4.00E-16 | Cytophaga hutchinsonii | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | |
| 23731, 23732 | 48855925 | 35 | 6.00E-21 | Cytophaga hutchinsonii | COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family [Cytophaga hutchinsonii] | | | 5.2.1.8 |
| 23733, 23734 | 31194279 | 38 | 3.00E-17 | Anopheles gambiae | ENSANGP00000023840 [Anopheles gambiae] | | | |
| 23735, 23736 | 48854578 | 46 | 1.00E-61 | Cytophaga hutchinsonii | COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii] | | | 2.3.2.- |
| 23737, 23738 | 32473118 | 34 | 4.00E-13 | Rhodospirillum rubrum SH 1 | hypothetical protein RB4459 [Rhodospirillum rubrum SH 1] emb CAD73798.1 conserved hypothetical protein [Pirellula sp.] | | | |
| 23739, 23740 | 53711839 | 38 | 7.00E-38 | Bacteroides fragilis YCH46 | putative mutS-like mismatch repair protein [Bacteroides fragilis YCH46] db BAD47297.1 putative mutS-like mismatch repair protein [Bacteroides fragilis YCH46] | | | |
| 23743, 23744 | 15614794 | 40 | 1.00E-35 | Bacillus halodurans C-125 | hypothetical protein BH2231 [Bacillus halodurans C-125] db BAB05950.1 BH2231 [Bacillus halodurans C-125] pir G83928 hypothetical protein BH2231 [imported] - Bacillus halodurans (strain C-125) | | | 2.-.-.- |
| 23745, 23746 | 28897175 | 23 | 4.00E-07 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VP0401 [Vibrio parahaemolyticus RIMD 2210633] db BAC58664.1 hypothetical protein [Vibrio parahaemolyticus] | | | |
| 23749, 23750 | 47826743 | 42 | 3.00E-31 | Streptomyces sp. AP77 | beta-1,3-glucanase [Streptomyces sp. AP77] | | | 3.2.1.- |
| 23751, 23752 | 50083970 | 49 | 1.00E-48 | Acinetobacter sp. ADP1 | putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] emb CAG67658.1 putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] | | | 4.1.99.4 |
| 23753, 23754 | 53712069 | 31 | 5.00E-22 | Bacteroides fragilis YCH46 | hypothetical protein BF0776 [Bacteroides fragilis YCH46] db BAD47527.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | |
|---|--|----------------------|---|--|--|--|--|------------------------------|
| 23755, 23756 23759, 23760 | 54297099 50 53797086 39 | 2.00E-21 2.00E-28 | Legionella pneumophila str. Paris Chloroflexus aurantiacus | hypothetical protein lpp1144 [Legionella pneumophila str. Paris] emb CAH112295.1 hypothetical protein [Legionella pneumophila str. Paris] COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus] | | | | |
| 23761, 23762 | 17227449 31 | 4.00E-17 | Nostoc sp. PCC 7120 | hypothetical protein all8075 [Nostoc sp. PCC 7120] pir AD2560 hypothetical protein all8075 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120gamma dbj BAB77405.1 ORF_ID:all8075--probable helicase [Nostoc sp. PCC 7120] | | | | 3.1.21.3 |
| 23763, 23764 | 56750215 53 | 9.00E-48 | Synechococcus elongatus PCC 6301 | D-lactate dehydrogenase [Synecococcus elongatus PCC 6301] dbj BAD78396.1 D-lactate dehydrogenase [Synecococcus elongatus PCC 6301] ref ZP_00164440.1 COG1052: Lactate dehydrogenase and related dehydrogenases [Synecococcus elongatus PCC 7942] | | | | 1.1.1.28 |
| 23765, 23766 | 29345572 51 | 3.00E-78 | Bacteroides thetataoamicon VPI-5482 | penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI- 5482] gb AAO75269.1 penicillin-binding protein 1C (PBP-1c) [Bacteroides thetataoamicon VPI-5482] | | | | 2.4.2.- |
| 23767, 23768 23769, 23770 | 15614651 39 21674237 36 | 8.00E-32 2.00E-28 | Bacillus halodurans C-125 Chlorobium tepidum TLS | hypothetical protein BH2088 [Bacillus halodurans C-125] dbj BAB05807.1 BH2088 [Bacillus halodurans C-125] pir H83910 hypothetical protein BH2088 [imported] - Bacillus halodurans (strain C-125) dbj BAA75367.1 Ydel [Bacillus halodurans] glycosyl transferase [Chlorobium tepidum TLS] gb AAM72644.1 glycosyl transferase [Chlorobium tepidum TLS] | | | | 2.4.1.83 |
| 2377, 2378 23771, 23772 | 15899755 27 48855208 36 | 3.00E-11 3.00E-26 | Sulfolobus solfataricus P2 Cytophaga hutchinsonii | hypothetical protein SSO3050 [Sulfolobus solfataricus P2] gb AAK43150.1 Hypothetical protein SSO3050 [Sulfolobus solfataricus P2] pir G90486 hypothetical protein SSO3050 [imported] - Sulfolobus solfataricus COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | | |
| 23773, 23774 | 29349387 40 | 1.00E-30 | Bacteroides thetataoamicon VPI-5482 | putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79084.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.1.1.- |
| 23775, 23776 23777, 23778 23783, 23784 | 34397409 62 48854653 59 21227244 29 | 1.00E-26 5.00E-83 | Porphyromonas gingivalis W83 Cytophaga hutchinsonii Methanosarcina mazel Go1 | DNA polymerase III, gamma and tau subunits [Porphyromonas gingivalis W83] ref NP_905573.1 DNA polymerase III, gamma and tau subunits [Porphyromonas gingivalis W83] COG0635: Coproporphyrinogen III oxidase and related Fe-S oxidoreductases [Cytophaga hutchinsonii] glycosyltransferase [Methanosarcina mazel Go1] gb AAM30838.1 glycosyltransferase [Methanosarcina mazel Go1] conserved hypothetical protein-putative acetyltransferase [Rhodopirellula ballica SH 1] emb CAD72907.1 conserved hypothetical protein-putative acetyltransferase [Pirellula sp.] | | | | 2.7.7.7 1.-.-. 2.4.1.- |
| 23789, 23790 | 32472229 43 | 9.00E-25 | Rhodopirellula ballica SH 1 | | | | | 2.3.1.12 8 |

| | | | | | | | | | | |
|-----------------|----------|----|----------|----------------------|----------------------|--|-------------------------------------|----|----------|----------|
| 2379, 2380 | 17229774 | 48 | 2.00E-26 | 7120 | Nostoc sp. PCC | serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120] pir AC2091 serine/threonine kinase with two-component sensor domain all 2282 [Imported] - Nostoc sp. (strain PCC 7120) dbj BAB73981.1 serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120] | | | | 2.7.3.- |
| 23791, 23792 | 53714606 | 47 | 1.00E-73 | YCH46 | Bacteroides fragilis | excinuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD50064.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46] | | | | |
| 23793, 23794 | 48854339 | 65 | 9.00E-67 | hutchinsonii | Cytophaga | COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii] | Desc:Restriction enzyme AccII gene. | | | |
| 23795, 23796 | 53711964 | 44 | 4.00E-65 | YCH46 | Bacteroides fragilis | aminopeptidase N [Bacteroides fragilis YCH46] | Org:Acinetobacter calcoaceticus | 87 | 1.00E-07 | 3.4.21.- |
| 23797, 23798 | 48855486 | 53 | 7.00E-38 | hutchinsonii | Cytophaga | aminopeptidase N [Bacteroides fragilis YCH46] | | | | 3.4.11.- |
| 23799, 23800 | 53711964 | 43 | 2.00E-24 | YCH46 | Bacteroides fragilis | COG1721: Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) [Cytophaga hutchinsonii] | | | | |
| 23801, 23802 | 52858290 | 28 | 9.00E-09 | gasserii | Lactobacillus | aminopeptidase N [Bacteroides fragilis YCH46] | | | | |
| 23803, 23804 | 48869750 | 35 | 2.00E-13 | acyl-carrier-protein | | COG2352: Phosphoenolpyruvate carboxylase [Lactobacillus gasserii] | | | | 4.1.1.31 |
| 2381, 2382 | 15899755 | 27 | 2.00E-10 | sofatarius P2 | Sulfolobus | COG0332: 3-oxoacyl-[acyl-carrier-protein] synthase II [Pediococcus pentosaceus ATCC 25745] | | | | 2.3.1.38 |
| 23811, 23812 | 53711614 | 42 | 1.00E-59 | YCH46 | Bacteroides fragilis | hypothetical protein SSO3050 [Sulfolobus solfataricus P2] gb AAK43150.1 Hypothetical protein SSO3050 [Sulfolobus solfataricus P2] pir G90486 | | | | |
| 23813, 23814 | 29350001 | 26 | 1.00E-07 | VPI-5482 | Bacteroides | hypothetical protein SSO3050 [Imported] - Sulfolobus solfataricus | | | | 3.1.5.1 |
| 23815, 23816 | 52853383 | 82 | 6.00E-66 | 273-4 | Psychrobacter sp. | dGTP triphosphohydrolase [Bacteroides fragilis YCH46] dbj BAD47072.1 dGTP triphosphohydrolase [Bacteroides fragilis YCH46] | | | | |
| 23817, 23818 | 52853382 | 78 | 6.00E-55 | 273-4 | Psychrobacter sp. | hypothetical protein BT4593 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79698.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23819, 23820 | 53713702 | 62 | 7.00E-99 | YCH46 | Bacteroides fragilis | COG0569: K+ transport systems, NAD-binding component [Psychrobacter sp. 273-4] | | | | |
| 23821, 23822 | 48855500 | 48 | 2.00E-55 | hutchinsonii | Cytophaga | hypothetical protein Psc03002036 [Psychrobacter sp. 273-4] | | | | |
| | | | | | | DNA gyrase A subunit [Bacteroides fragilis YCH46] dbj BAD49160.1 DNA gyrase A subunit [Bacteroides fragilis YCH46] | | | | 5.99.1.3 |
| | | | | | | COG0249: Mismatch repair ATPase (MutS family) [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|-------------|---------------|
| 23823, 23824 | 48854545 | 57 | 1.00E-38 | Cytophaga hutchinsonii | COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii] | | | 2.1.1.- |
| 23825, 23826 | 29346224 | 27 | 3.00E-18 | Bacteroides thetaiotaomicron VPI-5482 | conserved hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] gblAAO75921.1 conserved hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2383, 2384 | 22855032 | 34 | 1.00E-36 | Bacteriophage phi- 105 | ORF8 [Bacteriophage phi-105] pir T13548 hypothetical protein 8 - Bacillus phage phi-105 dbj BAA36665.1 ORF8 [Bacteriophage phi-105] | | | |
| 23831, 23832 | 46141389 | 38 | 3.00E-15 | Psychrobacter sp. 273-4 | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Psychrobacter sp. 273-4] | | | |
| 23835, 23836 | 28379927 | 36 | 6.00E-09 | Lactobacillus plantarum WCFS1 | sorbitol-6-phosphate 2-dehydrogenase [Lactobacillus plantarum WCFS1] emb CAD65697.1 sorbitol-6-phosphate 2-dehydrogenase [Lactobacillus plantarum WCFS1] | | | 1.1.1.14 0 |
| 23837, 23838 | 28852358 | 37 | 4.00E-41 | Pseudomonas syringae pv. tomato str. DC3000 | oxidoreductase, short chain dehydrogenase/reductase family [Pseudomonas syringae pv. tomato str. DC3000] ref NP_791737.1 oxidoreductase, short chain dehydrogenase/reductase family [Pseudomonas syringae pv. tomato str. DC3000] | | | 1.1.1.10 0 |
| 23843, 23844 | 48854525 | 69 | 1.00E-138 | Cytophaga hutchinsonii | COG0143: Methionyl-tRNA synthetase [Cytophaga hutchinsonii] | Bacteroides fragilis YCH46 DNA, complete genome | 82 3.00E-12 | 6.1.1.10 |
| 23845, 23846 | 56460315 | 37 | 5.00E-23 | Idiomarina loihlensis L2TR | Predicted metal-dependent amidohydrolase with the TIM-barrel fold [Idiomarina loihlensis L2TR] gblAAV82047.1 Predicted metal-dependent amidohydrolase with the TIM-barrel fold [Idiomarina loihlensis L2TR] | | | |
| 23847, 23848 | 29346648 | 67 | 1.00E-114 | Bacteroides thetaiotaomicron VPI-5482 | putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetaiotaomicron VPI-5482] gblAAO76345.1 putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetaiotaomicron VPI-5482] | Streptococcus mutans UA159 section 65 of 185 of the complete genome | 85 7.00E-07 | |
| 23849, 23850 | 48853628 | 51 | 6.00E-15 | Cytophaga hutchinsonii | COG0006: Xaa-Pro aminopeptidase [Cytophaga hutchinsonii] | | | |
| 2385, 2386 | 16125286 | 51 | 2.00E-87 | Caulobacter crescentus CB15 Microbulbifer | GTP-binding protein LepA [Caulobacter crescentus CB15] gblAAK23018.1 GTP-binding protein LepA [Caulobacter crescentus CB15] pir F87377 GTP- binding protein LepA [imported] - Caulobacter crescentus | | | 3.6.1.48 |
| 23851, 23852 | 48863907 | 41 | 9.00E-28 | degradans 2-40 | COG5651: PPE-repeat proteins [Microbulbifer degradans 2-40] | | | |
| 23853, 23854 | 57236797 | 54 | 5.00E-96 | Flavobacterium johnsoniae | SprA [Flavobacterium johnsoniae] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----|---------------|
| 23855, 23856 | 27363755 | 75 | 8.00E-46 | Vibrio vulnificus CMCP6 | hypothetical protein VV10277 [Vibrio vulnificus CMCP6] gb AAO08810.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] | | | | |
| 23857, 23858 | 9654540 | 47 | 3.00E-32 | Vibrio cholerae O1 biovar eltor str. N16961 | DPS family protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229797.1 DPS family protein [Vibrio cholerae O1 biovar eltor str. N16961] pir B82359 DPS family protein VC0139 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 23859, 23860 | 32140459 | 62 | 3.00E-37 | Polaribacter filamentus | tryptophan 2,3-dioxygenase [Polaribacter filamentus] | | | | |
| 23861, 23862 | 53715627 | 38 | 2.00E-24 | Bacteroides fragilis YCH46 | putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46] dbj BAD51085.1 putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46] | | | 84 | 1.00E-09 |
| 23863, 23864 | 53711798 | 53 | 2.00E-68 | Bacteroides fragilis YCH46 | riboflavin biosynthesis protein RibD [Bacteroides fragilis YCH46] dbj BAD47256.1 riboflavin biosynthesis protein RibD [Bacteroides fragilis YCH46] | | | | 1.1.1.19 3 |
| 23865, 23866 | 48855258 | 29 | 3.00E-20 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | | |
| 23867, 23868 | 53714264 | 45 | 3.00E-71 | Bacteroides fragilis YCH46 | folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46] | | | | 6.3.2.17 |
| 23869, 23870 | 45657718 | 48 | 2.00E-26 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | d-alanine-d-alanine ligase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70441.1 d-alanine-d-alanine ligase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | 6.3.2.4 |
| 2387, 2388 | 53714487 | 56 | 3.00E-44 | Bacteroides fragilis YCH46 | SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD49945.1 SsrA-binding protein [Bacteroides fragilis YCH46] | | | | |
| 23871, 23872 | 48856909 | 60 | 8.00E-44 | Cytophaga hutchinsonii | COG4276: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 23873, 23874 | 48854192 | 28 | 3.00E-12 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | | |
| 23875, 23876 | 34396999 | 56 | 3.00E-38 | Porphyromonas gingivalis W83 | response regulator [Porphyromonas gingivalis W83] ref NP_905164.1 response regulator [Porphyromonas gingivalis W83] | | | | |
| 23877, 23878 | 21674076 | 59 | 2.00E-69 | Chlorobium tepidum TLS | hydrolase, alpha/beta hydrolase fold family [Chlorobium tepidum TLS] gb AAM72483.1 hydrolase, alpha/beta hydrolase fold family [Chlorobium tepidum TLS] | | | | 3.1.1.1 |

| | | | | | | | | | |
|--------|----------|----|-----------|---|---|--|--|--|----------|
| 23883, | 53715650 | 26 | 6.00E-13 | Bacteroides fragilis YCH46 | putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD51108.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] | | | | |
| 23884, | | | | Cytophaga | | | | | |
| 23885, | 48854506 | 41 | 2.00E-18 | hutchinsonii | hypothetical protein Chut0202705 [Cytophaga hutchinsonii] | | | | |
| 23886 | | | | | biotin-acetyl-CoA-carboxylase ligase [Porphyromonas gingivalis W83] ref NP_905731.1 biotin-acetyl-CoA-carboxylase ligase [Porphyromonas gingivalis W83] | | | | 6.3.4.15 |
| 23887, | 34397568 | 37 | 7.00E-33 | Porphyromonas gingivalis W83 | COG0188: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit [Cytophaga hutchinsonii] | | | | 5.99.1.3 |
| 23888 | 48853785 | 58 | 1.00E-105 | Cytophaga hutchinsonii | hypothetical protein RPA2762 [Rhodopseudomonas palustris CGA009] | | | | |
| 23891, | | | | Rhodopseudomonas palustris CGA009 | emb CAE28204.1 conserved hypothetical protein [Rhodopseudomonas palustris CGA009] | | | | |
| 23892 | 39935829 | 32 | 8.00E-07 | s palustris CGA009 | 3-dehydroquininate synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79080.1 3-dehydroquininate synthase [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.2.3.4 |
| 23899, | | | | Bacteroides thetaiotaomicron | COG0030: Dimethyladenosine transferase (RNA methylation) [Cytophaga hutchinsonii] | | | | 2.1.1.- |
| 23900 | 29349383 | 43 | 4.00E-28 | VPI-5482 | DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] dbj BAD50897.1 DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] | | | | 2.7.7.6 |
| 239, | 48853962 | 58 | 8.00E-75 | Cytophaga hutchinsonii | COG1482: Phosphomannose isomerase [Cytophaga hutchinsonii] | | | | 5.3.1.8 |
| 23903, | 53715439 | 69 | 5.00E-80 | Bacteroides fragilis YCH46 | COG0179: 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) [Cytophaga hutchinsonii] | | | | 3.7.1.5 |
| 23904 | 48855901 | 51 | 9.00E-60 | Cytophaga hutchinsonii | serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] | | | | |
| 23905, | 48856479 | 54 | 5.00E-44 | hutchinsonii | DNA polymerase IV (family X) [Thermoanaerobacter tengcongensis MB4] gb AAM25645.1 DNA polymerase IV (family X) [Thermoanaerobacter tengcongensis MB4] | | | | 2.7.7.7 |
| 23907, | | | | Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130 | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_900602.1 hypothetical protein CV0932 [Chromobacterium violaceum ATCC 12472] | | | | |
| 23908 | 45658172 | 33 | 2.00E-34 | Thermoanaerobacter tengcongensis | putative sugar hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79068.1 putative sugar hydrolase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 23909, | 20808870 | 35 | 5.00E-22 | Chromobacterium violaceum ATCC 12472 | | | | | |
| 23910 | 34102240 | 44 | 1.00E-20 | Bacteroides thetaiotaomicron | | | | | |
| 23911, | | | | Bacteroides thetaiotaomicron VPI-5482 | | | | | |
| 23912 | 29349371 | 52 | 3.00E-74 | VPI-5482 | | | | | |
| 23913, | | | | | | | | | |
| 23914 | | | | | | | | | |
| 23915, | | | | | | | | | |
| 23916 | | | | | | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|---|--|--|--|----------|
| 23917, | 37222111 | 75 | 5.00E-90 | uncultured bacterium | Uvs062 [uncultured bacterium] | | | | |
| 23918 | 32475352 | 29 | 6.00E-20 | Rhodopirellula baltica SH 1 | hypothetical protein RB8406 [Rhodopirellula baltica SH 1] emb CAD78624.1 | | | | |
| 23919, | | | | | hypothetical protein [Pirellula sp.] | | | | |
| 23920 | 29349252 | 49 | 6.00E-72 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.6.1.- |
| 23921, | 53713725 | 62 | 1.00E-79 | Bacteroides fragilis YCH46 | prolyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD49183.1 prolyl-tRNA synthetase [Bacteroides fragilis YCH46] | | | | 6.1.1.15 |
| 23923, | 53796261 | 72 | 4.00E-39 | Chloroflexus aurantiacus | COG4898: Uncharacterized protein conserved in bacteria [Chloroflexus aurantiacus] | | | | |
| 23924 | | | | | | | | | |
| 23925, | | | | | | | | | 3.1.31.1 |
| 23926 | | | | | | | | | |
| 23927, | | | | | | | | | |
| 23928 | | | | | | | | | |
| 2393, | 48856599 | 44 | 6.00E-33 | Cytophaga hutchinsonii | COG0848: Biopolymer transport protein [Cytophaga hutchinsonii] | | | | |
| 2394 | | | | | | | | | |
| 23931, | 48893454 | 58 | 1.00E-26 | Trichodesmium erythraeum IMS101 | COG1012: NAD-dependent aldehyde dehydrogenases [Trichodesmium erythraeum IMS101] | | | | 1.2.1.16 |
| 23932 | | | | | | | | | |
| 23933, | | | | | | | | | |
| 23934 | 46142168 | 48 | 6.00E-63 | Methanococcoides burtonii DSM 6242 | COG1012: NAD-dependent aldehyde dehydrogenases [Methanococcoides burtonii DSM 6242] | | | | 1.2.1.16 |
| 23939, | | | | | | | | | |
| 23940 | 31194225 | 51 | 8.00E-41 | Anopheles gambiae | ENSANGP00000000349 [Anopheles gambiae] | | | | 1.5.1.3 |
| 23947, | | | | | | | | | |
| 23948 | 29347921 | 51 | 1.00E-31 | Bacteroides thetaiotaomicron VPI-5482 | putative transcription regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 2395, | | | | | | | | | |
| 2396 | 48833666 | 29 | 4.00E-19 | Magnetococcus sp. MC-1 | COG0702: Predicted nucleoside-diphosphate-sugar epimerases [Magnetococcus sp. MC-1] | | | | 5.1.3.13 |
| 23951, | | | | | | | | | |
| 23952 | 48856392 | 40 | 3.00E-25 | Cytophaga hutchinsonii | COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii] | | | | |
| 23953, | | | | | | | | | |
| 23954 | 24371625 | 50 | 9.00E-38 | Shewanella oneidensis MR-1 | hypothetical flavodoxin [Shewanella oneidensis MR-1] gb AA53112.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | | 1.3.3.4 |
| 23955, | | | | | | | | | |
| 23956 | 17229665 | 48 | 5.00E-19 | Nostoc sp. PCC 7120 | hypothetical protein air2173 [Nostoc sp. PCC 7120] pir AG2077 hypothetical protein air2173 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73872.1 | | | | |
| 23957, | | | | | | | | | |
| 23958 | 48854368 | 60 | 3.00E-52 | Cytophaga hutchinsonii | COG1137: ABC-type (unclassified) transport system, ATPase component [Cytophaga hutchinsonii] | | | | 1.8.-.- |

| | | | | | | | | | | |
|-----------------|----------|----|----------|--|--|--|--|--|--|---------------|
| 23959, 23960 | 28897146 | 37 | 3.00E-38 | Vibrio parahaemolyticus RIMD 2210633 | putative hemolysin [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58635.1 putative hemolysin [Vibrio parahaemolyticus] conserved domain protein [Porphyromonas gingivalis W83] ref NP_906133.1 hypothetical protein PG2071 [Porphyromonas gingivalis W83] | | | | | 2.3.1.51 |
| 23961, 23962 | 34397972 | 35 | 5.00E-36 | Porphyromonas gingivalis W83 | exodeoxyribonuclease III [Porphyromonas gingivalis W83] ref NP_904590.1 exodeoxyribonuclease III [Porphyromonas gingivalis W83] COG4753: Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain [Cytophaga hutchinsonii] | | | | | 3.1.11.2 |
| 23963, 23964 | 34396422 | 57 | 1.00E-87 | Porphyromonas gingivalis W83 | hypothetical protein LIC13303 [Leptospira interrogans serovar Copenhagen] str. Flocruz L1-130] gb AA571845.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] glutamine amidotransferase, class II/dipeptidase [Porphyromonas gingivalis W83] ref NP_905813.1 glutamine amidotransferase, class II/dipeptidase [Porphyromonas gingivalis W83] | | | | | 3.4.13.1 9 |
| 23965, 23966 | 48856986 | 36 | 3.00E-14 | Cytophaga hutchinsonii | Eps6E [Streptococcus thermophilus] unknown [uncultured bacterium] COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | | | 2.7.8.6 |
| 23967, 23968 | 45659122 | 31 | 3.00E-07 | Leptospira interrogans serovar Copenhagen str. Flocruz L1-130 | conserved hypothetical protein-putative integral membrane protein [Rhodopirellula baltica SH 1] emb CAD77840.1 conserved hypothetical protein-putative integral membrane protein [Pirellula sp.] | | | | | |
| 23969, 23970 | 34397650 | 35 | 1.00E-48 | Porphyromonas gingivalis W83 | COG0438: Glycosyltransferase [Pseudomonas fluorescens PfO-1] | | | | | |
| 2397, 2398 | 24637443 | 32 | 3.00E-15 | Streptococcus thermophilus uncultured | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase, putative [Coxiella burnetii RSA 493] gb AAO89605.1 (3R)-hydroxymyristoyl-(acyl-carrier- protein) dehydratase, putative [Coxiella burnetii RSA 493] | | | | | 4.2.1.- |
| 23975, 23976 | 29611405 | 26 | 7.00E-08 | bacterium | COG0627: Predicted esterase [Microbulifer degradans 2-40] | | | | | |
| 23977, 23978 | 48857000 | 37 | 3.00E-15 | Cytophaga hutchinsonii | putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD49534.1 putative glycosyltransferase [Bacteroides fragilis YCH46] | | | | | 2.4.1.- |
| 23981, 23982 | 32477769 | 56 | 4.00E-69 | Rhodopirellula baltica SH 1 | | | | | | |
| 23983, 23984 | 48731496 | 42 | 2.00E-50 | Pseudomonas fluorescens PfO-1 | | | | | | |
| 23985, 23986 | 48856125 | 46 | 7.00E-35 | Cytophaga hutchinsonii | | | | | | |
| 23987, 23988 | 29653399 | 35 | 8.00E-23 | Coxiella burnetii RSA 493 | | | | | | |
| 23989, 23990 | 48863772 | 31 | 7.00E-30 | Microbulifer degradans 2-40 | | | | | | |
| 2399, 2400 | 53714076 | 27 | 1.00E-14 | Bacteroides fragilis YCH46 | | | | | | |

| | | | | | | | | |
|--------|----------|----|----------|--------------------------------|--|--|--|----------|
| 23993, | 53711313 | 52 | 4.00E-63 | Bacteroides fragilis YCH46 | L-aspartate oxidase [Bacteroides fragilis YCH46] dbj BAD46771.1 L-aspartate oxidase [Bacteroides fragilis YCH46] | | | 1.4.3.16 |
| 23994 | | | | | | | | |
| 23995, | 48863242 | 33 | 1.00E-24 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02001316 [Microbulbifer degradans 2-40] | | | 2.4.1.- |
| 23996 | | | | | | | | |
| 23999, | | | | Vibrio vulnificus | putative hemolysin [Vibrio vulnificus YJ016] dbj BAC93559.1 putative hemolysin [Vibrio vulnificus YJ016] | | | |
| 24000 | 37678979 | 33 | 3.00E-34 | YJ016 | | | | |
| | | | | Vibrio | | | | |
| 24001, | | | | parahaemolyticus | putative hemolysin [Vibrio parahaemolyticus RIMD 2210633] | | | |
| 24002 | 28897146 | 38 | 1.00E-21 | RIMD 2210633 | dbj BAC58635.1 putative hemolysin [Vibrio parahaemolyticus] | | | |
| 24007, | | | | Shewanella | hypothetical spermidine synthase [Shewanella oneidensis MR-1] | | | |
| 24008 | 24372547 | 29 | 1.00E-08 | oneidensis MR-1 | gb AAN54034.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | 2.5.1.16 |
| | | | | Geobacter | | | | |
| 2401, | | | | metallireducens GS | | | | |
| 2402 | 48847339 | 34 | 2.00E-12 | 15 | COG0438: Glycosyltransferase [Geobacter metallireducens GS-15] | | | 2.4.1.- |
| | | | | | | | | |
| 24011, | | | | Bacteroides fragilis YCH46 | tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | |
| 24012 | 53713347 | 27 | 2.00E-22 | YCH46 | dbj BAD48805.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | |
| | | | | Bacteroides | | | | |
| 24013, | | | | thetataomicron | hypothetical protein BT4619 [Bacteroides thetataomicron VPI-5482] | | | |
| 24014 | 29350027 | 42 | 3.00E-21 | VPI-5482 | gb AAO79724.1 hypothetical protein [Bacteroides thetataomicron VPI-5482] | | | |
| 24015, | | | | Cytophaga | | | | |
| 24016 | 48856513 | 55 | 1.00E-26 | hutchinsonii | COG0307: Riboflavin synthase alpha chain [Cytophaga hutchinsonii] | | | 2.5.1.9 |
| 24017, | | | | Bacillus clausii | glycosyltransferase [Bacillus clausii KSM-K16] dbj BAD65698.1 | | | |
| 24018 | 56964929 | 52 | 9.00E-11 | KSM-K16 | glycosyltransferase [Bacillus clausii KSM-K16] | | | |
| | | | | Porphyromonas gingivalis W83 | hypothetical protein PG1492 [Porphyromonas gingivalis W83] | | | |
| 24019, | | | | | ref NP_905638.1 hypothetical protein PG1492 [Porphyromonas gingivalis W83] | | | |
| 24020 | 34397475 | 31 | 3.00E-08 | gingivalis W83 | | | | |
| 24021, | | | | Anopheles | | | | |
| 24022 | 31194161 | 54 | 3.00E-43 | gambiae | ENSANGP00000000334 [Anopheles gambiae] | | | |
| 24025, | | | | Cytophaga | COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii] | | | 2.4.2.14 |
| 24026 | 48854452 | 51 | 5.00E-93 | hutchinsonii | | | | |
| | | | | Treponema denticola ATCC 35405 | aminotransferase, DegT/DnrJ/EryC1 family [Treponema denticola ATCC 35405] gb AAS11943.1 aminotransferase, DegT/DnrJ/EryC1 family [Treponema denticola ATCC 35405] | | | |
| 24027, | | | | | | | | |
| 24028 | 42526934 | 53 | 3.00E-44 | 35405 | Trk system K+ uptake protein TrkA [Bacteroides fragilis YCH46] | | | |
| | | | | Bacteroides fragilis YCH46 | dbj BAD47623.1 Trk system K+ uptake protein TrkA [Bacteroides fragilis YCH46] | | | |
| 24029, | | | | | | | | |
| 24030 | 53712165 | 38 | 2.00E-41 | YCH46 | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|---|----|----------|----------|
| 2403, 2404 | 29349121 | 41 | 3.00E-49 | Bacteroides thetaiotaomicron VPI-5482 | D-alanine-D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78818.1 D-alanine-D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine-D-alanine ligase (D- alanylalanine synthetase) (D-Ala-D-Ala ligase) | | | | 6.3.2.4 |
| 24033, 24034 | 48854117 | 51 | 1.00E-32 | Cytophaga hutchinsonii | COG1846: Transcriptional regulators [Cytophaga hutchinsonii] | | | | |
| 24035, 24036 | 52548776 | 44 | 4.00E-70 | uncultured archaeon GZfos18F2 | asparagine synthetase protein [uncultured archaeon GZfos18F2] chloramphenicol acetyltransferase (CAT-III) [Bacteroides fragilis YCH46] dbj BAD49154.1 chloramphenicol acetyltransferase (CAT-III) [Bacteroides fragilis YCH46] | | | | 6.3.5.4 |
| 24037, 24038 | 53713696 | 41 | 3.00E-34 | Bacteroides fragilis YCH46 | hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232756.1 hypothetical protein VCA0361 [Vibrio cholerae O1 biovar eltor str. N16961] pir [H82467 hypothetical protein VCA0361 [imported] - Vibrio cholerae (strain N16961 serogroup O1)] | | | | 2.3.1.28 |
| 24039, 24040 | 9657761 | 32 | 3.00E-17 | Vibrio cholerae O1 biovar eltor str. N16961 | repAC1 [Buchnera aphidicola] | | | | |
| 24043, 24044 | 4160158 | 25 | 2.00E-07 | Buchnera aphidicola | | Desc:Listeria monocytogenes 4b contig DNA sequence #786. Org:Listeria monocytogenes 4b | 87 | 3.00E-12 | |
| 24045, 24046 | 48854713 | 54 | 2.00E-85 | Cytophaga hutchinsonii | COG0542: ATPases with chaperone activity, ATP-binding subunit [Cytophaga hutchinsonii] hypothetical protein PBPRB1077 [Photobacterium profundum SS9] emb CAG22949.1 conserved hypothetical protein [Photobacterium profundum] | | | | |
| 24047, 24048 | 54302756 | 39 | 2.00E-13 | Photobacterium profundum SS9 | D-alanine-D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78818.1 D-alanine-D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine-D-alanine ligase (D- alanylalanine synthetase) (D-Ala-D-Ala ligase) | | | | 6.3.2.4 |
| 2405, 24056 | 48856669 | 47 | 8.00E-54 | Cytophaga hutchinsonii | COG5587: Uncharacterized conserved protein [Cytophaga hutchinsonii] ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI- 5482] gb AAO77281.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | | |
| 24057, 24058 | 29347584 | 32 | 7.00E-25 | Bacteroides thetaiotaomicron VPI-5482 | | | | | |
| 24059, 24060 | 48856477 | 33 | 3.00E-12 | Cytophaga hutchinsonii | | | | | |
| 24061, 24062 | 48856922 | 45 | 5.00E-24 | Cytophaga hutchinsonii | COG0841: Cation/multidrug efflux pump [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|--|--|----------|
| 24063, 24064 | 17229898 | 33 | 1.00E-07 | Nostoc sp. PCC 7120 | hypothetical protein alr2407 [Nostoc sp. PCC 7120] pir AH2106 hypothetical protein alr2407 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB74106.1 alr2407 [Nostoc sp. PCC 7120] | | | | |
| 24065, 24066 | 9658341 | 30 | 7.00E-24 | Vibrio cholerae O1 biovar eltor str. N16961 | methyl-accepting chemotaxis protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_233291.1 methyl-accepting chemotaxis protein [Vibrio cholerae O1 biovar eltor str. N16961] pir H82402 methyl-accepting chemotaxis protein VCA0906 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 24067, 24068 | 48856487 | 40 | 2.00E-43 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 24069, 24070 | 53714999 | 38 | 1.00E-09 | Bacteroides fragilis YCH46 | polyphosphate kinase [Bacteroides fragilis YCH46] dbj BAD50457.1 | | | | 2.7.4.1 |
| 24071, 24072 | 52627365 | 46 | 8.00E-40 | Prevotella intermedia | polyphosphate kinase [Bacteroides fragilis YCH46] | | | | 2.4.2.3 |
| 24073, 24074 | 34396629 | 31 | 6.00E-31 | Porphyrromonas gingivalis W83 | phosphorylase family protein [Prevotella intermedia] | | | | |
| 24075, 24076 | 29347634 | 30 | 4.00E-23 | Bacteroides thetaiotaomicron VPI-5482 | conserved hypothetical protein [Porphyrromonas gingivalis W83] ref NP_904796.1 hypothetical protein PG0501 [Porphyrromonas gingivalis W83] | | | | |
| 24083, 24084 | 48855830 | 52 | 3.00E-36 | Cytophaga hutchinsonii | hypothetical protein BT2224 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77331.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 24087, 24088 | 52698755 | 34 | 7.00E-33 | Rickettsia akari str. Hartford | hypothetical protein Chut02001042 [Cytophaga hutchinsonii] | | | | |
| 24089, 24090 | 24374921 | 35 | 3.00E-48 | Shewanella oneidensis MR-1 | COG2194: Predicted membrane-associated, metal-dependent hydrolase [Rickettsia akari str. Hartford] | | | | |
| 2409, 2410 | 48854462 | 46 | 7.00E-26 | Cytophaga hutchinsonii | protease, putative [Shewanella oneidensis MR-1] gb AAN56408.1 protease, putative [Shewanella oneidensis MR-1] | | | | 3.4.21.- |
| 24091, 24092 | 4164093 | 25 | 1.00E-09 | Bacteroides fragilis | COG0796: Glutamate racemase [Cytophaga hutchinsonii] | | | | 5.1.1.3 |
| 24095, 24096 | 53711532 | 36 | 2.00E-23 | Bacteroides fragilis YCH46 | BfmC [Bacteroides fragilis] | | | | |
| 24097, 24098 | 53715046 | 48 | 1.00E-58 | Bacteroides fragilis YCH46 | RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD46990.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] | | | | |
| 24099, 24100 | 53712708 | 43 | 5.00E-71 | Bacteroides fragilis YCH46 | acetolactate synthase large subunit [Bacteroides fragilis YCH46] dbj BAD50504.1 acetolactate synthase large subunit [Bacteroides fragilis YCH46] | | | | 4.1.3.18 |
| 24103, 24104 | AAE3396 | 39 | 2.00E-39 | Bacteroides fragilis YCH46 | hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| | | | | | Desc:Acetobacter turbidans alpha-amino ester hydrolase mutant protein #4. | | | | |
| | | | | | Org:Acetobacter turbidans | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|--|--|--|--|----------|
| 24105, 24106 | 53691878 | 31 | 2.00E-22 | Desulfovibrio desulfuricans G20 | COG0739: Membrane proteins related to metalloendopeptidases [Desulfovibrio desulfuricans G20] | | | | |
| 24109, 24110 | 15893313 | 41 | 7.00E-25 | Clostridium acetobutylicum ATCC 824 | D-3-phosphoglycerate dehydrogenase [Clostridium acetobutylicum ATCC 824] gb AAK78002.1 D-3-phosphoglycerate dehydrogenase [Clostridium acetobutylicum ATCC 824] pir G96901 D-3-phosphoglycerate dehydrogenase [imported] - Clostridium acetobutylicum | | | | 1.1.1.95 |
| 24111, 24112 | 48853533 | 48 | 1.00E-40 | Cytophaga hutchinsonii | COG2825: Outer membrane protein [Cytophaga hutchinsonii] | | | | |
| 24111, 24112 | 34397297 | 42 | 2.00E-53 | Porphyromonas gingivalis W83 | conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_905461.1 hypothetical protein PG1280 [Porphyromonas gingivalis W83] | | | | |
| 24117, 24118 | 48853461 | 37 | 1.00E-27 | Cytophaga hutchinsonii | COG3839: ABC-type sugar transport systems, ATPase components [Cytophaga hutchinsonii] | | | | |
| 24121, 24122 | 48856700 | 54 | 1.00E-40 | Cytophaga hutchinsonii | COG1541: Coenzyme F390 synthetase [Cytophaga hutchinsonii] | | | | |
| 24123, 24124 | 9654589 | 46 | 2.00E-72 | Vibrio cholerae O1 biovar eltor str. N16961 | transposase, putative [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229842.1 transposase, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir D82355 probable transposase VC0185 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 24125, 24126 | 15895127 | 45 | 2.00E-56 | Clostridium acetobutylicum ATCC 824 | Magnesium and cobalt transport protein [Clostridium acetobutylicum ATCC 824] gb AAK79816.1 Magnesium and cobalt transport protein [Clostridium acetobutylicum ATCC 824] pir E97128 magnesium and cobalt transport protein CAC1852 [imported] - Clostridium acetobutylicum | | | | |
| 24127, 24128 | 53713469 | 56 | 6.00E-40 | Bacteroides fragilis YCH46 | putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46] | | | | |
| 24129, 24130 | 29653396 | 36 | 2.00E-08 | Coxiella burnetii RSA 493 | hypothetical protein CBU0033 [Coxiella burnetii RSA 493] gb AAO69602.1 hypothetical protein CBU0033 [Coxiella burnetii RSA 493] | | | | |
| 2413, 2414 | 53766201 | 42 | 1.00E-49 | Rubrobacter xylanophilus DSM 9941 | COG2141: Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases [Rubrobacter xylanophilus DSM 9941] | | | | 1.5.99.9 |
| 24131, 24132 | 23126057 | 22 | 9.00E-07 | Nostoc punctiforme PCC 73102 | COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102] | | | | |
| 24133, 24134 | 48860822 | 59 | 2.00E-36 | Microbubifer degradans 2-40 | COG0229: Conserved domain frequently associated with peptide methionine sulfoxide reductase [Microbubifer degradans 2-40] | | | | 1.8.4.6 |
| 24135, 24136 | 24371966 | 74 | 1.00E-118 | Shewanella oneidensis MR-1 | helicase [Shewanella oneidensis MR-1] gb AAN53453.1 helicase [Shewanella oneidensis MR-1] | | | | |

| | | | | | | | | |
|--------|----------|----|----------|--|---|--|--|----------|
| 24137, | 18311295 | 64 | 7.00E-77 | Clostridium perfringens str. 13 | hypothetical protein CPE2313 [Clostridium perfringens str. 13] dbj BAB82019.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | 4.2.1.70 |
| 24138 | | | | | | | | |
| 24143, | 56965587 | 28 | 7.00E-16 | Bacillus clausii KSM-K16 | nuclease inhibitor [Bacillus clausii KSM-K16] dbj BAD66360.1 nuclease inhibitor [Bacillus clausii KSM-K16] | | | |
| 24144 | | | | uncultured archaeon | | | | |
| 24145, | 52549170 | 40 | 6.00E-43 | GZfos26B2 | two-component sensor histidine kinase [uncultured archaeon GZfos26B2] | | | 2.7.3.- |
| 24146 | | | | | | | | |
| 24149, | 48893909 | 44 | 4.00E-25 | Trichodesmium erythraeum IMS101 | COG4251: Bacteriophytochrome (light-regulated signal transduction histidine kinase) [Trichodesmium erythraeum IMS101] | | | 2.7.3.- |
| 24150 | | | | | | | | |
| 2415, | 48858507 | 30 | 2.00E-07 | Clostridium thermocellum ATCC 27405 | COG3507: Beta-xylosidase [Clostridium thermocellum ATCC 27405] | | | |
| 2416 | | | | | | | | |
| 24151, | 15643773 | 52 | 1.00E-36 | Thermotoga maritima MSB8 | glutamate dehydrogenase [Thermotoga maritima MSB8] gb AAD36092.1 glutamate dehydrogenase [Thermotoga maritima MSB8] sp P96110 DHE3_THEME Glutamate dehydrogenase (GDH) pir G72305 glutamate dehydrogenase - Thermotoga maritima (strain MSB8) | | | 1.4.1.3 |
| 24152 | | | | | | | | |
| 24155, | 48854139 | 62 | 4.00E-59 | Cytophaga hutchinsonii | COG1066: Predicted ATP-dependent serine protease [Cytophaga hutchinsonii] | | | |
| 24156 | | | | | | | | |
| 24159, | 37675978 | 55 | 5.00E-45 | Vibrio vulnificus YJ016 | bacterial lipocalin [Vibrio vulnificus YJ016] dbj BAC96344.1 bacterial lipocalin [Vibrio vulnificus YJ016] | | | |
| 24160 | | | | | | | | |
| 24161, | | | | Xanthomonas campestris pv. campestris str. | hypothetical protein XCC3550 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM42820.1 conserved hypothetical protein | | | |
| 24162 | 21232979 | 32 | 6.00E-21 | ATCC 33913 | [Xanthomonas campestris pv. campestris str. ATCC 33913] Polyphosphate kinase [Vibrio vulnificus CMCP6] gb AAO08986.1 Polyphosphate kinase [Vibrio vulnificus CMCP6] sp Q8DEW2 PPK_VIBVU Polyphosphate kinase (Polyphosphoric acid kinase) (ATP-polyphosphate phosphotransferase) | | | 2.7.4.1 |
| 24163, | 27363931 | 42 | 5.00E-35 | Vibrio vulnificus CMCP6 | putative polyphosphate kinase [Photobacterium profundum SS9] emb CAG19139.1 putative polyphosphate kinase [Photobacterium profundum] | | | 2.7.4.1 |
| 24164 | | | | | | | | |
| 24165, | 54307921 | 55 | 2.00E-38 | Photobacterium profundum SS9 | periplasmic-binding protein of ABC transporter [Nostoc sp. PCC 7120] pir AH2309 periplasmic-binding protein of ABC transporter alr4031 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75730.1 periplasmic- binding protein of ABC transporter [Nostoc sp. PCC 7120] | | | |
| 24166 | | | | | | | | |
| 24167, | 17231523 | 35 | 1.00E-33 | Nostoc sp. PCC 7120 | Alpha/beta superfamily hydrolase [Idiomarina loihiensis L2TR] gb AAV82289.1 Alpha/beta superfamily hydrolase [Idiomarina loihiensis L2TR] | | | |
| 24168 | | | | | | | | |
| 24169, | 56460557 | 48 | 4.00E-47 | Idiomarina loihiensis L2TR | | | | |
| 24170 | | | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 2417, 2418 | 39996605 | 63 | 2.00E-91 | Geobacter sulfurreducens PCA | ABC transporter, ATP-binding protein [Geobacter sulfurreducens PCA] gb AAR34879.1 ABC transporter, ATP-binding protein [Geobacter sulfurreducens PCA] | | | 1.8.-.- |
| 24171, 24172 | 21673717 | 38 | 1.00E-43 | Chlorobium tepidum TLS | phosphoglycolate phosphatase [Chlorobium tepidum TLS] gb AAM72124.1 phosphoglycolate phosphatase [Chlorobium tepidum TLS] | | | 3.1.3.18 |
| 24173, 24174 | 53715107 | 33 | 4.00E-26 | Bacteroides fragilis YCH46 | putative N-acetylmuramoyl-L-alanine amidase AmiA [Bacteroides fragilis YCH46] db BAD50565.1 putative N-acetylmuramoyl-L-alanine amidase AmiA [Bacteroides fragilis YCH46] | | | 3.5.1.28 |
| 24175, 24176 | 56962411 | 28 | 9.00E-07 | Bacillus clausii KSM-K16 | hypothetical protein ABC0637 [Bacillus clausii KSM-K16] db BAD63176.1 hypothetical protein [Bacillus clausii KSM-K16] | | | |
| 24177, 24178 | 48838149 | 30 | 5.00E-36 | Methanosarcina barkeri str. fusaro | COG2202: FOG: PAS/PAC domain [Methanosarcina barkeri str. fusaro] | | | 2.7.3.- |
| 24179, 24180 | 45659150 | 43 | 2.00E-38 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS71873.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.7.3.- |
| 24181, 24182 | 21231194 | 38 | 6.00E-10 | Xanthomonas campestris pv. campestris str. ATCC 33913 | 2-oxo-3-deoxygalactonate kinase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM41035.1 2-oxo-3-deoxygalactonate kinase [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | 2.7.1.58 |
| 24183, 24184 | 52425546 | 59 | 5.00E-71 | Mannheimia succiniciproducens MBEL55E | CarB protein [Mannheimia succiniciproducens MBEL55E] gb AAU38098.1 CarB protein [Mannheimia succiniciproducens MBEL55E] | | | |
| 24185, 24186 | 48854285 | 32 | 1.00E-19 | Cytophaga hutchinsonii | COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 24187, 24188 | 29349036 | 43 | 1.00E-45 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3628 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78733.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 24189, 24190 | 56460695 | 47 | 3.00E-26 | Idiomarina lohiensis L2TR | Glyoxalase/dioxygenase superfamily protein [Idiomarina lohiensis L2TR] gb AAV82427.1 Glyoxalase/dioxygenase superfamily protein [Idiomarina lohiensis L2TR] | | | |
| 2419, 2420 | 2511751 | 58 | 1.00E-29 | Rhodobacter capsulatus | tyrosine-phenol-lyase [Rhodobacter capsulatus] sp O30971 TNAA_RHOCA Tryptophanase (L-tryptophan indole-lyase) (TNase) pir T45297 tyrosine phenol-lyase (EC 4.1.99.2) [Imported] - Rhodobacter capsulatus | | | 4.1.99.2 |
| 24191, 24192 | 46321822 | 34 | 1.00E-10 | Burkholderia cepacia R1808 | COG1522: Transcriptional regulators [Burkholderia cepacia R1808] | | | |
| 24193, 24194 | 48854355 | 64 | 1.00E-66 | Cytophaga hutchinsonii | COG1200: RecG-like helicase [Cytophaga hutchinsonii] | | | 3.6.1.- |

| | | | | | | | | |
|-------------------------------------|----------------------|----------|-----------------------|--|---|--|----------------|---------|
| 24197, 24198, 24199, 24200 | 48855120 48856384 | 70 22 | 1.00E-109 3.00E-10 | Cytophaga hutchinsonii Cytophaga hutchinsonii | COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii] hypothetical protein Chut02000101 [Cytophaga hutchinsonii] | Flavobacterium johnsoniae LeuS (leuS) gene, partial cds; and Fjo12 (fjo12), FtsX (ftsX), Fjo13 (fjo13), BacA (bacA), and TruB (truB) genes, complete cds | 80 4.00E-17 | 6.1.1.4 |
| 24201, 24202 | 28855211 | 34 | 4.00E-14 | Pseudomonas syringae pv. tomato str. DC3000 | esterase/lipase/thioesterase family protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794577.1 esterase/lipase/thioesterase family protein [Pseudomonas syringae pv. tomato str. DC3000] | | | |
| 24203, 24204 | 56480140 | 34 | 2.00E-07 | Shigella flexneri 2a str. 301 | hypothetical protein SF2623 [Shigella flexneri 2a str. 301] gb AA44120.2 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] ref NP_838134.1 hypothetical protein S2796 [Shigella flexneri 2a str. 24577] gb AAP17944.1 hypothetical protein S2796 [Shigella flexneri 2a str. 24577] | | | |
| 24208, 24210 | 29346727 | 53 | 2.00E-35 | Bacteroides thetaiotaomicron VPI-5482 | riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76424.1 riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] | | | 2.5.1.9 |
| 2421, 2422 | 4049885 | 33 | 3.00E-26 | Melanoplus sanguinipes entomopoxvirus | ORF MSV027 tryptophan repeat gene family protein [Melanoplus sanguinipes entomopoxvirus] pir T28188 hypothetical protein ORF29 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon) ref NP_048098.1 ORF MSV027 tryptophan repeat gene family protein [Melanoplus sanguinipes entomopoxvirus] | | | |
| 24211, 24212 | 23501247 | 28 | 4.00E-08 | Brucella suis 1330 | DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M) | | | |
| 24213, 24214 | 53712193 | 23 | 1.00E-20 | Bacteroides fragilis YCH46 | hypothetical protein BF0900 [Bacteroides fragilis YCH46] db BAD47651.1 hypothetical protein [Bacteroides fragilis YCH46] | | | 2.7.3.- |
| 24215, 24216 | 48856044 | 50 | 7.00E-74 | Cytophaga hutchinsonii | COG2908: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | 3.6.1.- |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|--|---------|--|--|----------|
| 24217, 24218 | 29348158 | 53 | 5.00E-49 | Bacteroides thetaiotaomicron VPI-5482 | putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77855.1 putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 24219, 24220 | 29348158 | 28 | 4.00E-20 | Bacteroides thetaiotaomicron VPI-5482 | putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77855.1 putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 24221, 24222 | 34397011 | 29 | 8.00E-25 | Porphyromonas gingivalis W83 | ABC transporter, permease protein, putative [Porphyromonas gingivalis W83] ref NP_905176.1 ABC transporter, permease protein, putative [Porphyromonas gingivalis W83] | | | | |
| 24225, 24226 | 48856113 | 36 | 2.00E-30 | Cytophaga hutchinsonii | COG0212: 5-formyltetrahydrofolate cyclo-ligase [Cytophaga hutchinsonii] probable transmembrane protein [Chromobacterium violaceum ATCC 12472] ref NP_903091.1 probable transmembrane protein [Chromobacterium violaceum ATCC 12472] | 6.3.3.2 | | | |
| 24227, 24228 | 34332880 | 56 | 1.00E-29 | Chromobacterium violaceum ATCC 12472 | COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii] | | | | |
| 24229, 24230 | 48853602 | 49 | 5.00E-53 | Cytophaga hutchinsonii | hypothetical protein Chut02002705 [Cytophaga hutchinsonii] putative transposase [Yersinia pestis] ref YP_071802.1 putative transposase [Yersinia pseudotuberculosis IP 32953] ref YP_070613.1 putative transposase [Yersinia pseudotuberculosis IP 32953] ref YP_069318.1 putative transposase-like protein [Yersinia pseudotuberculosis IP 32953] ref YP_069245.1 putative transposase [Yersinia pseudotuberculosis IP 32953] ref YP_068733.1 putative transposase for IS285 insertion element [Yersinia pseudotuberculosis IP 32953] ref NP_994772.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievallis str. 91001] ref NP_994258.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievallis str. 91001] ref NP_994158.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievallis str. 91001] ref NP_994064.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievallis str. 91001] ref NP_993887.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievallis str. 91001] ref NP_993762.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievallis str. 91001] ref NP | 3.6.1.- | | | |
| 24231, 24232 | 52788138 | 66 | 1.00E-123 | Yersinia pestis | COG4679: Phage-related protein [Cytophaga hutchinsonii] O6-methylguanine-DNA methyltransferase [Bacillus cereus G9241] gb EAL14768.1 O6-methylguanine-DNA methyltransferase [Bacillus cereus G9241] | | | | 2.1.1.63 |
| 24233, 24234 | 48856841 | 38 | 1.00E-07 | Cytophaga hutchinsonii | | | | | |
| 24235, 24236 | 47566806 | 51 | 1.00E-41 | Bacillus cereus G9241 | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|--|--|--|----------|
| 24237, 24238 | 53711669 | 29 | 2.00E-13 | Bacteroides fragilis YCH46 | putative TonB-dependent receptor [Bacteroides fragilis YCH46] dbj BAD47127.1 putative TonB-dependent receptor [Bacteroides fragilis YCH46] | | | |
| 24239, 24240 | 55377565 | 27 | 4.00E-15 | Haloarcula marismortui ATCC 43049 | universal stress protein [Haloarcula marismortui ATCC 43049] gb AAV45709.1 universal stress protein [Haloarcula marismortui ATCC 43049] | | | |
| 24241, 24242 | 34398043 | 29 | 2.00E-18 | Porphyromonas gingivalis W83 | LysM domain protein [Porphyromonas gingivalis W83] ref NP_906204.1 LysM domain protein [Porphyromonas gingivalis W83] | | | 3.2.1.- |
| 24245, 24246 | 48856971 | 61 | 7.00E-66 | Cytophaga hutchinsonii | COG0138: AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Afcu) [Cytophaga hutchinsonii] hypothetical protein TTHA1017 [Thermus thermophilus HB8] dbj BAD70840.1 conserved hypothetical protein [Thermus thermophilus HB8] | | | 2.1.2.3 |
| 24247, 24248 | 55980986 | 23 | 8.00E-11 | Thermus thermophilus HB8 | | | | |
| 24249, 24250 | 31195967 | 79 | 3.00E-41 | Anopheles gambiae | ENSANGP00000016322 [Anopheles gambiae] | | | 1.6.4.5 |
| 2425, 2426 | 48856035 | 40 | 2.00E-20 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | 2.-.-.- |
| 24251, 24252 | 51246763 | 36 | 1.00E-41 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb CAC37640.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 24253, 24254 | 56965073 | 55 | 1.00E-31 | Bacillus clausii KSM-K16 | hydrolase, HAD superfamily [Bacillus clausii KSM-K16] dbj BAD65844.1 hydrolase, HAD superfamily [Bacillus clausii KSM-K16] | | | |
| 24255, 24256 | 53712488 | 56 | 5.00E-55 | Bacteroides fragilis YCH46 | peptidyl-L-tyrosine hydrolase [Bacteroides fragilis YCH46] dbj BAD47946.1 peptidyl-L-tyrosine hydrolase [Bacteroides fragilis YCH46] | | | 3.1.1.29 |
| 24257, 24258 | 48856955 | 53 | 7.00E-68 | Cytophaga hutchinsonii | COG0134: Indole-3-glycerol phosphate synthase [Cytophaga hutchinsonii] | | | 4.1.1.48 |
| 24259, 24260 | 48854173 | 24 | 5.00E-08 | Cytophaga hutchinsonii | hypothetical protein Chut02002840 [Cytophaga hutchinsonii] | | | |
| 24261, 24262 | 48853326 | 47 | 5.00E-46 | Cytophaga hutchinsonii | COG1485: Predicted ATPase [Cytophaga hutchinsonii] | | | |
| 24263, 24264 | 27367774 | 61 | 1.00E-100 | Vibrio vulnificus CMCP6 | Phosphoglycerol transferase [Vibrio vulnificus CMCP6] gb AAO08291.1 Phosphoglycerol transferase [Vibrio vulnificus CMCP6] | | | 2.7.8.20 |
| 24267, 24268 | 32476849 | 42 | 4.00E-20 | Rhodopirella baltica SH 1 | hypothetical protein RB11207 [Rhodopirella baltica SH 1] emb CAD78986.1 conserved hypothetical protein [Pirella sp.] | | | |
| 2427, 2428 | 48856079 | 51 | 7.00E-67 | Cytophaga hutchinsonii | COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | 1.8.-.- |
| 24271, 24272 | 53712075 | 25 | 7.00E-18 | Bacteroides fragilis YCH46 | hypothetical protein BF0782 [Bacteroides fragilis YCH46] dbj BAD47533.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |

| | | | | | | |
|-----------------|----------|----|-----------|---|---|---------------------|
| 24273, 24274 | 17936192 | 31 | 3.00E-33 | Agrobacterium tumefaciens str. C58 | xanthine dehydrogenase [Agrobacterium tumefaciens str. C58] gb AAL43298.1 xanthine dehydrogenase [Agrobacterium tumefaciens str. C58] gb AAK88052.1 AGR_C_4202p [Agrobacterium tumefaciens str. C58] pir AD2860 xanthine dehydrogenase xdhA [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir C97637 xanthine dehydrogenase (PA1524) [imported] - Agrobacterium tumefaciens (strain C58, Cereon) ref NP_355267.1 hypothetical protein AGR_C_4202 [Agrobacterium tumefaciens str. C58] | 1.1.1.20 4 |
| 24275, 24276 | 53713423 | 29 | 1.00E-12 | Bacteroides fragilis YCH46 | hypothetical protein BF2134 [Bacteroides fragilis YCH46] dbj BAD48881.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | |
| 24277, 24278 | 29347250 | 67 | 2.00E-68 | Bacteroides thetaiotaomicron VPI-5482 | histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76947.1 histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI- 5482] sp Q8A6N7 SYH_BACTN Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS) | 6.1.1.21 |
| 24279, 24280 | 48855464 | 40 | 2.00E-28 | Cytophaga hutchinsonii | COG1999: Uncharacterized protein SCO1/SenC/PrC, involved in biogenesis of respiratory and photosynthetic systems [Cytophaga hutchinsonii] | |
| 24281, 24282 | 48859534 | 69 | 1.00E-100 | Clostridium thermocellum ATCC 27405 | COG0804: Urea amidohydrolase (urease) alpha subunit [Clostridium thermocellum ATCC 27405] | 89 1.00E-17 3.5.1.5 |
| 24283, 24284 | 52841315 | 57 | 7.00E-88 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27167.1 reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | 2.7.7.49 |
| 24285, 24286 | 17230079 | 21 | 9.00E-15 | Nostoc sp. PCC 7120 | transcriptional regulator [Nostoc sp. PCC 7120] dbj BAB74286.1 transcriptional regulator [Nostoc sp. PCC 7120] pir AD2129 transcription regulator alr2587 [imported] - Nostoc sp. (strain PCC 7120) | |
| 24287, 24288 | 15893983 | 44 | 2.00E-67 | Clostridium acetobutylicum ATCC 824 | Altronate oxidoreductase [Clostridium acetobutylicum ATCC 824] gb AAK78672.1 Altronate oxidoreductase [Clostridium acetobutylicum ATCC 824] pir E96985 altronate oxidoreductase CAC0695 [imported] - Clostridium acetobutylicum sp Q97L67 UXAB_CLOAB Altronate oxidoreductase (Tagaturonate reductase) (Tagaturonate dehydrogenase) | 1.1.1.58 |
| 24289, 24290 | 48855692 | 68 | 1.00E-117 | Cytophaga hutchinsonii | COG1080: Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes [Cytophaga hutchinsonii] | 2.8.1.6 |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|----|----------|---------|
| 2429, 2430 | 18310267 | 26 | 2.00E-14 | Clostridium perfringens str. 13 | hypothetical protein CPE1285 [Clostridium perfringens str. 13] dbj BAB80991.1 hypothetical protein [Clostridium perfringens str. 13] | | | | |
| 24291, 24292 | 48855692 | 61 | 4.00E-85 | Cytophaga hutchinsonii | COG1060: Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes [Cytophaga hutchinsonii] | | | | 2.8.1.6 |
| 24293, 24294 | 48854815 | 44 | 2.00E-57 | Cytophaga hutchinsonii | COG0719: ABC-type transport system involved in Fe-S cluster assembly, permease component [Cytophaga hutchinsonii] | | | | |
| 24295, 24296 | 48855375 | 42 | 1.00E-18 | Cytophaga hutchinsonii | COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 24301, 24302 | 48853518 | 39 | 6.00E-37 | Cytophaga hutchinsonii | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | | | | |
| 24305, 24306 | 47526988 | 25 | 5.00E-16 | Bacillus anthracis str. 'Ames Ancestor' | tpg/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] | | | | |
| 24307, 24308 | 48854601 | 44 | 4.00E-37 | Cytophaga hutchinsonii | COG4485: Predicted membrane protein [Cytophaga hutchinsonii] | | | | |
| 24309, 24310 | 15612709 | 61 | 5.00E-61 | Bacillus halodurans C-125 | 50S ribosomal protein L5 [Bacillus halodurans C-125] dbj BAB03865.1 50S ribosomal protein L5 [Bacillus halodurans C-125] pir T44395 ribosomal protein L5 (BL6) rplE [imported] - Bacillus halodurans (strain C-125) sp Q9Z9K2 RL5_BACHD 50S ribosomal protein L5 dbj BAA75283.1 rplE homologue (identity of 86% to B. subtilis) [Bacillus halodurans] | Spiroplasma kunkelii strain CR2- 3x partial genome sequence | 92 | 5.00E-19 | |
| 24311, 24312 | 31195605 | 70 | 1.00E-104 | Anopheles gambiae | ENSANGP00000013686 [Anopheles gambiae] hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229887.1 hypothetical protein VC0230 [Vibrio cholerae O1 biovar eltor str. N16961] pir H82348 hypothetical protein VC0230 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | Desc:Staphylococ- cus aureus DNA for cellular proliferation protein #1366. Org:Staphylococcus aureus | 85 | 1.00E-26 | |
| 24313, 24314 | 9654638 | 51 | 3.00E-40 | Vibrio cholerae O1 biovar eltor str. N16961 | | | | | |

| | | | | | | | | |
|--------|----------|----|-----------|---|--|---|-------------|----------|
| 24315, | 49484433 | 29 | 6.00E-12 | Staphylococcus aureus subsp. aureus MRSA252 | putative tRNA pseudouridine synthase [Staphylococcus aureus subsp. aureus MRSA252] emb[CAG41283.1] putative tRNA pseudouridine synthase [Staphylococcus aureus subsp. aureus MRSA252] sp Q6GEL6 TRUA_STAAR tRNA pseudouridine synthase A (Pseudouridylylase synthase I) (Pseudouridine synthase I) (Uracil hydrolyase) | | | 4.2.1.70 |
| 24319, | 31195671 | 53 | 3.00E-10 | Anopheles gambiae | ENSANGP000000000352 [Anopheles gambiae] | | | |
| 24320, | 48782075 | 30 | 4.00E-20 | Burkholderia fungorum LB400 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Burkholderia fungorum LB400] | | | 2.--- |
| 24323, | | | | Bacillus cereus ATCC 10987 | uroporphyrinogen-III synthase [Bacillus cereus ATCC 10987] | | | |
| 24324, | 42783600 | 31 | 2.00E-09 | Anopheles gambiae | ENSANGP0000000015562 [Anopheles gambiae] | | | 2.7.6.5 |
| 24325, | | | | Bdellovibrio bacteriovorus HD100 | ATP-dependent protease LA [Bdellovibrio bacteriovorus HD100] emb[CAE8111.1] ATP-dependent protease LA [Bdellovibrio bacteriovorus HD100] | Bdellovibrio bacteriovorus complete genome, strain HD100; segment 11/11 | 82 2.00E-10 | 3.4.21.5 |
| 24326, | 42525077 | 78 | 1.00E-108 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482] gb AAO76861.1 two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.3.- |
| 24331, | 29347164 | 43 | 8.00E-47 | Bacteroides fragilis YCH46 | C-terminal part of two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] dbj BAD47137.1 C-terminal part of two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] | | | |
| 24332, | | | | Magnetococcus sp. MC-1 | COG3176: Putative hemolysin [Magnetococcus sp. MC-1] | | | |
| 24333, | 53711679 | 33 | 2.00E-38 | Cytophaga hutchinsonii | COG2932: Predicted transcriptional regulator [Cytophaga hutchinsonii] | | | |
| 24334, | 48856470 | 35 | 9.00E-40 | Acinetobacter sp. ADP1 | putative ATP-dependent DNA helicase (PcrA) [Acinetobacter sp. ADP1] emb[CAG67422.1] putative ATP-dependent DNA helicase (PcrA) [Acinetobacter sp. ADP1] | | | 3.6.1.- |
| 24335, | 48833909 | 41 | 7.00E-53 | uncultured proteobacterium QS1 | conserved hypothetical protein [uncultured proteobacterium QS1] | | | |
| 24337, | | | | Anopheles gambiae | ENSANGP000000000334 [Anopheles gambiae] | | | |
| 24338, | 50083734 | 41 | 1.00E-69 | | | | | |
| 24339, | | | | | | | | |
| 24340, | | | | | | | | |
| 24347, | 50956565 | 25 | 7.00E-22 | | | | | |
| 24348, | | | | | | | | |
| 24349, | 31194161 | 66 | 2.00E-31 | | | | | |
| 24350, | | | | | | | | |

| | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|--|----|----------|
| 24351, | 53712250 | 54 | 7.00E-26 | Bacteroides fragilis YCH46 | DNA replication and repair protein RecF [Bacteroides fragilis YCH46] | | | 3.1.11.- |
| 24352 | | | | | dbj BAD47708.1 DNA replication and repair protein RecF [Bacteroides fragilis YCH46] | | | |
| 24353, | | | | Tolypothrix sp. | | | | |
| 24354 | 18642520 | 37 | 1.00E-36 | PCC 7601 | phytochrome-like protein [Tolypothrix sp. PCC 7601] | | | 2.7.3.- |
| 24357, | | | | Cytophaga hutchinsonii | COG0142: Geranylgeranyl pyrophosphate synthase [Cytophaga hutchinsonii] | | | |
| 24358 | 48855539 | 64 | 3.00E-90 | Bacteroides fragilis YCH46 | alpha-amylase [Bacteroides fragilis YCH46] | | | 2.5.1.- |
| 24359, | | | | | dbj BAD50039.1 alpha-amylase [Bacteroides fragilis YCH46] | | | |
| 24360 | 53714581 | 35 | 1.00E-08 | Bacteroides fragilis YCH46 | putative membrane peptidase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 24361, | | | | Bacteroides thetaiotaomicron VPI-5482 | gb AAO77110.1 putative membrane peptidase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 24362 | 29347413 | 32 | 2.00E-17 | Cytophaga hutchinsonii | COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii] | | | |
| 24363, | | | | | COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] | | | 2.7.7.7 |
| 24364 | 48853591 | 60 | 3.00E-27 | Cytophaga hutchinsonii | | | | |
| 24365, | | | | | COG0419: ATPase involved in DNA repair [Dechloromonas aromatica RCB] | | | |
| 24366 | 48853783 | 42 | 3.00E-40 | Cytophaga hutchinsonii | COG1556: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 24371, | | | | Dechloromonas aromatica RCB | COG0739: Membrane proteins related to metalloendopeptidases [Desulfovibrio desulfuricans G20] | | | |
| 24372 | 46140632 | 36 | 2.00E-37 | Cytophaga hutchinsonii | | | | 3.1.11.- |
| 24373, | | | | | | | | |
| 24374 | 48856043 | 28 | 3.00E-09 | Desulfovibrio desulfuricans G20 | | | | |
| 24377, | | | | | | | | |
| 24378 | 53691878 | 32 | 3.00E-24 | | | | | |
| | | | | | | Pasteurella multocida subsp. multocida str. Pm70 section 202 of 204 of the complete genome | 86 | 7.00E-13 |
| 24379, | | | | Cytophaga hutchinsonii | COG0020: Undecaprenyl pyrophosphate synthase [Cytophaga hutchinsonii] | | | 2.5.1.31 |
| 24380 | 48853531 | 54 | 2.00E-74 | Bacteroides fragilis YCH46 | DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] | | | |
| 24383, | | | | | dbj BAD51320.1 DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] | | | |
| 24384 | 53715862 | 66 | 3.00E-81 | Bacteroides fragilis YCH46 | DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482] | | | |
| | | | | | gb AAO78227.1 DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 24385, | | | | Bacteroides thetaiotaomicron VPI-5482 | sp Q8A334 MUTS_BACTN DNA mismatch repair protein mutS | | | |
| 24386 | 29348530 | 55 | 2.00E-75 | Geobacter sulfurreducens PCA | sensory box histidine kinase [Geobacter sulfurreducens PCA] | | | |
| 24387, | | | | | gb AAR36209.1 sensory box histidine kinase [Geobacter sulfurreducens PCA] | | | 2.7.3.- |
| 24388 | 39997908 | 29 | 5.00E-28 | | | | | |

| | | | | | | | | | |
|---|--|----|-----------|-------------------------------|---|---|----|----------|----------|
| 24389, 24390, 24391, 24392, 24395, 24396, 24397, 24398 | 30024199 46316555 29348695 | 27 | 1.00E-09 | Bacteriophage P2-EC53 | putative lysogenic conversion protein [Bacteriophage P2-EC53] | Vibrio vulnificus CMCP6 chromosome II section 2 of 6 of the complete sequence | 89 | 2.00E-13 | |
| 24399, 24400, 24401, 24402 | 48854339 48855592 | 65 | 1.00E-68 | Burkholderia cepacia R18194 | COG1289: Predicted membrane protein [Burkholderia cepacia R18194] | | | | |
| 24405, 24406, 24407, 24408, 24409, 24410 | 53714606 37222107 31790570 | 63 | 1.00E-109 | Bacteroides fragilis YCH46 | COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Cytophaga hutchinsonii] | Desc:Restriction enzyme AccIII gene. Org:Adinetobacter calcoaceticus | 87 | 1.00E-07 | 3.4.21.- |
| 24411, 24412 | 15606857 31195649 | 30 | 7.00E-11 | Aquifex aeolicus VF5 | excnuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD50084.1 excnuclease ABC subunit A [Bacteroides fragilis YCH46] | | | | 3.1.3.5 |
| 24413, 24414, 24415, 24416, 24417, 24418 | 34398008 48855689 52144400 | 29 | 7.00E-17 | Porphyrromonas gingivalis W83 | lysopene beta-monocyclase [marine bacterium P99-3] sulfur oxidation protein SoxB [Aquifex aeolicus VF5] gb AAC07634.1 sulfur oxidation protein SoxB [Aquifex aeolicus VF5] pir E70455 sulfur oxidation protein SoxB - Aquifex aeolicus | | | | |
| 24419, 24420, 24421, 24422 | 31195649 34398008 48855689 52144400 | 34 | 1.00E-28 | Anopheles gambiae | ENSANGP00000000282 [Anopheles gambiae] hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Porphyrromonas gingivalis W83] ref NP_906169.1 hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Porphyrromonas gingivalis W83] | | | | |
| 24423, 24424, 24425, 24426, 24427, 24428 | 34398008 48855689 52144400 | 29 | 7.00E-17 | Porphyrromonas gingivalis W83 | COG0351: Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [Cytophaga hutchinsonii] | | | | |
| 24429, 24430, 24431, 24432 | 48855689 52144400 | 40 | 2.00E-10 | Cytophaga hutchinsonii | hypothetical protein BCZK0824 [Bacillus cereus ZK] gb AAU19419.1 conserved hypothetical protein [Bacillus cereus ZK] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|--|--|--|--|---------|
| 24419, | 53797765 | 25 | 4.00E-11 | Chloroflexus aurantiacus | hypothetical protein Chio02001813 [Chloroflexus aurantiacus] | | | | |
| 24420 | | | | aurantiacus | COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii] | | | | |
| 24421, | 48854071 | 54 | 3.00E-54 | Cytophaga hutchinsonii | | | | | |
| 24422 | | | | Wolinella succinogenes DSM 1740 | hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 24423, | 34557509 | 44 | 2.00E-28 | | Translation IF2, GTPase [Clostridium acetobutylicum ATCC 824] | | | | |
| 24424 | | | | Clostridium acetobutylicum ATCC 824 | gb AAK79767.1 Translation IF2, GTPase [Clostridium acetobutylicum ATCC 824] pir D97122 translation IF2, GTPase [imported] - Clostridium acetobutylicum sp Q97151 IF2_CLOAB Translation Initiation factor IF-2 | | | | |
| 24425, | 15895078 | 64 | 6.00E-38 | | | | | | |
| 24426 | | | | Thermosynechococcus elongatus BP-1 | hypothetical protein tir1343 [Thermosynechococcus elongatus BP-1] db BAC08895.1 tir1343 [Thermosynechococcus elongatus BP-1] | | | | |
| 24431, | 22298886 | 62 | 5.00E-37 | Cytophaga hutchinsonii | COG3279: Response regulator of the LysR/AlgR family [Cytophaga hutchinsonii] | | | | |
| 24432, | 48855702 | 37 | 2.00E-34 | Cytophaga hutchinsonii | | | | | |
| 24433, | | | | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | | |
| 24434 | 48853433 | 42 | 1.00E-61 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3008 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78114.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 24437, | 29348417 | 38 | 2.00E-34 | | RNA polymerase ECF(extracytoplasmic function)-type sigma factor (sigma-Z) [Bacillus subtilis subsp. subtilis str. 168] emb CAB14625.1 RNA polymerase ECF(extracytoplasmic function)-type sigma factor (sigma-Z) [Bacillus subtilis subsp. subtilis str. 168] gb AAB80887.1 RNA polymerase sigma factor SigZ [Bacillus subtilis] pir C69707 RNA polymerase ECF-type sigma factor sigZ - Bacillus subtilis sp O05409 SIGZ_BACSU RNA polymerase sigma factor sigZ | | | | |
| 24441, | 16079737 | 32 | 3.00E-10 | Bacillus subtilis subsp. subtilis str. 168 | | | | | |
| 24442 | | | | Cytophaga hutchinsonii | COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii] | | | | 4.1.3.- |
| 24443, | 48856398 | 55 | 1.00E-44 | Bacteroides thetaiotaomicron VPI-5482 | argininosuccinate lyase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78838.1 argininosuccinate lyase [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.3.2.1 |
| 24444 | 29349141 | 59 | 2.00E-99 | | hypothetical protein LIC10662 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_713715.1 hypothetical protein LA3535 [Leptospira interrogans serovar Lai str. 56601] gb AAN50733.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS69283.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | |
| 24445, | 45656560 | 33 | 3.00E-22 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | | |
| 24446 | 48855183 | 45 | 2.00E-66 | Cytophaga hutchinsonii | | | | | |

| | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|----------|
| 24451, | 15899699 | 31 | 2.00E-22 | Sulfolobus solfataricus P2 | Diphosphomevalonate decarboxylase, putative [Sulfolobus solfataricus P2] gb AAK43094.1 Diphosphomevalonate decarboxylase, putative [Sulfolobus solfataricus P2] pir G90479 diphosphomevalonate decarboxylase, probable [Imported] - Sulfolobus solfataricus | 4.1.1.33 |
| 24452, | 10880727 | 50 | 3.00E-75 | Borrelia coriaceae | glycerophosphodiester phosphodiesterase GlpQ [Borrelia coriaceae] | 3.1.4.46 |
| 24453, | | | | Helicobacter pylori | hypothetical protein Jhp1070 [Helicobacter pylori J99] gb AAD06650.1 putative [Helicobacter pylori J99] pir D71853 hypothetical protein jhp1070 - Helicobacter pylori (strain J99) | |
| 24454, | 15612135 | 45 | 3.00E-58 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1057 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76164.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | |
| 24455, | 29346467 | 33 | 7.00E-40 | Bacillus methanolicus | putative replication initiator protein [Bacillus methanolicus] gb AAR39408.1 putative replication initiator protein [Bacillus methanolicus] | |
| 24456, | 41057059 | 28 | 4.00E-26 | Geobacillus stearothermophilus | methylase fusion protein [Geobacillus stearothermophilus] | 2.1.1.73 |
| 24457, | 34451616 | 34 | 1.00E-20 | Ornithobacterium rhinotracheale | MbpB [Ornithobacterium rhinotracheale] | |
| 24458, | 47059349 | 25 | 1.00E-07 | Psychrobacter sp. | Desc:Psychrobacter monas gingivalis protein PG83. Org:Psychrobacter monas gingivalis | |
| 24459, | AAV3442 | 32 | 3.00E-23 | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Psychrobacter sp. 273-4] | |
| 24460, | 46141287 | 46 | 9.00E-44 | Geobacter metallireducens GS-15 | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] | |
| 24461, | 48856125 | 42 | 2.00E-33 | Listeria innocua | COG0057: Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Geobacter metallireducens GS-15] | |
| 24462, | 48846053 | 33 | 8.00E-08 | Cytophaga hutchinsonii | hypothetical protein lin0833 [Listeria innocua Clip11262] emb CAC96065.1 lin0833 [Listeria innocua] pir A1536 hypothetical protein lin0833 [Imported] - Listeria innocua (strain Clip11262) | |
| 24463, | 16799907 | 47 | 8.00E-48 | Cytophaga hutchinsonii | COG1071: Pyruvate/2-oxoglutarate dehydrogenase complex, hutchinsonii | 1.2.4.1 |
| 24464, | 48856576 | 46 | 7.00E-38 | Bacteroides thetaiotaomicron VPI-5482 | mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75480.1 mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482] | 5.3.1.8 |
| 24465, | 29345783 | 49 | 1.00E-66 | Anopheles gambiae | ENSANGP00000000282 [Anopheles gambiae] | 2.7.1.37 |

| | | | | | | | | | |
|--------|----------|----|-----------|------------------------|--|---|----|----------|----------|
| 24487, | 48854985 | 60 | 9.00E-49 | Cytophaga hutchinsonii | hypothetical protein Chut02002044 [Cytophaga hutchinsonii] | | | | |
| 24488 | ABB8477 | | | | Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org: Cytophaga hutchinsonii | | | | 2.7.7.7 |
| 24490 | 1 | 51 | 1.00E-63 | | | | | | |
| 2449, | | | | Silicibacter sp. | | | | | 2.7.3.- |
| 2450 | 52011036 | 37 | 6.00E-26 | TM1040 | COG0642: Signal transduction histidine kinase [Silicibacter sp. TM1040] | | | | |
| 24491, | | | | Pseudoalteromonas | | Pseudoalteromonas | | | |
| 24492 | 46193747 | 88 | 3.00E-46 | s haloplanktis | DsbA protein [Pseudoalteromonas haloplanktis] | haloplanktis dsbA operon | 99 | 0 | |
| 24493, | | | | Bifidobacterium | possible alpha beta hydrolase [Bifidobacterium longum NCC2705] | | | | |
| 24494 | 23465361 | 44 | 2.00E-18 | longum NCC2705 | gb AAN24600.1 possible alpha beta hydrolase [Bifidobacterium longum NCC2705] | | | | 3.8.1.2 |
| 24497, | | | | Methanosarcina | hypothetical protein MM1155 [Methanosarcina mazei Go1] gb AAM30851.1 conserved protein [Methanosarcina mazei Go1] | | | | |
| 24498 | 21227257 | 27 | 3.00E-08 | mazei Go1 | ARA1 [Mycoplasma gallisepticum R] ref NP_853218.1 ARA1 [Mycoplasma gallisepticum R] | | | | 1.1.1.- |
| 24499, | | | | Mycoplasma | | | | | |
| 24500 | 31541486 | 48 | 2.00E-76 | gallisepticum R | | | | | |
| 245, | | | | Cytophaga | | | | | |
| 246 | 48856118 | 49 | 1.00E-46 | hutchinsonii | COG0242: N-formylmethionyl-tRNA deformylase [Cytophaga hutchinsonii] | | | | 3.5.1.88 |
| 24501, | | | | Bacteroides | putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79316.1 putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides thetaiotaomicron VPI-5482] | Bacteroides fragilis YCH46 DNA, complete genome | 88 | 7.00E-07 | 6.3.3.1 |
| 24502 | 29349619 | 80 | 1.00E-120 | VPI-5482 | | | | | |
| 24505, | | | | Flavobacterium | | | | | |
| 24506 | 55540763 | 56 | 1.00E-107 | columnare | MrcA [Flavobacterium columnare] | | | | 2.4.2.- |
| 24507, | | | | Shewanella | conserved hypothetical protein [Shewanella violacea] | | | | |
| 24508 | 32562918 | 31 | 1.00E-07 | violacea | | | | | |
| 24509, | | | | Cytophaga | | | | | |
| 24510 | 48856384 | 28 | 2.00E-17 | hutchinsonii | hypothetical protein Chut02000101 [Cytophaga hutchinsonii] | | | | |
| 2451, | | | | Nostoc sp. PCC | hypothetical protein air1565 [Nostoc sp. PCC 7120] dbj BAB77931.1 air1565 [Nostoc sp. PCC 7120] pir AG2001 hypothetical protein air1565 [Imported] - Nostoc sp. (strain PCC 7120) | | | | |
| 2452 | 17229057 | 38 | 5.00E-21 | 7120 | | | | | |
| 24511, | | | | Bacteroides | glycerol-3-phosphate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77230.1 glycerol-3-phosphate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.1.1.94 |
| 24512 | 29347533 | 63 | 3.00E-37 | VPI-5482 | | | | | |
| 24515, | | | | Cytophaga | COG0323: DNA mismatch repair enzyme (predicted ATPase) [Cytophaga hutchinsonii] | | | | |
| 24516 | 48854181 | 36 | 7.00E-45 | hutchinsonii | tyrosine-protein kinase [Bacteroides fragilis YCH46] dbj BAD49519.1 tyrosine-protein kinase [Bacteroides fragilis YCH46] | | | | |
| 24517, | | | | Bacteroides fragilis | | | | | |
| 24518 | 53714061 | 32 | 3.00E-19 | YCH46 | adenine specific DNA methylase MOD [Azoarcus sp. EbN1] emb CAI07479.1 Adenine specific DNA methylase MOD [Azoarcus sp. EbN1] | | | | 2.1.1.72 |
| 24519, | | | | | | | | | |
| 24520 | 56476791 | 53 | 2.00E-68 | Azoarcus sp. EbN1 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|-----------------------------------|---|---|--|--|----------|
| 24521, 24522 | 52008518 | 42 | 2.00E-16 | 25259 | Thiobacillus denitrificans ATCC | COG2189: Adenine specific DNA methylase Mod [Thiobacillus denitrificans ATCC 25259] | | | |
| 24523, 24524 | 54294349 | 30 | 2.00E-19 | 25259 | Legionella pneumophila str. | hypothetical protein lp1417 [Legionella pneumophila str. Lens] | | | |
| 24527, 24528 | 48856556 | 38 | 9.00E-32 | 25259 | Cytophaga hutchinsonii | hypothetical protein Chut02000288 [Cytophaga hutchinsonii] | | | |
| 24529, 24530 | 19704557 | 62 | 1.00E-39 | 25586 | Fusobacterium nucleatum subsp. nucleatum ATCC | hypothetical protein FN1222 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95418.1 Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | |
| 2453, 2454 | 28212149 | 48 | 1.00E-23 | E88 | Clostridium tetani | tRNA pseudouridine synthase A [Clostridium tetani E88] gb AAO37030.1 tRNA pseudouridine synthase A [Clostridium tetani E88] | | | |
| 24531, 24532 | 28210031 | 32 | 2.00E-10 | E88 | Clostridium tetani | sp Q890R5 TRA2_CLOTE tRNA pseudouridine synthase A 2 (Pseudouridylate synthase 1 2) (Pseudouridine synthase 1 2) (Uracil hydrolyase 2) | | | 4.2.1.70 |
| 24535, 24536 | 29349772 | 39 | 7.00E-27 | VPI-5482 | Bacteroides thetaiotaomicron | mannosyltransferase [Clostridium tetani E88] gb AAO34912.1 mannose 6-phosphate 4-epimerase [Clostridium tetani E88] | | | 2.4.1.- |
| 24537, 24538 | 48854863 | 23 | 9.00E-12 | hutchinsonii | Cytophaga hutchinsonii | hypothetical protein BT4364 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79469.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 24539, 24540 | 23502244 | 29 | 5.00E-11 | Brucella suis 1330 | Brucella suis 1330 | COG0358: DNA primase (bacterial type) [Cytophaga hutchinsonii] | | | |
| 24541, 24542 | 20092248 | 31 | 1.00E-15 | Methanosarcina acetivorans C2A | Methanosarcina acetivorans C2A | hypothetical protein BR1372 [Brucella suis 1330] ref NP_539548.1 hypothetical protein BMEI0631 [Brucella melitensis 16M] gb AAN30286.1 conserved hypothetical protein [Brucella suis 1330] gb AAL51812.1 hypothetical protein [Brucella melitensis 16M] pir A13330 hypothetical protein BMEI0631 [imported] - Brucella melitensis (strain 16M) | | | |
| 24543, 24544 | 53711898 | 49 | 1.00E-48 | YCH46 | Bacteroides fragilis | hypothetical protein MA3436 [Methanosarcina acetivorans C2A] gb AAM06803.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | |
| 24545, 24546 | 16272405 | 47 | 2.00E-25 | KW20 | Haemophilus influenzae Rd | L-asparaginase I [Bacteroides fragilis YCH46] db BAD47356.1 L-asparaginase I [Bacteroides fragilis YCH46] | | | 3.5.1.1 |
| | | | | | | hypothetical protein HI0457 [Haemophilus influenzae Rd KW20] gb AAC22115.1 conserved hypothetical protein [Haemophilus influenzae Rd KW20] pir E64069 yceG protein homolog HI0457 - Haemophilus influenzae (strain Rd KW20) sp P44720 YCEG_HAEIN Hypothetical protein HI0457 | | | 4.--- |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|----------|
| 24547, 24548 | 53797765 | 26 | 3.00E-27 | Chloroflexus aurantiacus | hypothetical protein Chio02001813 [Chloroflexus aurantiacus] | | | | |
| 24549, 24550 | 53685671 | 27 | 6.00E-16 | Desulfitobacterium hafniense DCB-2 | COG2207: AraC-type DNA-binding domain-containing proteins [Desulfitobacterium hafniense DCB-2] | | | | |
| 24551, 24552 | 54308659 | 32 | 2.00E-07 | Photobacterium profundum SS9 | putative methyl-accepting chemotaxis protein [Photobacterium profundum SS9] emb[CAG19877.1] putative methyl-accepting chemotaxis protein [Photobacterium profundum] | | | | |
| 24553, 24554 | 52549449 | 33 | 2.00E-21 | uncultured archaeon GZfos27E6 | carboxylesterase [uncultured archaeon GZfos27E6] | | | | 3.1.1.1 |
| 24555, 24556 | 27364673 | 29 | 5.00E-09 | Vibrio vulnificus CMCP6 | Transcriptional regulator [Vibrio vulnificus CMCP6] ref NP_935886.1 transcriptional regulator [Vibrio vulnificus YJ016] gb AAO09728.1 Transcriptional regulator [Vibrio vulnificus CMCP6] dbj BAC95857.1 transcriptional regulator [Vibrio vulnificus YJ016] | | | | |
| 24559, 24560 | 48855208 | 36 | 1.00E-25 | Cytophaga hutchinsonii | sigma24 homolog [Cytophaga hutchinsonii] | | | | |
| 24567, 24568 | 32473966 | 29 | 2.00E-10 | Rhodopirellula baltica SH 1 | serine/threonine protein phosphatase [Rhodopirellula baltica SH 1] emb CAD74502.1 serine/threonine protein phosphatase [Pirellula sp.] | | | | 3.1.3.16 |
| 24569, 24570 | 29348712 | 43 | 1.00E-45 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent RNA helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78409.1 ATP-dependent RNA helicase [Bacteroides thetaiotaomicron VPI-5482] | Desc:Bacillus anthracis variable region DNA sequence SEQ ID NO 85. Org:Bacillus anthracis | 97 | 5.00E-07 | 2.7.7.- |
| 2457, 2458 | 53797741 | 33 | 8.00E-32 | Chloroflexus aurantiacus | COG0438: Glycosyltransferase [Chloroflexus aurantiacus] | | | | 2.4.1.- |
| 24571, 24572 | 14531032 | 52 | 5.00E-82 | Flavobacterium johnsoniae | Flo14 [Flavobacterium johnsoniae] | | | | |
| 24579, 24580 | 23120384 | 27 | 7.00E-10 | Desulfitobacterium hafniense DCB-2 | COG0823: Periplasmic component of the Tol biopolymer transport system [Desulfitobacterium hafniense DCB-2] | | | | |
| 24583, 24584 | 34397168 | 47 | 8.00E-29 | Porphyromonas gingivalis W83 | ATP:cob(I)alamin adenosyltransferase, putative [Porphyromonas gingivalis W83] ref NP_905333.1 ATP:cob(I)alamin adenosyltransferase, putative [Porphyromonas gingivalis W83] | | | | 4.2.1.28 |
| 24587, 24588 | 53714518 | 22 | 1.00E-13 | Bacteroides fragilis YCH46 | DNA polymerase III subunit gamma/tau [Bacteroides fragilis YCH46] dbj BAD49976.1 DNA polymerase III subunit gamma/tau [Bacteroides fragilis YCH46] | | | | |

| | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|--|--|--|----------|
| 24589, | 53712040 | 39 | 2.00E-31 | Bacteroides fragilis YCH46 | putative methyltransferase [Bacteroides fragilis YCH46] dbj BAD47498.1 | | | 2.1.1.- |
| 24590 | | | | YCH46 | putative methyltransferase [Bacteroides fragilis YCH46] | | | |
| 2459, | 48856618 | 55 | 1.00E-86 | Cytophaga hutchinsonii | COG1562: Phytoene/squalene synthetase [Cytophaga hutchinsonii] | | | 2.5.1.32 |
| 2460 | | | | | | | | |
| 24591, | 5360168 | 53 | 8.00E-55 | Flavobacterium johnsoniae | GidB [Flavobacterium johnsoniae] | | | |
| 24592 | | | | | | | | |
| 24593, | 5360169 | 60 | 5.00E-35 | Flavobacterium johnsoniae | GidC [Flavobacterium johnsoniae] | | | |
| 24594 | | | | | | | | |
| 24595, | 52853314 | 27 | 4.00E-07 | Psychrobacter sp. 273-4 | COG2755: Lysophospholipase L1 and related esterases [Psychrobacter sp. 273-4] | | | |
| 24596 | | | | | | | | |
| 24597, | 52006884 | 33 | 3.00E-10 | Thiobacillus denitrificans ATCC 25259 | COG0543: 2-polypropenylphenol hydroxylase and related flavodoxin oxidoreductases [Thiobacillus denitrificans ATCC 25259] | | | |
| 24598 | | | | | | | | |
| 24599, | 52082356 | 45 | 3.00E-13 | Bacillus licheniformis ATCC 14580 | YwaF [Bacillus licheniformis ATCC 14580] gb AAU25509.1 YwaF [Bacillus licheniformis ATCC 14580] ref YP_093574.1 YwaF [Bacillus licheniformis ATCC 14580] gb AAU42881.1 YwaF [Bacillus licheniformis DSM 13] | | | |
| 24600 | | | | | | | | |
| 24601, | 53714270 | 66 | 3.00E-45 | Bacteroides fragilis YCH46 | DNA polymerase III epsilon chain [Bacteroides fragilis YCH46] dbj BAD49728.1 DNA polymerase III epsilon chain [Bacteroides fragilis YCH46] | | | 2.7.7.7 |
| 24602 | | | | | | | | |
| 24605, | 22958439 | 33 | 9.00E-08 | Rhodobacter sphaeroides 2.4.1 | COG1393: Arsenate reductase and related proteins, glutaredoxin family [Rhodobacter sphaeroides 2.4.1] | | | |
| 24606 | | | | | | | | |
| | | | | | hypothetical protein MA4225 [Methanosarcina acetivorans C2A] ref NP_618394.1 hypothetical protein MA3511 [Methanosarcina acetivorans C2A] ref NP_618264.1 hypothetical protein MA3375 [Methanosarcina acetivorans C2A] ref NP_617683.1 hypothetical protein MA2785 [Methanosarcina acetivorans C2A] gb AAM07570.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] gb AAM06874.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] gb AAM06744.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] gb AAM06163.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | |
| 24609, | 20093015 | 47 | 4.00E-15 | Methanosarcina acetivorans C2A | COG0504: CTP synthase (UTP-ammonia lyase) [Cytophaga hutchinsonii] | | | 6.3.4.2 |
| 24610 | | | | | | | | |
| 2461, | 48856944 | 59 | 1.00E-69 | Cytophaga hutchinsonii | putative ribosomal large chain pseudouridine synthase A [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61405.1 putative ribosomal large chain pseudouridine synthase A [Vibrio parahaemolyticus] | | | 4.2.1.70 |
| 2462 | | | | | | | | |
| 24617, | 28899917 | 57 | 1.00E-90 | Vibrio parahaemolyticus RIMD 2210633 | COG0441: Threonyl-tRNA synthetase [Cytophaga hutchinsonii] | | | 6.1.1.3 |
| 24618 | | | | | | | | |
| 24619, | 48853747 | 50 | 3.00E-32 | Cytophaga hutchinsonii | | | | |
| 24620 | | | | | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|---|----|----------|----------|
| 24621, | 48853518 | 48 | 1.00E-36 | Cytophaga hutchinsonii | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | Desc: Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2072 | 95 | 3.00E-07 | |
| 24622 | | | | Mesorhizobium loti | hypothetical protein ml5269 [Mesorhizobium loti MAFF303099] | Org: Staphylococcus epidermidis | | | |
| 24625, | 13474394 | 47 | 6.00E-16 | MAFF303099 | dbj BAB51748.1 ml5269 [Mesorhizobium loti MAFF303099] | | | | |
| 24626 | | | | Flavobacterium johnsoniae | gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [imported] - Flavobacterium johnsoniae | | | | |
| 24629, | 2281663 | 66 | 3.00E-43 | johnsoniae | | | | 1.8.- | |
| 24630 | | | | Mus musculus | Thimet oligopeptidase 1 [Mus musculus] | | | 3.4.24.1 | |
| 2463, | 21619359 | 43 | 3.00E-57 | Mus musculus | | | | 5 | |
| 2464 | | | | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | DNA-binding response regulator [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94742.1 DNA-binding response regulator [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | 2.7.3.- |
| 24631, | 46578675 | 56 | 2.00E-32 | Hildenborough | two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] dbj BAD51228.1 two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] | | | | |
| 24633, | 53715770 | 38 | 1.00E-28 | YCH46 | probable transcriptional regulator [Clostridium perfringens str. 13] | | | | |
| 24634 | | | | Clostridium perfringens str. 13 | dbj BAB82245.1 probable transcriptional regulator [Clostridium perfringens str. 13] | | | | |
| 24635, | 18311521 | 33 | 2.00E-19 | perfringens str. 13 | malate:quinone oxidoreductase [Oceanobacillus ihayensis HTE831] | | | | |
| 24636 | | | | Oceanobacillus ihayensis HTE831 | sp Q8CV11 MQO_OCEIH Probable malate:quinone oxidoreductase (Malate dehydrogenase [acceptor]) (MQO) dbj BAC12902.1 malate:quinone oxidoreductase [Oceanobacillus ihayensis HTE831] | | | 1.1.99.1 | 6 |
| 24637, | 23098401 | 46 | 3.00E-65 | ihayensis HTE831 | nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] | | | | |
| 24641, | | | | Coxiella burnetii | gb AAO90553.1 nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] | | | | 2.4.2.11 |
| 24642 | 29664347 | 58 | 2.00E-42 | RSA 493 | hypothetical protein Bd0852 [Bdellovibrio bacteriovorus HD100] | | | | |
| 24643, | | | | Bdellovibrio bacteriovorus | emb CAE78797.1 lepB [Bdellovibrio bacteriovorus HD100] | | | | |
| 24644 | 42522424 | 27 | 6.00E-07 | HD100 | hypothetical protein PBPRB1077 [Photobacterium profundum SS9] | | | | |
| 24645, | | | | Photobacterium profundum SS9 | emb CAG22949.1 conserved hypothetical protein [Photobacterium profundum] | | | | |
| 24646 | 54302756 | 38 | 2.00E-12 | profundum SS9 | | | | | |

| | | | | | | | | |
|--------|----------|----|----------|--|---|---------------|--|--|
| 24647, | 29345964 | 60 | 1.00E-73 | Bacteroides thetataoimicron VPI-5482 | glucosamine-fructose-6-phosphate aminotransferase [Bacteroides thetataoimicron VPI-5482] gb AAO75661.1 glucosamine-fructose-6- phosphate aminotransferase [Bacteroides thetataoimicron VPI-5482] sp Q8AAB1 GLMS_BACTN Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (Hexosephosphate aminotransferase) (D- fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6- phosphate amidotransferase) (Glucosamine-6-phosphate synthase) | 2.6.1.16 | | |
| 24648 | 31195963 | 58 | 1.00E-93 | Anopheles gambiae | ENSANGP00000000454 [Anopheles gambiae] | 4.2.1.22 | | |
| 24649, | 53796853 | 49 | 3.00E-68 | Chloroflexus aurantiacus | COG0210: Superfamily I DNA and RNA helicases [Chloroflexus aurantiacus] | 3.6.1.- | | |
| 24650 | | | | | | | | |
| 24651, | 53764144 | 43 | 1.00E-54 | Anabaena variabilis ATCC 29413 | COG1770: Protease II [Anabaena variabilis ATCC 29413] | 3.4.21.8 3 | | |
| 24652 | | | | | | | | |
| 24653, | 34397502 | 29 | 5.00E-21 | Porphyromonas gingivalis W83 | 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2- oxoglutarate decarboxylase [Porphyromonas gingivalis W83] ref NP_905665.1 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Porphyromonas gingivalis W83] | 4.1.1.71 | | |
| 24654 | | | | | | | | |
| 24657, | 21227543 | 46 | 2.00E-21 | Methanosarcina mazel Go1 | Inorganic pyrophosphatase [Methanosarcina mazel Go1] gb AAM31137.1 | 3.6.1.1 | | |
| 24658 | | | | | Inorganic pyrophosphatase [Methanosarcina mazel Go1] site-specific recombinase, phage integrase family [Methylococcus capsulatus str. Bath] ref YP_113189.1 site-specific recombinase, phage integrase family [Methylococcus capsulatus str. Bath] | | | |
| 24659, | 53758908 | 36 | 2.00E-32 | Methylococcus capsulatus str. Bath | | | | |
| 24660 | | | | | | | | |
| 24663, | 55246919 | 64 | 1.00E-68 | Anopheles gambiae str. PEST | ENSANGP00000016322 [Anopheles gambiae str. PEST] ref XP_561003.1 | 1.8.4.5 | | |
| 24664 | | | | | ENSANGP00000016322 [Anopheles gambiae str. PEST] | | | |
| 24665, | 48824812 | 54 | 1.00E-36 | Enterococcus faecium | COG0367: Asparagine synthase (glutamine-hydrolyzing) [Enterococcus faecium] | 6.3.5.4 | | |
| 24666 | | | | | | | | |
| 24667, | 21227240 | 35 | 2.00E-11 | Methanosarcina mazel Go1 | glycosyltransferase [Methanosarcina mazel Go1] gb AAM30834.1 | 2.4.1.- | | |
| 24668 | | | | | glycosyltransferase [Methanosarcina mazel Go1] hypothetical protein NE0847 [Nitrosomonas europaea ATCC 19718] emb CAD84758.1 conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] | | | |
| 24669, | 30248851 | 30 | 5.00E-07 | Nitrosomonas europaea ATCC 19718 | | | | |
| 24670 | | | | | | | | |
| 24671, | 29345970 | 29 | 3.00E-26 | Bacteroides thetataoimicron VPI-5482 | outer membrane efflux protein [Bacteroides thetataoimicron VPI-5482] gb AAO75667.1 outer membrane efflux protein [Bacteroides thetataoimicron VPI-5482] | | | |
| 24672 | | | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|--|--|----|-------------------|
| 24673, 24674 | 53712087 | 37 | 2.00E-54 | Bacteroides fragilis YCH46 | putative transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD47545.1 putative transcriptional regulator [Bacteroides fragilis YCH46] | | | |
| 24677, 24678 | 53715627 | 36 | 4.00E-27 | Bacteroides fragilis YCH46 | putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46] dbj BAD51085.1 putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46] | | | 3.3.2.3 |
| 24679, 24680 | 53713311 | 45 | 2.00E-44 | Bacteroides fragilis YCH46 | hypothetical protein BF2022 [Bacteroides fragilis YCH46] dbj BAD48769.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | Anopheles gambiae ENSANGP000000000 3278 (ENSANGG00000000 02643) mRNA, partial cds | 93 | 5.00E-07 3.4.13.9 |
| 24681, 24682 | 29345572 | 51 | 8.00E-80 | Bacteroides thetaiotaomicron VPI-5482 | penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI- 5482] gbl AAO75269.1 penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI-5482] | | | 2.4.2.- |
| 24683, 24684 | 48855337 | 54 | 1.00E-71 | Cytophaga hutchinsonii | COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii] | | | |
| 24685, 24686 | 55977207 | 37 | 7.00E-37 | Comamonas sp. JS46 | replicase [Comamonas sp. JS46] | | | |
| 24687, 24688 | 50083970 | 52 | 3.00E-37 | Acinetobacter sp. ADP1 | putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] emb CAG67658.1 putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] | | | 4.1.99.4 |
| 2469, 2470 | 34397012 | 47 | 4.00E-63 | Porphyrromonas gingivalis W83 | ABC transporter, ATP-binding protein [Porphyrromonas gingivalis W83] ref NP_905177.1 ABC transporter, ATP-binding protein [Porphyrromonas gingivalis W83] | | | 1.8.- |
| 24691, 24692 | 53713904 | 72 | 1.00E-120 | Bacteroides fragilis YCH46 | exonuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46] | Staphylococcus epidermidis ATCC 12228, section 2 of 9 of the complete genome | 87 | 2.00E-07 |
| 24699, 24700 | 53712212 | 45 | 1.00E-34 | Bacteroides fragilis YCH46 | phosphate starvation-inducible protein PhoH [Bacteroides fragilis YCH46] dbj BAD47670.1 phosphate starvation-inducible protein PhoH [Bacteroides fragilis YCH46] | | | |
| 24701, 24702 | 48854288 | 38 | 7.00E-35 | Cytophaga hutchinsonii | COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii] | | | |
| 24703, 24704 | 48855384 | 42 | 2.00E-39 | Cytophaga hutchinsonii | COG0601: ABC-type dipeptide/oligopeptide/nickel transport systems, permease components [Cytophaga hutchinsonii] | | | |
| 24705, 24706 | 48856104 | 42 | 4.00E-30 | Cytophaga hutchinsonii | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|----------|
| 24707, 24708 | 34397475 | 25 | 3.00E-13 | Porphyromonas gingivalis W83 | hypothetical protein PG1492 [Porphyromonas gingivalis W83] ref NP_905638.1 hypothetical protein PG1492 [Porphyromonas gingivalis W83] | | | |
| 24709, 24710 | 29347584 | 38 | 8.00E-11 | Bacteroides thetaiotaomicron VPI-5482 | ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO77281.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2471, 2472 | 53715428 | 55 | 1.00E-92 | Bacteroides fragilis YCH46 | histidine ammonia-lyase [Bacteroides fragilis YCH46] dbj BAD50886.1 histidine ammonia-lyase [Bacteroides fragilis YCH46] | | | 4.3.1.3 |
| 24711, 24712 | 45658399 | 46 | 2.00E-20 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC12558 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS71122.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 24713, 24714 | 48853960 | 32 | 3.00E-20 | Cytophaga hutchinsonii | COG0764: 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases [Cytophaga hutchinsonii] | | | |
| 24715, 24716 | 57506055 | 41 | 4.00E-21 | Campylobacter upsaliensis RM3195 | RioF, putative [Campylobacter upsaliensis RM3195] gb EAL52454.1 RioF, putative [Campylobacter upsaliensis RM3195] | | | |
| 24717, 24718 | 48854571 | 63 | 1.00E-61 | Cytophaga hutchinsonii | COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Cytophaga hutchinsonii] | | | 2.4.1.- |
| 24719, 24720 | 52853382 | 77 | 2.00E-27 | Psychrobacter sp. 273-4 | hypothetical protein Psyc03002036 [Psychrobacter sp. 273-4] | | | |
| 24723, 24724 | 48853807 | 36 | 2.00E-56 | Cytophaga hutchinsonii | COG0793: Periplasmic protease [Cytophaga hutchinsonii] | | | 3.4.21.- |
| 24725, 24726 | 48855800 | 63 | 2.00E-60 | Cytophaga hutchinsonii | COG0688: Phosphatidylserine decarboxylase [Cytophaga hutchinsonii] | | | 4.1.1.65 |
| 24727, 24728 | 53711474 | 37 | 1.00E-46 | Bacteroides fragilis YCH46 | hypothetical protein BF0183 [Bacteroides fragilis YCH46] dbj BAD46932.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 2473, 2474 | 42523724 | 44 | 4.00E-18 | Bdellovibrio bacteriovorus HD100 | putative potassium/proton antiporter [Bdellovibrio bacteriovorus HD100] emb CAE80097.1 putative potassium/proton antiporter [Bdellovibrio bacteriovorus HD100] | | | |
| 24735, 24736 | 30248520 | 31 | 3.00E-23 | Nitrosomonas europaea ATCC 19718 | riuD, ribosomal large subunit pseudouridine synthase D [Nitrosomonas europaea ATCC 19718] emb CAD84416.1 rluD, ribosomal large subunit pseudouridine synthase D [Nitrosomonas europaea ATCC 19718] sp Q82WZ5 RLUD_NITEU Ribosomal large subunit pseudouridine synthase D (Pseudouridylylase synthase) (Uracil hydrolyase) | | | 4.2.1.70 |
| 24737, 24738 | 29346053 | 58 | 2.00E-94 | Bacteroides thetaiotaomicron VPI-5482 | RNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75750.1 RNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8AA22 Y643_BACTN Hypothetical RNA methyltransferase BT0643 | | | 2.1.1.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|---|----|----------|----------|
| 24739, 24740 | 23103296 | 33 | 2.00E-35 | Azotobacter vinelandii | COG2194: Predicted membrane-associated, metal-dependent hydrolase [Azotobacter vinelandii] | | | | |
| 24741, 24742 | 29346131 | 33 | 5.00E-44 | Bacteroides thetaiotaomicron VPI-5482 | DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75828.1 DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 24743, 24744 | 48863475 | 44 | 3.00E-63 | Microbulifer degradans 2-40 | hypothetical protein Mdeg02001566 [Microbulifer degradans 2-40] | | | | |
| 24745, 24746 | 48856334 | 22 | 2.00E-07 | Cytophaga hutchinsonii | hypothetical protein Chut02000046 [Cytophaga hutchinsonii] | | | | |
| 24747, 24748 | AAW9778 | 35 | 6.00E-09 | | Desc:Bacillus subtilis serine protease SP1 (YUXL). Org:Bacillus subtilis imidazole glycerol phosphate synthase subunit hisH [Bacteroides fragilis YCH46] dbj BAD49801.1 imidazole glycerol phosphate synthase subunit hisH [Bacteroides fragilis YCH46] | | | 3.4.21.- | |
| 24749, 24750 | 53714343 | 55 | 5.00E-47 | Bacteroides fragilis YCH46 | peroxiredoxin [Rhodopirella batlica SH 1] emb CAD77542.1 peroxiredoxin [Pirella sp.] | | | | 2.4.2.- |
| 24751, 24752 | 32477471 | 38 | 4.00E-13 | Ralstonia metallidurans | COG0463: Glycosyltransferases involved in cell wall biogenesis [Ralstonia metallidurans CH34] | | | | 2.4.-.- |
| 24753, 24754 | 48771048 | 37 | 6.00E-29 | CH34 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Haemophilus somnus 2336] | | | | 2.4.1.- |
| 24757, 24758 | 53728512 | 43 | 9.00E-38 | Haemophilus sornus 2336 | hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1 hypothetical maturase [Photobacterium profundum] | Photobacterium profundum SS9 chromosome 2; segment 3/7 | 83 | 2.00E-16 | 2.7.7.49 |
| 24759, 24760 | 54302486 | 72 | 3.00E-99 | Photobacterium profundum SS9 | hypothetical protein BT9727_2788 [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA760154.1 conserved hypothetical protein [Bacillus thuringiensis serovar konkukian str. 97-27] | | | | |
| 24761, 24762 | 49477952 | 26 | 1.00E-22 | Bacillus thuringiensis serovar konkukian str. 97-27 | GTP-binding protein Era [Porphyromonas gingivalis W83] ref NP_906196.1 GTP-binding protein Era [Porphyromonas gingivalis W83] | | | | |
| 24765, 24766 | 34398035 | 43 | 6.00E-39 | Porphyromonas gingivalis W83 | hypothetical protein BT1057 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76164.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 24767, 24768 | 29346467 | 31 | 3.00E-16 | Bacteroides thetaiotaomicron VPI-5482 | putative DNA mismatch repair protein [Bacteroides fragilis YCH46] dbj BAD50625.1 putative DNA mismatch repair protein [Bacteroides fragilis YCH46] | | | | |
| 24769, 24770 | 53715167 | 37 | 4.00E-16 | Bacteroides fragilis YCH46 | hypothetical protein BF3279 [Bacteroides fragilis YCH46] dbj BAD50023.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|-----------------------|--|--|--|--|----------|
| 2477, | 28377430 | 55 | 5.00E-37 | Lactobacillus | hypoxanthine-guanine phosphoribosyltransferase [Lactobacillus plantarum WCFS1] emb CAD63163.1 hypoxanthine-guanine | | | | 2.4.2.8 |
| 2478 | | | | plantarum WCFS1 | phosphoribosyltransferase [Lactobacillus plantarum WCFS1] | | | | |
| 24771, | 48839913 | 31 | 7.00E-17 | Methanosarcina | COG2120: Uncharacterized proteins, LmbE homologs [Methanosarcina barkeri str. fusaro] | | | | |
| 24772 | | | | barkeri str. fusaro | | | | | |
| 24773, | 21228215 | 42 | 1.00E-34 | Methanosarcina | hypothetical protein MM2113 [Methanosarcina mazel Go1] gb AAM31809.1 | | | | |
| 24774 | | | | mazel Go1 | hypothetical protein [Methanosarcina mazel Go1] | | | | |
| 24775, | | | | | phosphoglycolate phosphatase (putative) [Lactobacillus plantarum WCFS1] | | | | |
| 24776 | 28379855 | 27 | 9.00E-07 | Lactobacillus | emb CAD65825.1 phosphoglycolate phosphatase (putative) [Lactobacillus plantarum WCFS1] | | | | |
| 24779, | | | | plantarum WCFS1 | | | | | |
| 24780 | 48855589 | 35 | 2.00E-34 | Cytophaga | COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii] | | | | 3.1.-.- |
| | | | | hutchinsonii | | | | | |
| 24781, | | | | | probable late competence protein [Clostridium perfringens str. 13] | | | | |
| 24782 | 18310639 | 38 | 2.00E-40 | Clostridium | dbj BAB81363.1 probable late competence protein [Clostridium perfringens str. 13] | | | | |
| | | | | perfringens str. 13 | | | | | |
| 24785, | | | | Cytophaga | COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii] | | | | 2.4.1.18 |
| 24786 | 48855019 | 44 | 1.00E-16 | hutchinsonii | | | | | 2 |
| 24787, | | | | Cytophaga | COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] | | | | |
| 24788 | 48854120 | 50 | 1.00E-81 | hutchinsonii | | | | | 6.2.1.3 |
| 24789, | | | | Mesorhizobium loti | hypothetical protein mlr2180 [Mesorhizobium loti MAFF303099] | | | | |
| 24790 | 13472020 | 33 | 5.00E-11 | MAFF303099 | dbj BAB49373.1 mlr2180 [Mesorhizobium loti MAFF303099] | | | | |
| | | | | Photorhabdus | | | | | |
| 2479, | | | | luminescens | hypothetical protein plu2609 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE14983.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] | | | | |
| 2480 | 37526500 | 52 | 2.00E-34 | subsp. laumondii TTO1 | | | | | |
| 24793, | | | | Cytophaga | COG0735: Fe2+/Zn2+ uptake regulation proteins [Cytophaga hutchinsonii] | | | | |
| 24794 | 48856297 | 55 | 2.00E-40 | hutchinsonii | oxygen-independent coproporphyrinogen III oxidase, putative [Pseudomonas putida KT2440] gb AAN70666.1 oxygen-independent coproporphyrinogen III oxidase, putative [Pseudomonas putida KT2440] | | | | 1.-.-.- |
| 24795, | | | | Pseudomonas | | | | | |
| 24796 | 26991777 | 35 | 6.00E-12 | putida KT2440 | hypothetical protein PG1493 [Porphyrinomonas gingivalis W83] | | | | |
| 24797, | | | | Porphyrinomonas | ref NP_905638.1 hypothetical protein PG1493 [Porphyrinomonas gingivalis W83] | | | | |
| 24798 | 34397476 | 33 | 4.00E-30 | gingivalis W83 | | | | | |
| | | | | | hypothetical protein MA2102 [Methanosarcina acetivorans C2A] | | | | |
| 24803, | | | | Methanosarcina | gb AAM05501.1 hypothetical protein (multi-domain) [Methanosarcina acetivorans str. C2A] | | | | |
| 24804 | 20090946 | 35 | 3.00E-24 | acetivorans C2A | | | | | 2.7.7.49 |
| | | | | | hypothetical protein AF1548 [Archaeoglobus fulgidus DSM 4304] | | | | |
| 24805, | | | | | gb AAB89701.1 A. fulgidus predicted coding region AF1548 [Archaeoglobus fulgidus DSM 4304] pir C69443 hypothetical protein AF1548 - | | | | |
| 24806 | 11499143 | 31 | 2.00E-20 | Archaeoglobus | Archaeoglobus fulgidus sp O28724 YF48_ARCFU Hypothetical protein AF1548 | | | | |
| | | | | fulgidus DSM 4304 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|--|--|----------|
| 24809, 24810 | 48853591 | 59 | 1.00E-102 | Cytophaga hutchinsonii | COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii] | | | | |
| 2481, 2482 | 29377430 | 55 | 5.00E-37 | Lactobacillus plantarum WCFS1 | hypoxanthine-guanine phosphoribosyltransferase [Lactobacillus plantarum WCFS1] emb CAD63163.1 hypoxanthine-guanine phosphoribosyltransferase [Lactobacillus plantarum WCFS1] | | | | 2.4.2.8 |
| 24811, 24812 | 10717100 | 38 | 2.00E-37 | Streptococcus thermophilus | putative HsdS [Streptococcus thermophilus] | | | | 3.1.21.3 |
| 24813, 24814 | 48855375 | 37 | 4.00E-21 | Cytophaga hutchinsonii | COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 24815, 24816 | 29349055 | 50 | 3.00E-31 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3647 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78752.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 24817, 24818 | 48856944 | 56 | 2.00E-26 | Cytophaga hutchinsonii | COG0504: CTP synthase (UTP-ammonia lyase) [Cytophaga hutchinsonii] | | | | 6.3.4.2 |
| 24827, 24828 | 46120271 | 47 | 2.00E-59 | Crocospaera watsonii WH 8501 | hypothetical protein Cwat03000671 [Crocospaera watsonii WH 8501] penicillin-binding protein AmpH, putative [Caulobacter crescentus CB15] gb AAK25451.1 penicillin-binding protein AmpH, putative [Caulobacter crescentus CB15] pir G87681 penicillin-binding protein AmpH, probable [imported] - Caulobacter crescentus | | | | |
| 2483, 2484 | 16127719 | 30 | 1.00E-27 | Caulobacter crescentus CB15 | COG0286: Type I restriction-modification system methyltransferase subunit [Burkholderia cepacia R1808] | | | | |
| 24835, 24836 | 46320397 | 30 | 3.00E-08 | Burkholderia cepacia R1808 | COG0286: Type I restriction-modification system methyltransferase subunit [Burkholderia cepacia R1808] | | | | |
| 24837, 24838 | 46320397 | 27 | 3.00E-15 | Burkholderia cepacia R1808 | COG0286: Type I restriction-modification system methyltransferase subunit [Burkholderia cepacia R1808] | | | | |
| 24839, 24840 | 48891775 | 43 | 7.00E-10 | Trichodesmium erythraeum IMS101 | COG1112: Superfamily I DNA and RNA helicases and helicase subunits [Trichodesmium erythraeum IMS101] | | | | 3.6.1.- |
| 24841, 24842 | 16766038 | 25 | 7.00E-09 | Phage Fels-2 | hypothetical protein STM2726 [Phage Fels-2] gb AAL21612.1 Fels-2 prophage protein [Salmonella typhimurium LT2] | | | | |
| 24843, 24844 | 56480140 | 34 | 2.00E-07 | Shigella flexneri 2a str. 301 | hypothetical protein SF2623 [Shigella flexneri 2a str. 301] gb AAN44120.2 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] ref NP_838134.1 hypothetical protein S2796 [Shigella flexneri 2a str. 2457T] gb AAP17944.1 hypothetical protein S2796 [Shigella flexneri 2a str. 2457T] | | | | |
| 24845, 24846 | 34396493 | 44 | 1.00E-30 | Porphyromonas gingivalis W83 | ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] ref NP_904560.1 ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] | | | | 3.6.1.- |
| 24847, 24848 | 29611044 | 51 | 2.00E-44 | NiFe | putative [NiFe] hydrogenase expression/formation protein [Streptomyces avermitilis MA-4680] ref NP_828553.1 putative [NiFe] hydrogenase expression/formation protein [Streptomyces avermitilis MA-4680] | | | | |

| | | | | | | | | | | |
|--------|----------|----|----------|----------------------------|---|--|--|--|--|---------|
| 24849, | 37527577 | 26 | 3.00E-07 | TT01 | Photorhabdus luminescens subsp. laumondii | hypothetical protein plu3714 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16086.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] | | | | |
| 24850 | | | | | | | | | | |
| 24857, | 42761500 | 41 | 3.00E-20 | Dictyostelium discoideum | hypothetical protein [Dictyostelium discoideum] | | | | | |
| 24858 | | | | | | | | | | |
| 24859, | 39545768 | 34 | 2.00E-18 | Aeromonas hydrophila | putative ADP-heptose-LPS [Aeromonas hydrophila] | | | | | 2.4.1.- |
| 24860 | | | | | | | | | | |
| 24861, | | | | | Legionella pneumophila subsp. pneumophila | | | | | |
| 24862 | 52842406 | 42 | 2.00E-25 | Philadelphina 1 | sulfate transporter [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28258.1 sulfate transporter [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | | |
| 24863, | | | | | Legionella | | | | | |
| 24864 | 54298940 | 40 | 1.00E-37 | pneumophila str. Paris | hypothetical protein lpp3007 [Legionella pneumophila str. Paris] emb CAH14160.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | | |
| 24865, | | | | | Legionella | | | | | |
| 24866 | 54295786 | 35 | 3.00E-39 | pneumophila str. Lens | hypothetical protein lpl2876 [Legionella pneumophila str. Lens] emb CAH17120.1 hypothetical protein [Legionella pneumophila str. Lens] | | | | | |
| 24867, | | | | | Thermotoga | | | | | |
| 24868 | 15643211 | 41 | 1.00E-34 | maritima MSB8 | hypothetical protein TM0445 [Thermotoga maritima MSB8] gb AAD35530.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir [H72377 conserved hypothetical protein - Thermotoga maritima (strain MSB8) COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] ref ZP_00146915.2 COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] | | | | | |
| 24869, | 52853435 | 89 | 1.00E-85 | Psychrobacter sp. 273-4 | hypothetical protein BF3882 [Bacteroides fragilis YCH46] db [BAD50624.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | | |
| 24871, | 53715166 | 30 | 4.00E-08 | Bacteroides fragilis YCH46 | hypothetical protein BT2180 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77287.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | | |
| 24872 | | | | | Bacteroides thetaiotaomicron | | | | | |
| 24875, | 29347590 | 50 | 7.00E-59 | VPI-5482 | hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | | |
| 24876 | | | | | Cytophaga | | | | | |
| 24877, | 48853745 | 29 | 1.00E-09 | hutchinsonii | hypothetical protein Chut02003380 [Cytophaga hutchinsonii] | | | | | |
| 24878 | | | | | | | | | | |
| 24883, | | | | | Porphyrromonas | | | | | |
| 24884 | 34396570 | 26 | 2.00E-17 | gingivallis W83 | capsular polysaccharide transport protein, putative [Porphyrromonas gingivallis W83] ref NP_904737.1 capsular polysaccharide transport protein, putative [Porphyrromonas gingivallis W83] | | | | | |
| 24885, | | | | | Bacteroides | | | | | |
| 24886 | 29346006 | 29 | 7.00E-12 | thetaitotaomicron VPI-5482 | putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO75703.1 putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | | |
| 24891, | 28210167 | 57 | 3.00E-35 | E88 | hypothetical protein CTC00414 [Clostridium tetani E88] conserved protein [Clostridium tetani E88] | | | | | |
| 24892 | | | | | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|--|---|--|----|-------------------|
| 24895, 24896 | 29606128 | 38 | 2.00E-15 | Streptomyces avermittilis MA-4680 | hypothetical protein [Streptomyces avermittilis MA-4680] ref NP_823656.1 hypothetical protein SAV2480 [Streptomyces avermittilis MA-4680] | | | |
| 24897, 24898 | 48854298 | 43 | 7.00E-22 | Cytophaga hutchinsonii | COG4867: Uncharacterized protein with a von Willebrand factor type A (vWA) domain [Cytophaga hutchinsonii] | | | |
| 24899, 24900 | 48856451 | 50 | 6.00E-21 | Cytophaga hutchinsonii | COG0040: ATP phosphoribosyltransferase [Cytophaga hutchinsonii] | | | 2.4.2.17 |
| 24903, 24904 | 34397714 | 63 | 1.00E-113 | Porphyrromonas gingivalis W83 | transcription-repair coupling factor [Porphyrromonas gingivalis W83] ref NP_905876.1 transcription-repair coupling factor [Porphyrromonas gingivalis W83] | Streptococcus mutans UA159 section 1 of 185 of the complete genome | 85 | 5.00E-113 3.6.1.- |
| 24905, 24906 | 48853984 | 44 | 2.00E-30 | Cytophaga hutchinsonii | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | |
| 24907, 24908 | 31194223 | 57 | 1.00E-72 | Anopheles gambiae | ENSANGP00000015562 [Anopheles gambiae] | | | 2.7.6.5 |
| 24909, 24910 | 56480140 | 41 | 7.00E-08 | Shigella flexneri 2a str. 301 | hypothetical protein SF2623 [Shigella flexneri 2a str. 301] gb AA044120.2 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] ref NP_838134.1 hypothetical protein S2796 [Shigella flexneri 2a str. 2457T] gb AAP17944.1 hypothetical protein S2796 [Shigella flexneri 2a str. 2457T] two-component sensor histidine kinase [Nostoc sp. PCC 7120] pit AH2051 two-component sensor histidine kinase air1966 [imported] - Nostoc sp. (strain PCC 7120) db BAB73665.1 two-component sensor histidine kinase [Nostoc sp. PCC 7120] | | | 2.7.3.- |
| 24911, 24912 | 17229458 | 24 | 8.00E-19 | Bdellovibrio bacteriovorus HD100 | glutamate synthase [Bdellovibrio bacteriovorus HD100] emb CAE80072.1 glutamate synthase [Bdellovibrio bacteriovorus HD100] | | | 1.4.1.13 |
| 24919, 24920 | 42523699 | 48 | 8.00E-29 | Shewanella oneidensis MR-1 | GGDEF domain protein [Shewanella oneidensis MR-1] gb AA055538.1 GGDEF domain protein [Shewanella oneidensis MR-1] | | | |
| 24921, 24922 | 24374051 | 48 | 2.00E-46 | Anabaena variabilis ATCC 29413 | COG2021: Homoserine acetyltransferase [Anabaena variabilis ATCC 29413] | | | 2.3.1.31 |
| 24923, 24924 | 53764561 | 32 | 2.00E-19 | Cytophaga hutchinsonii | COG1674: DNA segregation ATPase Fisk/SpoIIIE and related proteins [Cytophaga hutchinsonii] | | | |
| 24925, 24926 | 48854535 | 40 | 1.00E-43 | Cytophaga hutchinsonii | COG1674: DNA segregation ATPase Fisk/SpoIIIE and related proteins [Cytophaga hutchinsonii] | | | |
| 24929, 24930 | 48854535 | 42 | 2.00E-51 | Listeria monocytogenes str. 4b F2365 | hypothetical protein LMO2365_2347 [Listeria monocytogenes str. 4b F2365] gb AA05113.1 conserved domain protein [Listeria monocytogenes str. 4b F2365] | | | |
| 24930 | 46908547 | 31 | 2.00E-21 | 4b F2365 | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|--|--|---|----|----------|----------|
| 2493, 2494 | 48838849 | 81 | 8.00E-89 | Methanosarcina barkeri str. fusaro | COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro] | Methanosarcina acetivorans str. C2A, section 22 of 534 of the complete genome | 81 | 2.00E-27 | |
| 24931, 24932 | 46908547 | 29 | 1.00E-24 | Listeria monocytogenes str. 4b F2365 | hypothetical protein LMO2365_2347 [Listeria monocytogenes str. 4b F2365] gb AAU05113.1 conserved domain protein [Listeria monocytogenes str. 4b F2365] | | | | |
| 24933, 24934 | 55980986 | 25 | 7.00E-13 | Thermus thermophilus HB8 | hypothetical protein TTHA1017 [Thermus thermophilus HB8] dbj BAD70840.1 conserved hypothetical protein [Thermus thermophilus HB8] | | | | 3.6.1.- |
| 24935, 24936 | 48868352 | 49 | 3.00E-48 | Haemophilus influenzae 86- 028NP | COG0732: Restriction endonuclease S subunits [Haemophilus influenzae 86- 028NP] | | | | 3.1.21.3 |
| 24937, 24938 | 48868352 | 55 | 3.00E-68 | Haemophilus influenzae 86- 028NP | COG0732: Restriction endonuclease S subunits [Haemophilus influenzae 86- 028NP] | | | | 3.1.21.3 |
| 24939, 24940 | 52080497 | 40 | 1.00E-14 | Bacillus licheniformis ATCC 14580 | hypothetical protein BL01869 [Bacillus licheniformis ATCC 14580] gb AAU23650.1 conserved hypothetical protein [Bacillus licheniformis ATCC 14580] ref YP_091706.1 Ydel [Bacillus licheniformis ATCC 14580] gb AAU41013.1 Ydel [Bacillus licheniformis DSM 13] | | | | |
| 24941, 24942 | ABB4832 4 | 40 | 6.00E-25 | | Desc:Listeria monocytogenes protein #1028. Org:Listeria monocytogenes Predicted nucleotide-binding protein related to universal stress protein UspA [Methanopyrus kandleri AV19] gb AAM01736.1 Predicted nucleotide-binding protein related to universal stress protein UspA [Methanopyrus kandleri AV19] | | | | |
| 24943, 24944 | 20093959 | 30 | 9.00E-11 | Methanopyrus kandleri AV19 | Predicted nucleotide-binding protein related to universal stress protein UspA [Methanopyrus kandleri AV19] gb AAM01736.1 Predicted nucleotide-binding protein related to universal stress protein UspA [Methanopyrus kandleri AV19] | | | | |
| 24945, 24946 | 20093959 | 30 | 9.00E-11 | Methanopyrus kandleri AV19 | | | | | |
| 24947, 24948 | 38145972 | 30 | 1.00E-13 | Haemophilus influenzae | HIO869 [Haemophilus influenzae] | | | | |
| 2495, 2496 | 21674173 | 33 | 2.00E-28 | Chlorobium tepidum TLS | ABC transporter efflux protein [Chlorobium tepidum TLS] gb AAM72580.1 ABC transporter efflux protein [Chlorobium tepidum TLS] | | | | |
| 24951, 24952 | 48853325 | 36 | 3.00E-11 | Cytophaga hutchinsonii | hypothetical protein Chut02003941 [Cytophaga hutchinsonii] | | | | |
| 24953, 24954 | 48853326 | 44 | 3.00E-22 | Cytophaga hutchinsonii | COG1485: Predicted ATPase [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|---|---|----|----------|---------|
| 24955, | 48853325 | 30 | 2.00E-13 | Cytophaga | hypothetical protein Chuf02003941 [Cytophaga hutchinsonii] | | | | |
| 24956 | ABP7812 | | | hutchinsonii | Desc.N. gonorrhoeae amino acid sequence SEQ ID 2786. Org:Neisseria gonorrhoeae | | | | |
| 24957, | 8 | 28 | 3.00E-18 | | | | | | |
| 24958 | | | | | | | | | |
| 24959, | | | | | | | | | |
| 24960 | 34396448 | 57 | 7.00E-81 | Porphyrromonas gingivalis W83 | phosphoribosylformylglycinamide synthase, putative [Porphyrromonas gingivalis W83] refNP_904615.1 phosphoribosylformylglycinamide synthase, putative [Porphyrromonas gingivalis W83] | Bacteroides thetaiotaomicron VPI-5482, section 8 of 21 of the complete genome | 92 | 9.00E-09 | 6.3.5.3 |
| 24961, | | | | | | | | | |
| 24962 | 50083943 | 29 | 2.00E-08 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD0721 [Acinetobacter sp. ADP1] embjCAG67631.1 conserved hypothetical protein [Acinetobacter sp. ADP1] | | | | |
| 24963, | | | | | | | | | |
| 24964 | 48854312 | 39 | 3.00E-47 | Cytophaga hutchinsonii | COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii] | | | | |
| 24969, | | | | | | | | | |
| 24970 | 21673117 | 45 | 8.00E-32 | Chlorobium tepidum TLS | RNA polymerase sigma-70 factor, ECF subfamily [Chlorobium tepidum TLS] gb AAAM71524.1 RNA polymerase sigma-70 factor, ECF subfamily [Chlorobium tepidum TLS] | | | | |
| 2497, | | | | | | | | | |
| 2498 | 14521885 | 37 | 2.00E-21 | Pyrococcus abyssi GE5 | hypothetical protein PAB1106 [Pyrococcus abyssi GE5] emb CAB50591.1 Hypothetical protein [Pyrococcus abyssi] pir A75019 hypothetical protein PAB1106 - Pyrococcus abyssi (strain Orsay) splQ9UY21 YG87_PYRAB Hypothetical UPF0218 protein PYRAB16870 | | | | |
| 24971, | | | | | | | | | |
| 24972 | 21673117 | 45 | 2.00E-34 | Chlorobium tepidum TLS | RNA polymerase sigma-70 factor, ECF subfamily [Chlorobium tepidum TLS] gb AAAM71524.1 RNA polymerase sigma-70 factor, ECF subfamily [Chlorobium tepidum TLS] | | | | |
| 24973, | | | | | | | | | |
| 24974 | 48861126 | 35 | 5.00E-24 | Microbulifer degradans 2-40 | COG2303: Choline dehydrogenase and related flavoproteins [Microbulifer degradans 2-40] | | | | 1.-.- |
| 24975, | | | | | | | | | |
| 24976 | 46140301 | 47 | 5.00E-61 | Dechloromonas aromatica RCB | COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Dechloromonas aromatica RCB] | | | | 2.7.3.- |
| 24977, | | | | | | | | | |
| 24978 | 48845156 | 43 | 2.00E-62 | Geobacter metallireducens GS-15 | COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Geobacter metallireducens GS-15] | | | | 2.7.3.- |
| 24983, | | | | | | | | | |
| 24984 | 29345890 | 30 | 8.00E-28 | Bacteroides thetaiotaomicron VPI-5482 | glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.8.6 |
| 24985, | | | | | | | | | |
| 24986 | 46142542 | 36 | 3.00E-19 | Methanococcoides burtonii DSM 6242 | COG0367: Asparagine synthase (glutamine-hydrolyzing) [Methanococcoides burtonii DSM 6242] | | | | 6.3.5.4 |
| 24987, | | | | | | | | | |
| 24988 | 29346171 | 32 | 1.00E-47 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0761 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75868.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |

| | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|----------|
| 24989, | 29346171 | 30 | 3.00E-31 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0761 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75868.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 24990 | | | | | | | | |
| 2499, | 46401879 | 34 | 2.00E-11 | Bacteriophage T5 | putative prohead protease [Bacteriophage T5] | | | |
| 2500 | | | | | | | | |
| 24991, | | | | | type I restriction-modification system, M subunit, putative [Shewanella | | | |
| 24992 | 24373032 | 40 | 1.00E-45 | Shewanella oneidensis MR-1 | oneidensis MR-1 gb AAN54519.1 type I restriction-modification system, M subunit, putative [Shewanella oneidensis MR-1] | | | 2.1.1.72 |
| | | | | | type I restriction-modification system, M subunit, putative [Shewanella | | | |
| 24993, | | | | | oneidensis MR-1 gb AAN54519.1 type I restriction-modification system, M | | | |
| 24994 | 24373032 | 36 | 1.00E-52 | Shewanella oneidensis MR-1 | subunit, putative [Shewanella oneidensis MR-1] | | | 2.1.1.72 |
| 24995, | | | | | COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga | | | |
| 24996 | 48854243 | 34 | 2.00E-10 | Cytophaga hutchinsonii | hutchinsonii] | | | |
| | | | | | transcription regulator [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 24997, | | | | | gb AAO77449.1 transcription regulator [Bacteroides thetaiotaomicron VPI- | | | |
| 24998 | 29347752 | 26 | 2.00E-09 | Bacteroides thetaiotaomicron VPI-5482 | 5482] | | | |
| | | | | | | | | |
| 24999, | | | | | COG3604: Transcriptional regulator containing GAF, AAA-type ATPase, and | | | |
| 25000 | 48845094 | 54 | 2.00E-72 | Geobacter metallireducens GS-15 | DNA binding domains [Geobacter metallireducens GS-15] | | | |
| | | | | | hypothetical protein Bd1537 [Bdellovibrio bacteriovorus HD100] | | | |
| 25, | 42523044 | 34 | 5.00E-37 | Bdellovibrio bacteriovorus HD100 | emb CAE79417.1 hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100] | | | |
| 25001, | | | | | | | | |
| 25002 | 48855252 | 31 | 2.00E-14 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 25003, | | | | | | | | |
| 25004 | 48831933 | 29 | 1.00E-16 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 25007, | | | | | ATP-dependent protease [Bacteroides fragilis YCH46] db BAD49051.1 ATP | | | 3.4.21.5 |
| 25008 | 53713593 | 59 | 6.00E-85 | Bacteroides fragilis YCH46 | dependent protease [Bacteroides fragilis YCH46] | | | 3 |
| 25009, | | | | | COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga | | | 3.4.21.5 |
| 25010 | 48853586 | 46 | 1.00E-10 | Cytophaga hutchinsonii | hutchinsonii] | | | 3 |
| | | | | | Superfamily I DNA and RNA helicase [Methanosarcina mazel Go1] | | | |
| 2501, | | | | | gb AAM29724.1 Superfamily I DNA and RNA helicase [Methanosarcina | | | |
| 2502 | 21226130 | 34 | 1.00E-20 | Methanosarcina mazel Go1 | mazel Goe1] | | | 3.6.1.- |
| | | | | | | | | |
| 25011, | | | | | uncultured gamma | | | |
| 25012 | 47779387 | 41 | 1.00E-50 | proteobacterium eBACHOT4E07 | predicted HsdR [uncultured gamma proteobacterium eBACHOT4E07] | | | 3.1.21.3 |
| 25015, | | | | | COG0046: Phosphoribosylformylglycinamide (FGAM) synthase, | | | |
| 25016 | 48853770 | 71 | 2.00E-88 | Cytophaga hutchinsonii | synthetase domain [Cytophaga hutchinsonii] | | | 6.3.5.3 |

| | | | | | | | | | |
|--------|----------|----|-----------|----------------------------------|--|---|----|----------|---------|
| 25017, | 34398448 | 61 | 1.00E-106 | Porphyrromonas gingivalis W83 | phosphoribosylformylglycinamide synthase, putative [Porphyrromonas gingivalis W83] ref NP_904615.1 phosphoribosylformylglycinamide synthase, putative [Porphyrromonas gingivalis W83] | Bacteroides thetaiotaomicron VPI-5482, section 8 of 21 of the complete genome | 92 | 1.00E-08 | 6.3.5.3 |
| 25018, | 48853326 | 47 | 7.00E-21 | Cytophaga hutchinsonii | COG1485: Predicted ATPase [Cytophaga hutchinsonii] | | | | |
| 25019, | | | | Bdellovibrio | | | | | |
| 25020, | 42523322 | 24 | 1.00E-11 | bacteriovorus HD100 | oxaloductase [Bdellovibrio bacteriovorus HD100] emb CAE79695.1 oxaloductase [Bdellovibrio bacteriovorus HD100] | | | | |
| 25023, | | | | Bdellovibrio | | | | | |
| 25024, | 42523322 | 29 | 1.00E-11 | bacteriovorus HD100 | oxaloductase [Bdellovibrio bacteriovorus HD100] emb CAE79695.1 oxaloductase [Bdellovibrio bacteriovorus HD100] | | | | |
| 25025, | | | | Bacteroides fragilis | putative DNA mismatch repair protein [Bacteroides fragilis YCH46] dbj BAD50625.1 putative DNA mismatch repair protein [Bacteroides fragilis YCH46] | | | | |
| 25026, | 53715167 | 37 | 4.00E-16 | Bacteroides fragilis YCH46 | putative DNA mismatch repair protein [Bacteroides fragilis YCH46] dbj BAD50625.1 putative DNA mismatch repair protein [Bacteroides fragilis YCH46] | | | | |
| 25027, | | | | Nostoc sp. PCC 7120 | hypothetical protein alr7052 [Nostoc sp. PCC 7120] dbj BAB78136.1 alr7052 [Nostoc sp. PCC 7120] pir AD2484 hypothetical protein alr7052 [Imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha | | | | |
| 25028, | 17233068 | 28 | 4.00E-07 | uncultured cyanobacterium | putative transposase [uncultured cyanobacterium] pir S16892 probable transposase (insertion sequence IS702) - Calothrix sp. (PCC 7601) sp Q00462 T702_FREDI Probable transposase for insertion sequence element IS702 | | | | |
| 25031, | 581004 | 43 | 3.00E-24 | uncultured cyanobacterium | putative transposase [uncultured cyanobacterium] pir S16892 probable transposase (insertion sequence IS702) - Calothrix sp. (PCC 7601) sp Q00462 T702_FREDI Probable transposase for insertion sequence element IS702 | | | | |
| 25032, | | | | uncultured cyanobacterium | putative transposase [uncultured cyanobacterium] pir S16892 probable transposase (insertion sequence IS702) - Calothrix sp. (PCC 7601) sp Q00462 T702_FREDI Probable transposase for insertion sequence element IS702 | | | | |
| 25033, | 581004 | 43 | 3.00E-24 | Cytophaga hutchinsonii | COG1196: Chromosome segregation ATPases [Cytophaga hutchinsonii] | | | | |
| 25034, | 48854028 | 38 | 5.00E-36 | Burkholderia | | | | | |
| 25037, | | | | capacia R18194 | hypothetical protein Bcep03007254 [Burkholderia cepacia R18194] putative flagellar motor protein MotB [Bacteroides thetaiotaomicron VPI- 5482] gb AA078235.1 putative flagellar motor protein MotB [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 25038, | 46310883 | 36 | 4.00E-26 | Bacteroides thetaiotaomicron | | | | | |
| 25045, | | | | VPI-5482 | | | | | |
| 25046, | 29348538 | 30 | 6.00E-34 | Microbulifer | COG0784: FOG: CheY-like receiver [Microbulifer degradans 2-40] | | | | 2.7.3.- |
| 25047, | | | | degradans 2-40 | | | | | |
| 25048, | 48864200 | 27 | 9.00E-31 | | | | | | |
| 25049, | | | | | | | | | |
| 25050, | | | | | | | | | |

| | | | | | | | | |
|--------|----------|----|-----------|-------------------------------------|---|--|----|----------|
| 25053, | 15896323 | 40 | 2.00E-40 | Clostridium acetobutylicum ATCC 824 | Mannose-1-phosphate guanylyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK81012.1 Mannose-1-phosphate guanylyltransferase [Clostridium acetobutylicum ATCC 824] pir J97278 mannose-1-phosphate guanylyltransferase [imported] - Clostridium acetobutylicum | | | 2.7.7.22 |
| 25054, | 48838445 | 51 | 2.00E-59 | Methanosarcina barkeri str. fusaro | COG0696: Phosphoglyceromutase [Methanosarcina barkeri str. fusaro] | | | 5.4.2.1 |
| 25055, | 48855722 | 33 | 1.00E-09 | Cytophaga hutchinsonii | hypothetical protein Chut02000926 [Cytophaga hutchinsonii] | | | |
| 25056, | 17229681 | 39 | 2.00E-28 | Nostoc sp. PCC 7120 | regulatory protein [Nostoc sp. PCC 7120] dbj BAB73888.1 regulatory protein [Nostoc sp. PCC 7120] pir JAG2079 regulatory protein at2189 [imported] - Nostoc sp. (strain PCC 7120) | | | |
| 25057, | 18310182 | 43 | 1.00E-53 | Clostridium perfringens str. 13 | hypothetical protein CPE1200 [Clostridium perfringens str. 13] dbj BAB80906.1 hypothetical protein [Clostridium perfringens str. 13] | | | |
| 25058, | 48838061 | 86 | 1.00E-127 | Methanosarcina barkeri str. fusaro | COG3385: FOG: Transposase and inactivated derivatives [Methanosarcina barkeri str. fusaro] | | | |
| 25059, | 48854139 | 58 | 2.00E-51 | Cytophaga hutchinsonii | COG1066: Predicted ATP-dependent serine protease [Cytophaga hutchinsonii] | | 89 | 0 |
| 25060, | 20091497 | 60 | 1.00E-49 | Methanosarcina acetivorans C2A | inorganic pyrophosphatase [Methanosarcina acetivorans C2A] gb AAM06052.1 inorganic pyrophosphatase [Methanosarcina acetivorans str. C2A] sp Q8TMI3 PYR_METAC inorganic pyrophosphatase | | | 3.6.1.1 |
| 25061, | 53712258 | 53 | 1.00E-57 | Bacteroides fragilis YCH46 | (Pyrophosphate phospho-hydrolase) (PPase) peptidyl-dipeptidase [Bacteroides fragilis YCH46] dbj BAD47716.1 peptidyl-dipeptidase [Bacteroides fragilis YCH46] | | | 3.4.15.5 |
| 25062, | 53712055 | 34 | 2.00E-15 | Bacteroides fragilis YCH46 | putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46] | | | |
| 25063, | 48854967 | 54 | 4.00E-24 | Cytophaga hutchinsonii | COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 25064, | 13476784 | 32 | 1.00E-09 | Mesorhizobium loti MAFF303099 | transcriptional regulator [Mesorhizobium loti MAFF303099] dbj BAB53814.1 transcriptional regulator [Mesorhizobium loti MAFF303099] | | | |
| 25065, | 30019270 | 31 | 2.00E-33 | Bacillus cereus ATCC 14579 | Transcriptional regulator, AraC family [Bacillus cereus ATCC 14579] gb AAP08102.1 Transcriptional regulator, AraC family [Bacillus cereus ATCC 14579] | | | 2.1.1.63 |
| 25066, | 28974569 | 52 | 5.00E-60 | Pseudomonas sp. Y2 | putative ring-oxidation complex protein 5 [Pseudomonas sp. Y2] | | | 1.6.99.7 |
| 25067, | 48853628 | 49 | 4.00E-34 | Cytophaga hutchinsonii | COG0006: Xaa-Pro aminopeptidase [Cytophaga hutchinsonii] | | | 3.4.11.9 |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|--|--|----|---------------|
| 25093, 25094 | 48854571 | 63 | 2.00E-59 | Cytophaga hutchinsonii | COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Cytophaga hutchinsonii] | | | 2.4.1.- |
| 25095, 25096 | 22094897 | 48 | 1.00E-41 | Flavobacterium johnsoniae | MurF [Flavobacterium johnsoniae] | | | 6.3.2.15 |
| 25097, 25098 | 48856302 | 54 | 1.00E-12 | Cytophaga hutchinsonii | COG1396: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 25099, 25100 | 29349623 | 46 | 2.00E-28 | Bacteroides thetataoamicon VPI-5482 | shikimate 5-dehydrogenase [Bacteroides thetataoamicon VPI-5482] gb AAO79320.1 shikimate 5-dehydrogenase [Bacteroides thetataoamicon VPI-5482] | | | 1.1.1.25 |
| 251, 252 | 53712013 | 50 | 7.00E-29 | Bacteroides fragilis YCH46 | putative ATP/GTP hydrolase [Bacteroides fragilis YCH46] dbj BAD47471.1 putative ATP/GTP hydrolase [Bacteroides fragilis YCH46] | | | |
| 25101, 25102 | 53711995 | 48 | 1.00E-25 | Bacteroides fragilis YCH46 | hypothetical protein BF0706 [Bacteroides fragilis YCH46] dbj BAD47453.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | 3.1.- |
| 25103, 25104 | 48853536 | 45 | 4.00E-24 | Cytophaga hutchinsonii | COG1619: Uncharacterized proteins, homologs of microcin C7 resistance protein MccF [Cytophaga hutchinsonii] | | | 3.4.17.1 3 |
| 25105, 25106 | 53711995 | 48 | 1.00E-25 | Bacteroides fragilis YCH46 | hypothetical protein BF0706 [Bacteroides fragilis YCH46] dbj BAD47453.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | 3.1.- |
| 25107, 25108 | 23508812 | 36 | 2.00E-07 | Plasmodium falci-parum 3D7 | hypothetical protein PFL0575w [Plasmodium falci-parum 3D7] gb AAN36204.1 hypothetical protein PFL0575w [Plasmodium falci-parum 3D7] | | | |
| 25109, 25110 | 23508812 | 36 | 2.00E-07 | Plasmodium falci-parum 3D7 | hypothetical protein PFL0575w [Plasmodium falci-parum 3D7] gb AAN36204.1 hypothetical protein PFL0575w [Plasmodium falci-parum 3D7] | | | |
| 2511, 2512 | 53712708 | 40 | 1.00E-60 | Bacteroides fragilis YCH46 | hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 25111, 25112 | 48853940 | 53 | 5.00E-62 | Cytophaga hutchinsonii | COG0036: Pentose-5-phosphate-3-epimerase [Cytophaga hutchinsonii] | | | 5.1.3.1 |
| 25113, 25114 | 57471283 | 91 | 1.00E-101 | Flavobacterium johnsoniae | RpoD [Flavobacterium johnsoniae] | Treponema denticola ATCC 35405, section 4 of 10 of the complete genome | 94 | 3.00E-11 |
| 25117, 25118 | 53728512 | 35 | 2.00E-39 | Haemophilus sommus 2336 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Haemophilus sommus 2336] | | | 2.4.1.- |
| 25119, 25120 | 53712106 | 45 | 5.00E-11 | Bacteroides fragilis YCH46 | probable glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD47564.1 probable glycosyltransferase [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 25123, 25124 | 15895588 | 40 | 2.00E-07 | Clostridium acetobutylicum ATCC 824 | Predicted glycosyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK80277.1 Predicted glycosyltransferase [Clostridium acetobutylicum ATCC 824] pir B97186 probable glycosyltransferase CAC2321 [imported] - Clostridium acetobutylicum | | | | |
| 25127, 25128 | 53711566 | 22 | 7.00E-07 | Bacteroides fragilis YCH46 | RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD47024.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] | | | | |
| 2513, 2514 | 46317628 | 28 | 2.00E-12 | Burkholderia cepacia R18194 | COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Burkholderia cepacia R18194] | | | | |
| 25131, 25132 | 53732951 | 27 | 1.00E-18 | Haemophilus influenzae R2846 | COG0842: Signal transduction histidine kinase [Haemophilus influenzae R2846] | | | | |
| 25133, 25134 | 41690757 | 97 | 2.00E-34 | Psychrobacter sp. 273-4 | COG2975: Uncharacterized protein conserved in bacteria [Psychrobacter sp. 273-4] | | | | |
| 25135, 25136 | 41690757 | 97 | 2.00E-34 | Psychrobacter sp. 273-4 | COG2975: Uncharacterized protein conserved in bacteria [Psychrobacter sp. 273-4] | | | | |
| 25137, 25138 | 54302404 | 31 | 4.00E-21 | Photobacterium profundum SS9 | hypothetical protein PBPRB0725 [Photobacterium profundum SS9] emb CAG22597.1 hypothetical protein [Photobacterium profundum] | | | | |
| 25139, 25140 | 45656536 | 28 | 3.00E-14 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC10638 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69259.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 25145, 25146 | 23097681 | 30 | 6.00E-16 | Oceanobacillus ihayensis HTE831 | mevalonate diphosphate decarboxylase [Oceanobacillus ihayensis HTE831] dbj BAC12182.1 mevalonate diphosphate decarboxylase [Oceanobacillus ihayensis HTE831] | | | | 4.1.1.33 |
| 25147, 25148 | 45357986 | 29 | 2.00E-14 | Methanococcus maripaludis S2 | hypothetical protein MMP0423 [Methanococcus maripaludis S2] emb CAF29979.1 hypothetical [Methanococcus maripaludis S2] | | | | |
| 25149, 25150 | 46100870 | 37 | 5.00E-08 | Ustilago maydis 521 | hypothetical protein UM05700.1 [Ustilago maydis 521] ref XP_403315.1 hypothetical protein UM05700.1 [Ustilago maydis 521] | | | | |
| 25151, 25152 | 29345677 | 37 | 2.00E-40 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase/response regulator, hybrid (one component system) [Bacteroides thetaiotaomicron VPI-5482] gb AAO75374.1 two-component system sensor histidine kinase/response regulator, hybrid (one component system) [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|----------|--|--|--|
| 25153, 25154 | 15902916 | 33 | 1.00E-24 | Streptococcus pneumoniae R6 | Formamidopyrimidine-DNA glycosylase [Streptococcus pneumoniae R6] gb AAK99676.1 Formamidopyrimidine-DNA glycosylase [Streptococcus pneumoniae R6] sp Q8DQ33 FPG_STRR6 Formamidopyrimidine-DNA glycosylase (Fapy-DNA glycosylase) (DNA-(apurinic or apyrimidinic site) lyase mutM) (AP lyase mutM) pir H97980 DNA-formamidopyrimidine glycosylase (EC 3.2.2.23) [imported] - Streptococcus pneumoniae (strain R6) | 3.2.2.23 | | | |
| 25155, 25156 | 15902916 | 34 | 3.00E-20 | Streptococcus pneumoniae R6 | Formamidopyrimidine-DNA glycosylase [Streptococcus pneumoniae R6] gb AAK99676.1 Formamidopyrimidine-DNA glycosylase [Streptococcus pneumoniae R6] sp Q8DQ33 FPG_STRR6 Formamidopyrimidine-DNA glycosylase (Fapy-DNA glycosylase) (DNA-(apurinic or apyrimidinic site) lyase mutM) (AP lyase mutM) pir H97980 DNA-formamidopyrimidine glycosylase (EC 3.2.2.23) [imported] - Streptococcus pneumoniae (strain R6) | 3.2.2.23 | | | |
| 25157, 25158 | 15894287 | 34 | 2.00E-19 | Clostridium acetobutylicum ATCC 824 | Uncharacterized protein, homolog of yhfF B. subtilis [Clostridium acetobutylicum ATCC 824] gb AAK78976.1 Uncharacterized protein, homolog of yhfF B. subtilis [Clostridium acetobutylicum ATCC 824] pir E97023 uncharacterized protein, homolog of yhfF B. subtilis [imported] - Clostridium acetobutylicum | | | | |
| 25161, 25162 | 48855355 | 31 | 8.00E-42 | Cytophaga hutchinsonii | COG4796: Type II secretory pathway, component HofQ [Cytophaga hutchinsonii] | | | | |
| 25163, 25164 | 56459804 | 34 | 3.00E-26 | Idiomarina loihensis L2TR | Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR] | | | | |
| 25165, 25166 | 56459804 | 33 | 2.00E-23 | Idiomarina loihensis L2TR | Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR] | | | | |
| 25167, 25168 | 49478685 | 37 | 3.00E-30 | Bacillus thuringiensis serovar konkukian str. 97-27 | pseudouridylylase synthase [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAAT60887.1 pseudouridylylase synthase [Bacillus thuringiensis serovar konkukian str. 97-27] | 4.2.1.70 | | | |
| 25173, 25174 | 53715188 | 39 | 1.00E-08 | Bacteroides fragilis YCH46 | putative chloride channel protein [Bacteroides fragilis YCH46] dbj BAD50646.1 putative chloride channel protein [Bacteroides fragilis YCH46] | | | | |
| 25175, 25176 | 48892234 | 58 | 1.00E-29 | Trichodesmium erythraeum IMS101 | COG1132: ABC-type multidrug transport system, ATPase and permease components [Trichodesmium erythraeum IMS101] | 3.4.21.- | | | |
| 25177, 25178 | 48856952 | 44 | 2.00E-36 | Cytophaga hutchinsonii | COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii] | 4.1.3.27 | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|----|----------|----------|
| 25179, 25180 | 56460975 | 36 | 5.00E-26 | Idiomarina loihlensis L2TR | hypothetical protein IL1875 [Idiomarina loihlensis L2TR] gb AAV82707.1 Uncharacterized conserved protein [Idiomarina loihlensis L2TR] | | | | |
| 25187, 25188 | 53715101 | 31 | 2.00E-19 | Bacteroides fragilis YCH46 | hypothetical protein BF3817 [Bacteroides fragilis YCH46] dbj BAD50559.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 25191, 25192 | 53711382 | 55 | 3.00E-73 | Bacteroides fragilis YCH46 | DNA polymerase I [Bacteroides fragilis YCH46] dbj BAD46840.1 DNA polymerase I [Bacteroides fragilis YCH46] | | | | 2.7.7.7 |
| 25193, 25194 | 53711382 | 42 | 2.00E-67 | Bacteroides fragilis YCH46 | DNA polymerase I [Bacteroides fragilis YCH46] dbj BAD46840.1 DNA polymerase I [Bacteroides fragilis YCH46] | | | | 2.7.7.7 |
| 25199, 25200 | 48855224 | 36 | 4.00E-12 | Cytophaga hutchinsonii | COG0010: Arginase/agmatinase/formimionoglutamate hydrolase, arginase family [Cytophaga hutchinsonii] | | | | |
| 25201, 25202 | 29606128 | 39 | 2.00E-16 | Streptomyces avermitilis MA-4680 | hypothetical protein [Streptomyces avermitilis MA-4680] ref NP_823656.1 hypothetical protein SAV2480 [Streptomyces avermitilis MA-4680] | | | | |
| 25203, 25204 | 28900996 | 65 | 8.00E-40 | Vibrio parahaemolyticus RIMD 2210633 | gamma-carboxymuconolactone decarboxylase [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62484.1 gamma-carboxymuconolactone decarboxylase [Vibrio parahaemolyticus] | | | | 4.1.1.44 |
| 25207, 25208 | 53714372 | 49 | 2.00E-27 | Bacteroides fragilis YCH46 | hypothetical protein BF3085 [Bacteroides fragilis YCH46] dbj BAD49830.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 25209, 25210 | 53714371 | 63 | 1.00E-67 | Bacteroides fragilis YCH46 | putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] dbj BAD49829.1 putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] | | | | |
| 25211, 25212 | 48854073 | 44 | 2.00E-58 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] putative transcriptional regulator [Bacteroides fragilis YCH46] | | | | 2.7.3.- |
| 25213, 25214 | 53715260 | 52 | 2.00E-33 | Bacteroides fragilis YCH46 | dbj BAD50718.1 putative transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 25215, 25216 | 38195402 | 48 | 8.00E-25 | Flavobacterium johnsoniae | GidI [Flavobacterium johnsoniae] | | | | |
| 25219, 25220 | 48853532 | 31 | 1.00E-16 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | | |
| 25227, 25228 | 48855336 | 71 | 9.00E-57 | Cytophaga hutchinsonii | | Desc:Haemophilus influenzae complete genome sequence. Org:Haemophilus influenzae | 86 | 3.00E-07 | 6.1.1.22 |
| 25229, 25230 | 29348988 | 47 | 3.00E-56 | Bacteroides thetalaotomicron VPI-5482 | COG0017: Aspartyl/asparaglyl-tRNA synthetases [Cytophaga hutchinsonii] topoisomerase IV subunit A [Bacteroides thetalaotomicron VPI-5482] gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetalaotomicron VPI-5482] | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|---------------|
| 2523, 2524 | 34396289 | 39 | 9.00E-19 | Porphyrionas gingivalis W83 | conserved domain protein [Porphyrionas gingivalis W83] ref NP_904457.1 hypothetical protein PG0113 [Porphyrionas gingivalis W83] | | | |
| 25231, 25232 | 53714264 | 61 | 8.00E-65 | Bacteroides fragilis YCH46 | folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46] | | | 6.3.2.17 |
| 25233, 25234 | 53711292 | 62 | 2.00E-52 | Bacteroides fragilis YCH46 | tRNA/rRNA methyltransferase [Bacteroides fragilis YCH46] dbj BAD48750.1 tRNA/rRNA methyltransferase [Bacteroides fragilis YCH46] | | | 2.1.1.- |
| 25235, 25236 | 29348700 | 29 | 2.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3291 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78397.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 25237, 25238 | 46156085 | 27 | 1.00E-10 | Haemophilus sommus 2336 | COG3298: Predicted 3'-5' exonuclease related to the exonuclease domain of PolB [Haemophilus somnus 2336] | | | |
| 25239, 25240 | 48854571 | 58 | 4.00E-51 | Cytophaga hutchinsonii | COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Cytophaga hutchinsonii] | | | 2.4.1.- |
| 25241, 25242 | 34397452 | 22 | 8.00E-12 | Porphyrionas gingivalis W83 | type I restriction-modification system, M subunit, putative [Porphyrionas gingivalis W83] ref NP_905615.1 type I restriction-modification system, M subunit, putative [Porphyrionas gingivalis W83] | | | |
| 25243, 25244 | 54302903 | 60 | 6.00E-45 | Photobacterium profundum SS9 | putative transcriptional regulator [Photobacterium profundum SS9] emb CAG23096.1 putative transcriptional regulator [Photobacterium profundum] | | | |
| 25245, 25246 | 46446568 | 43 | 1.00E-42 | Parachlamydia sp. UWE25 | hypothetical protein pc0934 [Parachlamydia sp. UWE25] emb CAF23658.1 conserved hypothetical protein [Parachlamydia sp. UWE25] | | | 5.4.2.6 |
| 25247, 25248 | 48862250 | 68 | 4.00E-35 | Microbulbifer degradans 240 | COG0386: Glutathione peroxidase [Microbulbifer degradans 240] | | | 1.11.1.9 |
| 25251, 25252 | 50364936 | 41 | 1.00E-10 | Mesoplasma florum L1 | deoxyribose-phosphate aldolase [Mesoplasma florum L1] gb AAT75477.1 deoxyribose-phosphate aldolase [Mesoplasma florum L1] | | | 4.1.2.4 |
| 25255, 25256 | 15608643 | 47 | 9.00E-50 | Mycobacterium tuberculosis H37Rv | hypothetical protein Rv1505c [Mycobacterium tuberculosis H37Rv] ref NP_855195.1 hypothetical protein Mb1543c [Mycobacterium bovis AF2122/97] pir D70713 hypothetical protein Rv1505c - Mycobacterium tuberculosis (strain H37Rv) emb CAB02019.1 CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv] emb CAD96210.1 CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium bovis AF2122/97] | | | 2.3.1.11 7 |
| 25257, 25258 | 53715360 | 40 | 2.00E-27 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50818.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] | | | 3.6.1.- |

| | | | | | | | | | |
|--------|----------|----|----------|------------------------|---|--|--|--|----------|
| 25259, | 48854804 | 51 | 1.00E-70 | Cytophaga hutchinsonii | COG0661: Predicted unusual protein kinase [Cytophaga hutchinsonii] | | | | |
| 25260 | | | | | hypothetical protein DP0077 [Desulfotalea psychrophila LSV54] | | | | |
| 25261, | | | | Desulfotalea | emb[CAG34806.1] conserved hypothetical protein [Desulfotalea | | | | |
| 25262 | 51243929 | 56 | 3.00E-65 | psychrophila LSV54 | psychrophila LSV54] | | | | |
| | | | | | c-di-GMP phosphodiesterase A-related protein [Vibrio cholerae O1 biovar | | | | |
| 25263, | | | | Vibrio cholerae O1 | eltor str. N16961] ref[NP_230302.1] c-di-GMP phosphodiesterase A-related | | | | |
| 25264 | 9655090 | 43 | 4.00E-19 | N16961 | protein [Vibrio cholerae O1 biovar eltor str. N16961] pir[H82296 c-di-GMP | | | | |
| 25265, | | | | | phosphodiesterase A-related protein VC0653 [imported] - Vibrio cholerae | | | | |
| 25266 | 48856860 | 40 | 5.00E-23 | Cytophaga hutchinsonii | (strain N16961 serogroup O1) | | | | |
| 25267, | | | | uncultured | COG0781: Transcription termination factor [Cytophaga hutchinsonii] | | | | |
| 25268 | 40062908 | 40 | 9.00E-42 | bacterium 442 | metallo-beta-lactamase family protein [uncultured bacterium 442] | | | | 3.-.-.- |
| | | | | Bacillus | | | | | |
| 25269, | | | | thermoamyloliquefa | | | | | |
| 25270 | 13027221 | 33 | 9.00E-32 | ciens | alpha-glucosidase III [Bacillus thermoamyloliquefaciens] | | | | 3.2.1.20 |
| 2527, | | | | | | | | | |
| 2528 | 48854564 | 53 | 5.00E-67 | Cytophaga hutchinsonii | COG0745: Response regulators consisting of a CheY-like receiver domain | | | | |
| 25271, | | | | | and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 25272 | 48856559 | 37 | 9.00E-25 | Cytophaga hutchinsonii | COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga | | | | |
| 25273, | | | | Methanosarcina | hutchinsonii] | | | | |
| 25274 | 21227229 | 29 | 8.00E-08 | mazei Go1 | glycosyltransferase [Methanosarcina mazei Go1] gb[AAM30823.1] | | | | |
| | | | | | glycosyltransferase [Methanosarcina mazei Goe1] | | | | |
| 25281, | | | | Chromobacterium | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] | | | | |
| 25282 | 34101691 | 41 | 2.00E-20 | violaceum ATCC 12472 | ref[NP_900051.1] hypothetical protein CV0381 [Chromobacterium violaceum | | | | |
| | | | | Clostridium | ATCC 12472] | | | | |
| 25285, | | | | thermocellum | COG4585: Signal transduction histidine kinase [Clostridium thermocellum | | | | |
| 25286 | 48860369 | 30 | 9.00E-24 | ATCC 27405 | ATCC 27405] | | | | 2.7.3.- |
| 25289, | | | | Bacteroides | TraG-like [Bacteroides thetaiotaomicron] ref[NP_818964.1] TraG-like protein | | | | |
| 25290 | 29335925 | 32 | 2.00E-35 | thetaiotaomicron | [Bacteroides thetaiotaomicron] | | | | |
| | | | | | | | | | |
| 25293, | | | | Bacteroides fragilis | hypothetical protein BF2394 [Bacteroides fragilis YCH46] dbj[BAD49143.1] | | | | |
| 25294 | 53713685 | 52 | 8.00E-37 | YCH46 | conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 25295, | | | | | | | | | |
| 25296 | 48855491 | 40 | 2.00E-17 | Cytophaga hutchinsonii | hypothetical protein Chut02001830 [Cytophaga hutchinsonii] | | | | |

| | | | | | | | |
|-------------------------------------|----------------------|----------|----------------------|--|--|---|----------|
| 25297, 25298, 25299, 25300 | 29349770 48855551 | 66 37 | 4.00E-92 3.00E-21 | Bacteroides thetaiotaomicron VPI-5482 Cytophaga hutchinsonii | preprotein translocase SecA subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO79467.1 preprotein translocase SecA subunit [Bacteroides thetaiotaomicron VPI-5482] COG3569: Topoisomerase IB [Cytophaga hutchinsonii] hypothetical protein NE1380 [Nitrosomonas europaea ATCC 19718] emb CAD85291.1 hypothetical protein [Nitrosomonas europaea ATCC 19718] hypothetical protein BT4349 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79454.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] COG1132: ABC-type multidrug transport system, ATPase and permease components [Cytophaga hutchinsonii] hypothetical protein Chut02000915 [Cytophaga hutchinsonii] Predicted membrane protein [Vibrio vulnificus CMCP6] gb AAO08140.1 Predicted membrane protein [Vibrio vulnificus CMCP6] PREDICTED: similar to 3-mercaptopyruvate sulfurtransferase [Canis familiaris] iron(III) ABC transporter, ATP-binding protein, putative [Chlorobium tepidum TLS] gb AAM71658.1 iron(III) ABC transporter, ATP-binding protein, putative [Chlorobium tepidum TLS] | Bacteroides thetaiotaomicron VPI-5482, section 20 of 21 of the complete genome 83 1.00E-11 | |
| 25301, 25302 | 30249356 | 40 | 4.00E-09 | Nitrosomonas europaea ATCC 19718 | | | |
| 25307, 25308 | 29349757 | 31 | 2.00E-10 | Bacteroides thetaiotaomicron VPI-5482 | | | |
| 25309, 25310 | 48855938 | 40 | 4.00E-49 | Cytophaga hutchinsonii | | | |
| 25311, 25312 | 48855711 | 34 | 6.00E-22 | Cytophaga hutchinsonii | | | |
| 25317, 25318 | 27367623 | 42 | 3.00E-22 | Vibrio vulnificus CMCP6 | | | |
| 25321, 25322 | 57092777 | 35 | 3.00E-08 | Canis familiaris | | | 2.8.1.2 |
| 25323, 25324 | 21673251 | 46 | 4.00E-40 | Chlorobium tepidum TLS | | | 1.8.-.- |
| 25325, 25326 | 19879252 | 65 | 5.00E-89 | Flavobacterium johnsoniae | | Flavobacterium johnsoniae beta-lactamase JOHN-1 (blaJOHN-1), hypothetical primosomal replication factor Y, hypothetical pseudouridine synthase, and hypothetical transcription regulator protein genes, complete cds 84 1.00E-07 4.2.1.70 | |
| 25327, 25328 | 48854116 | 55 | 1.00E-65 | Cytophaga hutchinsonii | hypothetical pseudouridine synthase [Flavobacterium johnsoniae] COG1250: 3-hydroxyacyl-CoA dehydrogenase [Cytophaga hutchinsonii] | | 1.1.1.35 |

| | | | | | | | | | | | | |
|--------|----------|----|----------|--|--|---------------------------------|--|--|--|--|----------|--|
| 25329, | | | | | | Leptospira | TonB-dependent outer membrane hemin receptor [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69575.1 TonB-dependent outer membrane hemin receptor [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | | |
| 25330 | 45656852 | 38 | 4.00E-25 | | | Copenhageni str. Flocruz L1-130 | | | | | | |
| 25331, | | | | | | Cytophaga | COG3021: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | | |
| 25332 | 48853539 | 33 | 5.00E-33 | | | hutchinsonii | | | | | | |
| 25333, | | | | | | Erwinia carotovora | dTDP-4-dehydrohamnose reductase [Erwinia carotovora subsp. atroseptica SCR1043] emb CAG74350.1 dTDP-4-dehydrohamnose reductase | | | | 1.1.1.13 | |
| 25334 | 50120379 | 46 | 9.00E-50 | | | subsp. atroseptica SCR1043 | [Erwinia carotovora subsp. atroseptica SCR1043] | | | | 3 | |
| 25335, | | | | | | Clostridium | hypothetical protein CPE1460 [Clostridium perfringens str. 13] | | | | | |
| 25336 | 18310442 | 32 | 3.00E-20 | | | perfringens str. 13 | dbj BAB81166.1 hypothetical protein [Clostridium perfringens str. 13] | | | | | |
| 25337, | | | | | | Bacteroides | FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor) [Bacteroides thetaiotaomicron VPI-5482] gb AAO78946.1 FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor) [Bacteroides thetaiotaomicron VPI-5482] | | | | | |
| 25338 | 29349249 | 41 | 2.00E-29 | | | thetaitaomicron VPI-5482 | hypothetical protein STH2170 [Symbiobacterium thermophilum IAM 14863] dbj BAD41155.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863] | | | | | |
| 25339, | | | | | | Symbiobacterium | DNA-binding response regulator RprY [Porphyromonas gingivalis W83] | | | | 2.7.3.- | |
| 25340 | 51893308 | 26 | 4.00E-16 | | | thermophilum IAM 14863 | ref NP_905303.1 DNA-binding response regulator RprY [Porphyromonas gingivalis W83] | | | | | |
| 25341, | | | | | | Porphyromonas | hypothetical protein BT3618 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78723.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | | |
| 25342 | 34397138 | 51 | 5.00E-47 | | | gingivalis W83 | | | | | | |
| 25343, | | | | | | Bacteroides | | | | | | |
| 25344 | 29349026 | 40 | 2.00E-10 | | | thetaitaomicron VPI-5482 | | | | | | |
| 25345, | | | | | | Anabaena variabilis | hypothetical protein Avar03004767 [Anabaena variabilis ATCC 29413] | | | | | |
| 25346 | 53763669 | 27 | 8.00E-07 | | | ATCC 29413 | RNA methyltransferase [Bacteroides fragilis YCH46] dbj BAD49288.1 RNA methyltransferase [Bacteroides fragilis YCH46] | | | | 2.1.1.- | |
| 25347, | | | | | | Bacteroides fragilis | | | | | | |
| 25348 | 53713830 | 66 | 9.00E-83 | | | YCH46 | | | | | | |
| 25349, | | | | | | Escherichia coli | putative GlcNAc transferase [Escherichia coli] | | | | | |
| 25350 | 2586167 | 29 | 3.00E-14 | | | | | | | | | |
| 25351, | | | | | | Cytophaga | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | | 2.4.1.- | |
| 25352 | 48856222 | 22 | 4.00E-07 | | | hutchinsonii | | | | | | |
| 25353, | | | | | | Novosphingobium | hypothetical protein Saro02003107 [Novosphingobium aromaticivorans DSM 12444] | | | | | |
| 25354 | 48848300 | 35 | 9.00E-11 | | | aromaticivorans DSM 12444 | putative thioredoxin family protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78428.1 putative thioredoxin family protein [Bacteroides thetaiotaomicron VPI-5482] | | | | | |
| 25355, | | | | | | Bacteroides | | | | | | |
| 25356 | 29348731 | 36 | 2.00E-08 | | | thetaitaomicron VPI-5482 | | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|----|----------------|
| 25357, 25358 | 48854257 | 34 | 2.00E-22 | Cytophaga hutchinsonii | hypothetical protein Chui02002927 [Cytophaga hutchinsonii] | | | | |
| 25363, 25364 | 54024369 | 44 | 6.00E-22 | Nocardia farcinica IFM 10152 | putative acetyltransferase [Nocardia farcinica IFM 10152] dbj BAD57247.1 putative acetyltransferase [Nocardia farcinica IFM 10152] | | | | |
| 25365, 25366 | 29346516 | 66 | 1.00E-49 | Bacteroides thetaiotaomicron VPI-5482 | fructose-bisphosphate aldolase class I [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76213.1 fructose-bisphosphate aldolase class I [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.1.2.13 |
| 2537, 2538 | 21673456 | 34 | 2.00E-17 | Chlorobium tepidum TLS | transcriptional regulator, NusG/RfaH family [Chlorobium tepidum TLS] gb AAM71863.1 transcriptional regulator, NusG/RfaH family [Chlorobium tepidum TLS] | | | | |
| 25379, 25380 | 45658436 | 26 | 2.00E-17 | Leptospira interrogans serovar Copenhagen str. Flocruz L1-130 | alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhagen] str. Flocruz L1-130 ref NP_711250.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AAV48268.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AAS71159.1 alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhagen] str. Flocruz L1-130] | | | | |
| 25381, 25382 | 48854545 | 47 | 1.00E-19 | Cytophaga hutchinsonii | COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii] | | | | 2.1.1.- |
| 25383, 25384 | 56461428 | 39 | 2.00E-56 | Idiomarina loihensis L2TR | Dipeptidyl aminopeptidase [Idiomarina loihensis L2TR] gb AAV83160.1 Dipeptidyl aminopeptidase [Idiomarina loihensis L2TR] | | | | 3.4.14.- |
| 25387, 25388 | 48854949 | 28 | 4.00E-18 | Cytophaga hutchinsonii | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | | | | |
| 25389, 25390 | 48853612 | 38 | 4.00E-19 | Cytophaga hutchinsonii | COG1452: Organic solvent tolerance protein OstA [Cytophaga hutchinsonii] | | | | |
| 25397, 25398 | 46141605 | 62 | 2.00E-45 | Psychrobacter sp. 273-4 | hypothetical protein Pyc03000593 [Psychrobacter sp. 273-4] | | | | |
| 25399, 25400 | 46141620 | 59 | 3.00E-28 | Psychrobacter sp. 273-4 | COG3335: Transposase and inactivated derivatives [Psychrobacter sp. 273- 4] | | | | |
| 25401, 25402 | 56461359 | 68 | 7.00E-82 | Idiomarina loihensis L2TR | ABC-type multidrug transport system, ATPase component [Idiomarina loihensis L2TR] gb AAV83091.1 ABC-type multidrug transport system, ATPase component [Idiomarina loihensis L2TR] | | | 86 | 2.00E-22 1.8.- |
| 25403, 25404 | 1944167 | 35 | 7.00E-28 | Actinobacillus actinomycetemcomitans | unnamed protein product [Actinobacillus actinomycetemcomitans] | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|---|---|---|----|---|----------|
| 25409, | 48854730 | 49 | 5.00E-26 | Cytophaga hutchinsonii | COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii] | | | | |
| 25410 | | | | Mycobacteriophage Che9d | gp109 [Mycobacteriophage Che9d] ref NP_818074.1 gp109 | | | | |
| 2541, | 29425233 | 37 | 1.00E-09 | | [Mycobacteriophage Che9d] | | | | |
| 2542 | | | | Nostoc sp. PCC 7120 | regulatory protein [Nostoc sp. PCC 7120] dbj BAB73888.1 regulatory protein [Nostoc sp. PCC 7120] pir AG2079 regulatory protein alr2189 [imported] - Nostoc sp. (strain PCC 7120) | | | | 2.1.1.63 |
| 25411, | 17229681 | 30 | 5.00E-20 | | alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. 'Ames Ancestor'] ref YP_026463.1 alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. Sterne] ref NP_842740.1 alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. Ames] gb AAP24226.1 alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. Ames] | | | | |
| 25413, | | | | Bacillus anthracis str. 'Ames' | gb AAT29260.1 alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. 'Ames Ancestor'] gb AAT52514.1 alcohol dehydrogenase, zinc- containing [Bacillus anthracis str. Sterne] | | | | 1.1.1.1 |
| 25414 | 47525436 | 42 | 5.00E-31 | Ancestor' | | Moraxella sp. O245 insertion sequence IS1599, isolate O245 | 96 | 0 | |
| 25415, | | | | | transposase [Moraxella sp. O245] | | | | |
| 25416 | 28611027 | 95 | 1.00E-125 | Moraxella sp. O245 | COG5009: Membrane carboxypeptidase/penicillin-binding protein | | | | 2.4.2.- |
| 25417, | | | | Cytophaga hutchinsonii | [Cytophaga hutchinsonii] | | | | |
| 25418 | 48855155 | 39 | 2.00E-16 | | COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii] | | | | |
| 25419, | 48853613 | 37 | 2.00E-09 | Cytophaga hutchinsonii | putative type II restriction enzyme methylase subunit [Salmonella typhimurium LT2] gb AAL23313.1 putative type II restriction enzyme, methylase subunit [Salmonella typhimurium LT2] | | | | 3.1.21.4 |
| 25421, | | | | Salmonella typhimurium LT2 | | | | | |
| 25422 | 16767739 | 28 | 2.00E-22 | Thiobacillus denitrificans ATCC | COG0796: Glutamate racemase [Thiobacillus denitrificans ATCC 25259] | | | | 5.1.1.3 |
| 25423, | | | | | hypothetical protein BT2838 [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 25424 | 52007969 | 46 | 2.00E-13 | Bacteroides thetaitaomicron | gb AAO77944.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482] | | | | |
| 25425, | | | | | probable aminopeptidase [Rhodopirellula baetica SH 1] emb CAD78184.1 | | | | 3.4.11.- |
| 25426 | 29348247 | 29 | 2.00E-34 | VPI-5482 | probable aminopeptidase [Pirellula sp.] | | | | |
| 25427, | 32473409 | 38 | 8.00E-43 | Rhodopirellula baetica SH 1 | two-component response regulator [Bradyrhizobium japonicum USDA 110] | | | | 4.6.1.1 |
| 25428 | | | | (Bradyrhizobium japonicum USDA 110) | ref NP_904597.1 two-component response regulator [Bradyrhizobium japonicum USDA 110] | | | | |
| 25429, | 27377975 | 37 | 3.00E-32 | | conserved hypothetical protein [Porphyromonas gingivalis W83] | | | | |
| 25430 | | | | Porphyromonas gingivalis W83 | ref NP_904597.1 hypothetical protein PG0276 [Porphyromonas gingivalis W83] | | | | |
| 25433, | | | | | | | | | |
| 25434 | 34396430 | 37 | 2.00E-27 | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|----------|
| 25435, 25436 | 15669547 | 34 | 6.00E-42 | Methanocaldococcus jannaschii DSM 2661 | potassium channel protein, putative [Methanocaldococcus jannaschii DSM 2661] gb AAB99365.1 potassium channel protein, putative [Methanocaldococcus jannaschii DSM 2661] sp Q58752 MJ_K2_MET_JA | | | |
| 25437, 25438 | 53713469 | 64 | 2.00E-46 | Bacteroides fragilis YCH46 | Probable potassium channel protein 2 (MjK2) p I D64469 potassium channel homolog - Methanocaldococcus jannaschii | | | |
| 25439, 25440 | 9950580 | 36 | 9.00E-21 | Pseudomonas aeruginosa PAO1 | putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46] | | | 3.1.11.5 |
| 25441, 25442 | 48858490 | 41 | 2.00E-18 | Clostridium thermocellum ATCC 27405 | conserved hypothetical protein [Pseudomonas aeruginosa PAO1] ref ZP_00137838.2 COG3124: Uncharacterized protein conserved in bacteria [Pseudomonas aeruginosa UC8PP-PA14] p I A83102 conserved hypothetical protein PA4353 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253043.1 hypothetical protein PA4353 [Pseudomonas aeruginosa PAO1] | | | |
| 25443, 25444 | 34397809 | 65 | 1.00E-84 | Porphyromonas gingivalis W83 | COG3867: Arabinogalactan endo-1,4-beta-galactosidase [Clostridium thermocellum ATCC 27405] | | | |
| 25445, 25446 | 52078781 | 32 | 3.00E-41 | Bacillus licheniformis ATCC 14580 | GTP-binding protein HflX [Porphyromonas gingivalis W83] ref NP_905971.1 GTP-binding protein HflX [Porphyromonas gingivalis W83] | | | |
| 25449, 25450 | 53712371 | 31 | 1.00E-22 | Bacteroides fragilis YCH46 | penicillin-binding protein [Bacillus licheniformis ATCC 14580] gb AAU21934.1 penicillin-binding protein [Bacillus licheniformis ATCC 14580] ref YP_089980.1 hypothetical protein BLI00328 [Bacillus licheniformis ATCC 14580] gb AAU39287.1 putative protein [Bacillus licheniformis DSM 13] | | | |
| 2545, 2546 | 50119383 | 39 | 9.00E-13 | Erwinia carotovora subsp. atroseptica SCR11043 | hypothetical protein BF1079 [Bacteroides fragilis YCH46] dbj BAD47829.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 25451, 25452 | 48854288 | 55 | 9.00E-21 | Cytophaga hutchinsonii | hypothetical protein ECA0432 [Erwinia carotovora subsp. atroseptica SCR11043] emb CAG73347.1 conserved hypothetical protein [Erwinia carotovora subsp. atroseptica SCR11043] | | | |
| 25453, 25454 | 48845905 | 54 | 1.00E-72 | Geobacter metallireducens GS-15 | COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii] | | | |
| 25465, 25466 | 41689416 | 78 | 3.00E-54 | Psychrobacter sp. 273-4 | COG1640: 4-alpha-glucanotransferase [Geobacter metallireducens GS-15] | | | 2.4.1.25 |
| 25467, 25468 | 53711359 | 72 | 2.00E-72 | Bacteroides fragilis YCH46 | COG1393: Arsenate reductase and related proteins, glutaredoxin family [Psychrobacter sp. 273-4] | | | 1.--- |
| | | | | | tyrosyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD46817.1 tyrosyl-tRNA synthetase [Bacteroides fragilis YCH46] | | | 6.1.1.1 |

| | | | | | | | | | |
|-----------------|--------------|----|----------|---|---|--|--|--|----------|
| 25471, 25472 | 41408154 | 37 | 8.00E-19 | Mycobacterium avium subsp. paratuberculosis str. k10 | hypothetical protein MAP2056c [Mycobacterium avium subsp. paratuberculosis str. k10] gb AA04373.1 hypothetical protein MAP2056c [Mycobacterium avium subsp. paratuberculosis str. k10] | | | | |
| 25473, 25474 | 41408154 | 37 | 8.00E-19 | Mycobacterium avium subsp. paratuberculosis str. k10 | hypothetical protein MAP2056c [Mycobacterium avium subsp. paratuberculosis str. k10] gb AA04373.1 hypothetical protein MAP2056c [Mycobacterium avium subsp. paratuberculosis str. k10] | | | | |
| 25475, 25476 | 48856725 | 56 | 3.00E-72 | Cytophaga hutchinsonii | COG0159: Tryptophan synthase alpha chain [Cytophaga hutchinsonii] | | | | |
| 25477, 25478 | 48770125 | 37 | 3.00E-24 | Ralstonia metallidurans CH34 | COG0642: Signal transduction histidine kinase [Ralstonia metallidurans CH34] | | | | 2.7.3.- |
| 25479, 25480 | 48787591 | 36 | 4.00E-24 | Burkholderia fungorum LB400 | COG0210: Superfamily I DNA and RNA helicases [Burkholderia fungorum LB400] | | | | 3.6.1.- |
| 25483, 25484 | AAO2094 8 | 41 | 6.00E-45 | | Desc:Protein of the Bpm1 M1 methylase gene (Bpm1M1). Org: Bacillus pumilus | | | | |
| 25485, 25486 | 45157173 | 52 | 4.00E-76 | Escherichia coli | endonuclease [Escherichia coli] sp P25239 T257_ECOLI Type IIS restriction enzyme Eco57I (Endonuclease Eco57I) [Includes: Adenine-specific methyltransferase activity Eco57IA (M.Eco57IA)] | | | | 2.1.1.72 |
| 25487, 25488 | AAB6907 4 | 56 | 3.00E-84 | | Desc:Aquifex aeolicus VF5 1,4-alpha-glucan branching enzyme SEQ ID NO:1. Org:Aquifex aeolicus | | | | 2.4.1.18 |
| 25489, 25490 | 48854720 | 41 | 1.00E-45 | Cytophaga hutchinsonii | COG1559: Predicted periplasmic solute-binding protein [Cytophaga hutchinsonii] | | | | 4.-.-.- |
| 2549, 2550 | 53714487 | 56 | 9.00E-44 | Bacteroides fragilis YCH46 | SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD49945.1 SsrA- binding protein [Bacteroides fragilis YCH46] | | | | |
| 25491, 25492 | 34332880 | 56 | 2.00E-29 | Chromobacterium violaceum ATCC 12472 | probable transmembrane protein [Chromobacterium violaceum ATCC 12472] ref NP_903091.1 probable transmembrane protein [Chromobacterium violaceum ATCC 12472] | | | | |
| 25493, 25494 | 48863063 | 45 | 3.00E-29 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02001127 [Microbulbifer degradans 2-40] | | | | |
| 25495, 25496 | 48854920 | 36 | 6.00E-35 | Cytophaga hutchinsonii | COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Cytophaga hutchinsonii] | | | | 3.4.21.- |
| 255, 256 | 29346772 | 47 | 5.00E-18 | Bacteroides thetaiotaomicron VPI-5482 | flavoprotein [Bacteroides thetaiotaomicron VPI-5482] gb AA076489.1 flavoprotein [Bacteroides thetaiotaomicron VPI-5482] | | | | 6.3.2.5 |
| 25505, 25506 | 29654347 | 55 | 6.00E-27 | Coxiella burnetii RSA 493 | nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] gb AA090553.1 nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|--|--|--|--|----------|
| 25507, 25508 | 29654347 | 58 | 3.00E-43 | Coxiella burnetii RSA 493 | nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] gb AAO90553.1 nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] | | | | 2.4.2.11 |
| 25509, 25510 | 23099137 | 42 | 3.00E-10 | Oceanobacillus ihayensis HTE831 | cytochrome c biogenesis [Oceanobacillus ihayensis HTE831] dbj BAC13638.1 cytochrome c biogenesis (thiol:disulfide interchange protein) [Oceanobacillus ihayensis HTE831] | | | | |
| 2551, 2552 | 29349611 | 49 | 1.00E-22 | Bacteroides thetaiotaomicron VPI-5482 | tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79308.1 tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A018 MAA_BACTN tRNA delta(2)-isopentenylpyrophosphate transferase (IPP transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase) (IPTase) (IPT) | | | | 2.5.1.8 |
| 25511, 25512 | 23099137 | 42 | 3.00E-10 | Oceanobacillus ihayensis HTE831 | cytochrome c biogenesis [Oceanobacillus ihayensis HTE831] dbj BAC13638.1 cytochrome c biogenesis (thiol:disulfide interchange protein) [Oceanobacillus ihayensis HTE831] | | | | |
| 25513, 25514 | 48859742 | 31 | 3.00E-14 | Clostridium thermocellum ATCC 27405 | hypothetical protein Chte02000885 [Clostridium thermocellum ATCC 27405] | | | | |
| 25515, 25516 | 48859742 | 31 | 5.00E-29 | Clostridium thermocellum ATCC 27405 | hypothetical protein Chte02000885 [Clostridium thermocellum ATCC 27405] | | | | |
| 25517, 25518 | 48856112 | 40 | 2.00E-52 | Cytophaga hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 25519, 25520 | 48854446 | 42 | 2.00E-12 | Cytophaga hutchinsonii | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii] | | | | |
| 25521, 25522 | 56461337 | 27 | 2.00E-11 | Idiomarina lohiensis L2TR | Peptidase, M23/M37 family [Idiomarina lohiensis L2TR] gb AAV83069.1 Peptidase, M23/M37 family [Idiomarina lohiensis L2TR] | | | | |
| 25523, 25524 | 37528207 | 57 | 1.00E-102 | Photorhabdus luminescens subsp. laumondii TTO1 | glucose-6-phosphate isomerase (GPI) (phosphoglucose isomerase) (PGI) (phosphohexose isomerase) (PHI) [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16751.1 glucose-6-phosphate isomerase (GPI) (phosphoglucose isomerase) (PGI) (phosphohexose isomerase) (PHI) [Photorhabdus luminescens subsp. laumondii TTO1] | | | | 5.3.1.9 |
| 25525, 25526 | 29349609 | 29 | 4.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT4201 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79306.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 25527, 25528 | 48855337 | 54 | 2.00E-76 | Cytophaga hutchinsonii | COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii] | | | | |
| 2553, 2554 | 34396896 | 61 | 4.00E-48 | Porphyrromonas gingivalis W83 | polyA polymerase family protein [Porphyrromonas gingivalis W83] ref NP_905062.1 polyA polymerase family protein [Porphyrromonas gingivalis W83] | | | | 2.7.7.19 |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|----|----------|
| 25535, 25536 | 48854286 | 32 | 3.00E-30 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 25539, 25540 | 29347849 | 42 | 2.00E-34 | Bacteroides thetaiotaomicron VPI-5482 | beta-N-acetylglucosaminidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77546.1 beta-N-acetylglucosaminidase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 25541, 25542 | 29347849 | 42 | 6.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | beta-N-acetylglucosaminidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77546.1 beta-N-acetylglucosaminidase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 25543, 25544 | 48854034 | 33 | 3.00E-09 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |
| 2555, 2556 | 53712197 | 33 | 9.00E-14 | Bacteroides fragilis YCH46 | hypothetical protein BF0904 [Bacteroides fragilis YCH46] dbj BAD47655.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 25551, 25552 | 5198184 | 66 | 1.00E-111 | Yersinia pseudotuberculosis IP 32953 | possible type I restriction enzyme (restriction subunit) [Yersinia pseudotuberculosis IP 32953] emb CAH23117.1 possible type I restriction enzyme (restriction subunit) [Yersinia pseudotuberculosis IP 32953] | | | 3.1.21.3 |
| 25555, 25556 | 52081206 | 45 | 2.00E-55 | Bacillus licheniformis ATCC 14580 | cystathionine gamma-lyase YrhB [Bacillus licheniformis ATCC 14580] gb AAU24359.1 cystathionine gamma-lyase YrhB [Bacillus licheniformis ATCC 14580] ref YP_092416.1 YrhB [Bacillus licheniformis ATCC 14580] gb AAU41723.1 YrhB [Bacillus licheniformis DSM 13] | | | 4.4.1.8 |
| 25559, 25560 | 46141805 | 94 | 1.00E-121 | Psychrobacter sp. 273-4 | COG3328: Transposase and inactivated derivatives [Psychrobacter sp. 273- 4] | Erwinia sp. Ejp 556 plasmid pEJ30, complete sequence | 87 | 1.00E-07 |
| 25561, 25562 | 48855899 | 58 | 3.00E-71 | Cytophaga hutchinsonii | COG0321: Lipote-protein ligase B [Cytophaga hutchinsonii] | | | 6.--- |
| 25565, 25566 | 48855572 | 47 | 4.00E-21 | Cytophaga hutchinsonii | COG1733: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 25567, 25568 | 48853984 | 38 | 8.00E-14 | Cytophaga hutchinsonii | COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] | | | |
| 2557, 2558 | 53795203 | 31 | 1.00E-20 | Chloroflexus aurantiacus | COG1680: Beta-lactamase class C and other penicillin binding proteins [Chloroflexus aurantiacus] | | | 3.5.2.6 |
| 25573, 25574 | 52627365 | 47 | 1.00E-49 | Prevotella intermedia | phosphorylase family protein [Prevotella intermedia] | | | 2.4.2.3 |
| 25579, 25580 | 48855702 | 37 | 2.00E-40 | Cytophaga hutchinsonii | COG3279: Response regulator of the LysR/AlgR family [Cytophaga hutchinsonii] | | | 3.1.1.61 |
| 25581, 25582 | 28899875 | 37 | 7.00E-10 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA0020 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61363.1 conserved hypothetical protein [Vibrio parahaemolyticus] | | | 2.7.3.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|--|----|----------|
| 25583, 25584 | 48855703 | 30 | 2.00E-18 | Cytophaga hutchinsonii | COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 25585, 25586 | 16945755 | 51 | 1.00E-20 | Photobacterium damselfae subsp. piscicida | hypothetical protein [Photobacterium damselfae subsp. piscicida] | | | |
| 2559, 2560 | 52549895 | 44 | 4.00E-50 | uncultured archaeon | trehalose-6-phosphate synthase [uncultured archaeon GZfos33E1] | | | 2.4.1.15 |
| 25591, 25592 | 29348143 | 63 | 1.00E-93 | Bacteroides thetaiotaomicron VPI-5482 | DNA-directed RNA polymerase beta chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO77840.1 DNA-directed RNA polymerase beta chain [Bacteroides thetaiotaomicron VPI-5482] sp Q8A469 RPOB_BACTN DNA-directed RNA polymerase beta chain (RNAP beta subunit) (Transcriptase beta chain) (RNA polymerase beta subunit) | Porphyrromonas gingivalis W83 section 2 of 8 of the complete genome | 85 | 3.00E-15 |
| 25593, 25594 | 32475491 | 42 | 2.00E-24 | Rhodopirellula baltica SH 1 | probable oxidoreductase [Rhodopirellula baltica SH 1] emb CAD75862.1 probable oxidoreductase [Pirellula sp.] | | | 1.3.- |
| 25595, 25596 | 32475491 | 43 | 3.00E-26 | Rhodopirellula baltica SH 1 | probable oxidoreductase [Rhodopirellula baltica SH 1] emb CAD75862.1 | | | 1.3.- |
| 25597, 25598 | 53715737 | 43 | 2.00E-54 | Bacteroides fragilis YCH46 | hypothetical protein BF4458 [Bacteroides fragilis YCH46] dbj BAD51195.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 25603, 25604 | 53713063 | 34 | 3.00E-25 | Bacteroides fragilis YCH46 | [S110 family transposase [Bacteroides fragilis YCH46] dbj BAD48521.1 [S110 family transposase [Bacteroides fragilis YCH46] | | | |
| 25605, 25606 | 48853783 | 45 | 7.00E-25 | Cytophaga hutchinsonii | COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] | | | 2.7.7.7 |
| 25607, 25608 | 48853783 | 37 | 3.00E-42 | Cytophaga hutchinsonii | COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] | | | 2.7.7.7 |
| 25609, 25610 | 53730177 | 47 | 1.00E-48 | Dechloromonas aromatica RCB | COG2308: Uncharacterized conserved protein [Dechloromonas aromatica RCB] | | | |
| 2561, 2562 | 48853533 | 45 | 2.00E-36 | Cytophaga hutchinsonii | COG2825: Outer membrane protein [Cytophaga hutchinsonii] | | | |
| 25611, 25612 | 53730177 | 48 | 2.00E-50 | Dechloromonas aromatica RCB | COG2308: Uncharacterized conserved protein [Dechloromonas aromatica RCB] | | | |
| 25613, 25614 | 53715757 | 35 | 4.00E-32 | Bacteroides fragilis YCH46 | hypothetical protein BF4478 [Bacteroides fragilis YCH46] dbj BAD51215.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 25615, 25616 | 30023424 | 36 | 1.00E-31 | Bacillus cereus ATCC 14579 | Potassium channel protein [Bacillus cereus ATCC 14579] gb AAP12556.1 Potassium channel protein [Bacillus cereus ATCC 14579] | | | |
| 25617, 25618 | 25809040 | 55 | 9.00E-63 | Gram-negative bacterium 0471 | hypothetical protein [Gram-negative bacterium 0471] | | | 3.1.21.3 |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|--|--|----------|
| 25619, 25620 | 28897799 | 60 | 9.00E-32 | Vibrio parahaemolyticus RIMD 2210633 | putative beta-ketoadipate enol-lactone hydrolase [Vibrio parahaemolyticus RIMD 2210633] dbj BAC59288.1 putative beta-ketoadipate enol-lactone hydrolase [Vibrio parahaemolyticus] | | | 3.1.1.1 |
| 25625, 25626 | 24376152 | 65 | 7.00E-37 | Shewanella oneidensis MR-1 | hypothetical protein SO4680 [Shewanella oneidensis MR-1] gb AA57639.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | |
| 25627, 25628 | 51246929 | 46 | 3.00E-59 | Desulfotalea psychrophila LSV54 | probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] emb CAG37806.1 probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] | | | 3.4.21.- |
| 25629, 25630 | 29347578 | 38 | 4.00E-17 | Bacteroides thetaiotaomicron VPI-5482 | coproporphyrinogen III oxidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77275.1 coproporphyrinogen III oxidase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2563, 2564 | 48855581 | 61 | 3.00E-36 | Cytophaga hutchinsonii | COG0112: Glycine/serine hydroxymethyltransferase [Cytophaga hutchinsonii] | | | 2.1.2.1 |
| 25631, 25632 | 29347578 | 41 | 6.00E-23 | Bacteroides thetaiotaomicron VPI-5482 | coproporphyrinogen III oxidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77275.1 coproporphyrinogen III oxidase [Bacteroides thetaiotaomicron VPI-5482] | | | 1.-.-.- |
| 25633, 25634 | 53712075 | 26 | 2.00E-12 | Bacteroides fragilis YCH46 | hypothetical protein BF0782 [Bacteroides fragilis YCH46] dbj BAD47553.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 25635, 25636 | 32474967 | 48 | 5.00E-63 | Rhodopirellula baltica SH 1 | hypothetical protein RB7682 [Rhodopirellula baltica SH 1] emb CAD75508.1 hypothetical protein [Pirellula sp.] | | | |
| 25637, 25638 | 41725421 | 44 | 2.00E-24 | Dechloromonas aromatica RCB | hypothetical protein Daro03000355 [Dechloromonas aromatica RCB] COG0551: Zn-finger domain associated with topoisomerase type I | | | |
| 25639, 25640 | 52853389 | 66 | 1.00E-103 | Psychrobacter sp. 273-4 | [Psychrobacter sp. 273-4] | | | |
| 25641, 25642 | 32475496 | 42 | 2.00E-32 | Rhodopirellula baltica SH 1 | chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1] emb CAD75867.1 chloromuconate cycloisomerase YkfB1 [Pirellula sp.] | | | 5.5.-.- |
| 25643, 25644 | 48854032 | 53 | 4.00E-22 | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] COG1778: Low specificity phosphatase (HAD superfamily) [Cytophaga hutchinsonii] | | | |
| 25645, 25646 | 48856974 | 54 | 6.00E-46 | Cytophaga hutchinsonii | hypothetical protein MS129 [Microscilla sp. PRE1] gb AAK62851.1 MS129, hypothetical protein [Microscilla sp. PRE1] | | | 3.1.3.29 |
| 25649, 25650 | 14518334 | 37 | 4.00E-21 | Microscilla sp. PRE1 | hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Porphyromonas gingivalis W83] ref NP_906169.1 hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Porphyromonas gingivalis W83] | | | |
| 25655, 25656 | 34398008 | 29 | 7.00E-17 | Porphyromonas gingivalis W83 | COG0352: Thiamine monophosphate synthase [Cytophaga hutchinsonii] | | | 2.5.1.3 |
| 25657, 25658 | 48855690 | 49 | 1.00E-32 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|---|--|--|----------|
| 25659, | 48855689 | 38 | 2.00E-13 | Cytophaga hutchinsonii | COG0351: Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [Cytophaga hutchinsonii] | | | |
| 25660 | | | | Bacteroides | | | | |
| 25661, | 37962667 | 52 | 3.00E-58 | uniformis | Tn10-like transposase [Bacteroides uniformis] | | | |
| 25665, | | | | | unknown [Escherichia coli] | | | |
| 25666 | 37927544 | 47 | 3.00E-14 | Escherichia coli | conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_162420.1 hypothetical protein ZMO0685 [Zymomonas mobilis subsp. mobilis ZM4] | | | |
| 25667, | | | | Zymomonas mobilis subsp. mobilis ZM4 | | | | |
| 25668 | 56543155 | 33 | 1.00E-14 | Cytophaga hutchinsonii | hypothetical protein Chut02001282 [Cytophaga hutchinsonii] | | | |
| 25669, | 48856049 | 51 | 2.00E-45 | Cytophaga hutchinsonii | COG3021: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 25670 | | | | Cytophaga hutchinsonii | | | | |
| 2567, | 48853539 | 40 | 5.00E-23 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62612.1 hypothetical protein [Vibrio parahaemolyticus] | | | |
| 25673, | 28901124 | 45 | 3.00E-48 | Rhodopirellula | probable oxidoreductase [Rhodopirellula baltica SH ⁺] emb CAD75862.1 | | | 1.3.3.4 |
| 25677, | 32475491 | 43 | 1.00E-47 | baltica SH ⁺ | probable oxidoreductase [Pirellula sp.] | | | |
| 25678 | | | | Cytophaga hutchinsonii | COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Cytophaga hutchinsonii] | | | 6.2.1.1 |
| 25679, | 48856843 | 57 | 9.00E-71 | Cytophaga hutchinsonii | | | | |
| 25680 | | | | Cytophaga hutchinsonii | | | | |
| 25681, | 48854812 | 42 | 1.00E-19 | Desulfotalea psychrophila LSV54 | COG1522: Transcriptional regulators [Cytophaga hutchinsonii] related to isochorismate synthase (MenF) [Desulfotalea psychrophila LSV54] emb CAG34983.1 related to isochorismate synthase (MenF) [Desulfotalea psychrophila LSV54] | | | 5.4.99.6 |
| 25683, | 51244106 | 43 | 3.00E-22 | Bacteroides thetaiotaomicron VPI-5482 | 2-oxoglutarate decarboxylase and 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacteroides thetaiotaomicron VPI-5482] gbl AAO79806.1 2-oxoglutarate decarboxylase and 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 25684 | | | | Cytophaga hutchinsonii | | | | |
| 25685, | 29350109 | 34 | 7.00E-11 | Cytophaga hutchinsonii | COG0436: Aspartate/lysine/aromatic aminotransferase [Cytophaga hutchinsonii] | | | 2.6.1.17 |
| 25686 | 48856186 | 49 | 3.00E-67 | Ralstonia solanacearum GM1000 | hypothetical protein RS03686 [Ralstonia solanacearum GM1000] emb CAD17429.1 HYPOTHETICAL PROTEIN [Ralstonia solanacearum] | | | |
| 25687, | | | | Lactobacillus gasseri | | | | |
| 25688 | | | | Bdellovibrio bacteriovorus HD100 | COG0266: Formamidopyrimidine-DNA glycosylase [Lactobacillus gasseri] putative Ni,Fe-hydrogenase I cytochrome b subunit [Bdellovibrio bacteriovorus HD100] emb CAE79300.1 putative Ni,Fe-hydrogenase I cytochrome b subunit [Bdellovibrio bacteriovorus HD100] | | | 3.2.2.23 |
| 25689, | 17548499 | 46 | 1.00E-13 | | | | | |
| 25690 | | | | | | | | |
| 2569, | 23003059 | 33 | 1.00E-23 | | | | | |
| 2570 | | | | | | | | |
| 25691, | 42522927 | 28 | 6.00E-10 | | | | | |
| 25692 | | | | | | | | |

| | | | | | | | | | |
|-----------------|--------------|----|----------|--------------------------------------|---|--|--|---------|----------|
| 25693, 25694 | 53715357 | 26 | 6.00E-18 | Bacteroides fragilis YCH46 | hypothetical protein BF4073 [Bacteroides fragilis YCH46] dbj BAD50815.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 25695, 25696 | 53764561 | 28 | 4.00E-23 | Anabaena variabilis ATCC 29413 | COG2021: Homoserine acetyltransferase [Anabaena variabilis ATCC 29413] | | | | 2.3.1.31 |
| 25697, 25698 | 53797271 | 27 | 3.00E-16 | Chloroflexus aurantiacus | COG0249: Mismatch repair ATPase (MutS family) [Chloroflexus aurantiacus] | | | | |
| 25701, 25702 | 48854285 | 39 | 1.00E-46 | Cytophaga hutchinsonii | COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 25703, 25704 | 15610037 | 42 | 7.00E-47 | Mycobacterium tuberculosis H37Rv | POSSIBLE FORMATE DEHYDROGENASE H FDHF (FORMATE-HYDROGEN-LYASE-LINKED, SELENOCYSTEINE-CONTAINING POLYPEPTIDE) (FORMATE DEHYDROGENASE-H ALPHA SUBUNIT) (FDH-H) [Mycobacterium tuberculosis H37Rv] ref NP_856569.1 POSSIBLE FORMATE DEHYDROGENASE H FDHF (FORMATE-HYDROGEN-LYASE-LINKED, SELENOCYSTEINE-CONTAINING POLYPEPTIDE) (FORMATE DEHYDROGENASE-H ALPHA SUBUNIT) (FDH-H) [Mycobacterium bovis AF2122/97] ref NP_337480.1 formate dehydrogenase, alpha subunit, putative [Mycobacterium tuberculosis CDC1551] gb AAK47294.1 formate dehydrogenase, alpha subunit, putative [Mycobacterium tuberculosis CDC1551] sp P65409 YT24_MYCBO Hypothetical protein Mb2924c sp P65408 YT00_MYCTU Hypothetical protein Rv2900c/MT2968 pir G70926 probable fdhF protein - Mycobacterium tuberculosis (strain H37Rv) emb CAA98338.1 POSSIBLE FORMATE DEHYDROGENASE H FDHF (FORMATE-HYDROGEN-LYASE-LINKED, SELENOCYSTEINE-CONTAINING POLYPEPTIDE) (FORMATE DEHYDROGENASE-H ALPHA SUBUNIT) (FDH-H) [Mycobacterium tuberculosis H37Rv] emb CAD96611.1 POSSIBLE FORMATE DEHYDROGENASE H FDHF (FORMATE-HYDROGEN-LYASE-LINKED, SELENOCYSTEINE-CONTAINING POLYPEP | | | 1.2.1.2 | |
| 25709, 25710 | 37521791 | 33 | 2.00E-11 | Gloeobacter violaceus PCC 7421 | L-2,4-diaminobutyrate decarboxylase [Gloeobacter violaceus PCC 7421] dbj BAC90163.1 L-2,4-diaminobutyrate decarboxylase [Gloeobacter violaceus PCC 7421] | | | | 4.1.1.- |
| 2571, 2572 | 17547014 | 26 | 7.00E-16 | Ralstonia solanacearum GMI1000 | HYPOTHETICAL SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum GMI1000] emb CAD16002.1 HYPOTHETICAL SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] | | | | |
| 25713, 25714 | AAG9091 0 | 47 | 2.00E-10 | | Desc:C glutamicum protein fragment SEQ ID NO: 4664. Org:Corynebacterium glutamicum | | | | |
| 25715, 25716 | 28210167 | 56 | 3.00E-36 | Clostridium tetani E88 | hypothetical protein CTC00414 [Clostridium tetani E88] gb AAO35048.1 conserved protein [Clostridium tetani E88] | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|---------------|
| 25719, 25720 | 24375159 | 50 | 8.00E-64 | Shewanella oneidensis MR-1 | sigma-54 dependent transcriptional regulator/sensory box protein [Shewanella oneidensis MR-1] gb AAN56646.1 sigma-54 dependent transcriptional regulator/sensory box protein [Shewanella oneidensis MR-1] | | | | |
| 25723, 25724 | 29347290 | 36 | 1.00E-15 | Bacteroides thetaiotaomicron VPI-5482 | tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76987.1 tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.1.13 0 |
| 25725, 25726 | 53759291 | 42 | 3.00E-19 | Methylobacillus flagellatus KT | COG2895: GTPases - Sulfate adenylylate transferase subunit 1 [Methylobacillus flagellatus KT] | | | | 2.7.7.4 |
| 25731, 25732 | 21244950 | 36 | 4.00E-10 | Xanthomonas axonopodis pv. citri str. 306 | bleomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM390088.1 bleomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 25733, 25734 | 48853549 | 55 | 5.00E-27 | Cytophaga hutchinsonii | COG0277: FAD/FMN-containing dehydrogenases [Cytophaga hutchinsonii] hypothetical protein BT4201 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79306.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.1.3.15 |
| 25737, 25738 | 29349609 | 30 | 4.00E-07 | Bacteroides thetaiotaomicron VPI-5482 | D-amino acid dehydrogenase [Bdellovibrio bacteriovorus HD100] emb CAE77978.1 D-amino acid dehydrogenase [Bdellovibrio bacteriovorus HD100] | | | | 1.4.99.1 |
| 25741, 25742 | 42521944 | 38 | 5.00E-25 | Bdellovibrio bacteriovorus HD100 | dGTP triphosphohydrolase [Bacteroides fragilis YCH46] db BAD47072.1 dGTP triphosphohydrolase [Bacteroides fragilis YCH46] COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | | 3.1.5.1 |
| 25743, 25744 | 53711614 | 32 | 2.00E-10 | Bacteroides fragilis YCH46 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | 2.7.3.- |
| 25745, 25746 | 48855448 | 27 | 9.00E-17 | Cytophaga hutchinsonii | COG0564: Pseudouridylyl synthases, 23S RNA-specific [Cytophaga hutchinsonii] | | | | 4.2.1.70 |
| 25749, 25750 | 45657883 | 60 | 5.00E-32 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | hypothetical protein BF3706 [Bacteroides fragilis YCH46] db BAD50449.1 conserved hypothetical protein [Bacteroides fragilis YCH46] conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_906110.1 hypothetical protein PG2044 [Porphyromonas gingivalis W83] | | | | |
| 25751, 25752 | 48854010 | 49 | 2.00E-42 | Cytophaga hutchinsonii | COG0615: Cytidylyltransferase [Pediococcus pentosaceus ATCC 25745] | | | | 2.7.7.39 |
| 25753, 25754 | 53714991 | 57 | 4.00E-48 | Bacteroides fragilis YCH46 | | | | | |
| 25755, 25756 | 48854010 | 49 | 2.00E-42 | Cytophaga hutchinsonii | | | | | |
| 25757, 25758 | 34397949 | 51 | 1.00E-41 | Porphyromonas gingivalis W83 | | | | | |
| 25759, 25760 | 48869829 | 30 | 3.00E-07 | Pediococcus pentosaceus ATCC 25745 | | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|---|--|----|----------|----------|
| 25761, | 52853382 | 78 | 6.00E-31 | Psychrobacter sp. 273-4 | hypothetical protein Psc03002036 [Psychrobacter sp. 273-4] | | | | |
| 25762, | | | | | | | | | |
| 25763, | 48854536 | 51 | 2.00E-65 | Cytophaga hutchinsonii | COG0167: Dihydroorotate dehydrogenase [Cytophaga hutchinsonii] | | | | 1.3.3.1 |
| 25764, | | | | | tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | | |
| 25765, | | | | | dbj BAD47405.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | | |
| 25766, | 53711947 | 33 | 6.00E-07 | Bacteroides fragilis YCH46 | hypothetical protein RB11227 [Rhodopirellula baltica SH 1] | | | | 3.1.2.6 |
| 25767, | | | | | emb CAD78999.1 conserved hypothetical protein [Pirellula sp.] | | | | |
| 25768, | 32476862 | 48 | 1.00E-10 | Rhodopirellula baltica SH 1 | putative restriction modification enzyme S subunit [Escherichia coli O157:H7] ref NP_290962.1 putative restriction modification enzyme S subunit [Escherichia coli O157:H7 EDL933] ref NP_313333.1 type I restriction-modification enzyme S subunit [Escherichia coli O157:H7] dbj BAB38729.1 type I restriction-modification enzyme S subunit [Escherichia coli O157:H7] pir E86133 hypothetical protein Z5946 [imported] - Escherichia coli (strain O157:H7, substrain EDL933) pir B91292 hypothetical protein ECs5306 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) unnamed protein product [Kluyveromyces fragilis] emb CAH02391.1 unnamed protein product [Kluyveromyces fragilis NRRL Y-1140] | | 88 | 8.00E-15 | 3.1.21.3 |
| 25769, | 12519366 | 68 | 3.00E-77 | Escherichia coli O157:H7 | two-component sensor histidine kinase [uncultured archaeon GZfos26B2] | | | | 2.7.3.- |
| 25770, | | | | | conserved hypothetical protein [Porphyromonas gingivalis W83] | | | | |
| 25775, | 50304097 | 31 | 7.00E-10 | Kluyveromyces fragilis | ref NP_904796.1 hypothetical protein PG0501 [Porphyromonas gingivalis W83] | | | | |
| 25776, | | | | | putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.4.1.83 |
| 25777, | | | | | gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 25778, | 52549170 | 42 | 2.00E-30 | uncultured archaeon GZfos26B2 | putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47806.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] | | | | |
| 25781, | | | | | COG4704: Uncharacterized protein conserved in bacteria [Geobacter metallireducens GS-15] | | | | |
| 25782, | 34396629 | 37 | 2.00E-32 | Porphyromonas gingivalis W83 | two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO76183.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |
| 25789, | | | | | | | | | |
| 25790, | 29349972 | 65 | 1.00E-89 | Bacteroides thetaiotaomicron VPI-5482 | | | | | |
| 25791, | | | | | | | | | |
| 25792, | 53712348 | 33 | 7.00E-10 | Bacteroides fragilis YCH46 | | | | | |
| 25793, | | | | | | | | | |
| 25794, | 48847033 | 32 | 4.00E-17 | Geobacter metallireducens GS-15 | | | | | |
| 25795, | | | | | | | | | |
| 25796, | 29346486 | 48 | 2.00E-29 | Bacteroides thetaiotaomicron VPI-5482 | | | | | |

| | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|----|----------|
| 25797, 25798 | 29345596 | 39 | 9.00E-17 | Bacteroides thetaiotaomicron VPI-5482 | thiol:disulfide interchange protein dsbD precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO75293.1 thiol:disulfide interchange protein dsbD precursor [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 25799, 25800 | 56459804 | 35 | 4.00E-21 | Idiomarina loihiensis L2TR | Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihiensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihiensis L2TR] | | | |
| 25801, 25802 | 56460815 | 58 | 4.00E-25 | Idiomarina loihiensis L2TR | Anti-anti-sigma regulatory factor [Idiomarina loihiensis L2TR] gb AAV82547.1 Anti-anti-sigma regulatory factor [Idiomarina loihiensis L2TR] | Idiomarina loihiensis L2TR, complete genome | 88 | 1.00E-06 |
| 25803, 25804 | 53712688 | 25 | 9.00E-09 | Bacteroides fragilis YCH46 | hypothetical protein BF1395 [Bacteroides fragilis YCH46] dbj BAD48146.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 25805, 25806 | 48854662 | 30 | 4.00E-16 | Cytophaga hutchinsonii | COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Cytophaga hutchinsonii] | | | |
| 25809, 25810 | 50084459 | 34 | 4.00E-14 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD1273 [Acinetobacter sp. ADP1] emb CAG68147.1 conserved hypothetical protein [Acinetobacter sp. ADP1] | | | |
| 2581, 2582 | 48838849 | 72 | 1.00E-103 | Methanosarcina barkeri str. fusaro | COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro] | Methanosarcina acetivorans str. C2A, section 22 of 534 of the complete genome | 81 | 3.00E-27 |
| 25813, 25814 | 53712512 | 33 | 1.00E-26 | Bacteroides fragilis YCH46 | Iron(III) ABC transporter periplasmic iron-binding protein [Bacteroides fragilis YCH46] dbj BAD47970.1 Iron(III) ABC transporter periplasmic iron-binding protein [Bacteroides fragilis YCH46] | | | |
| 25817, 25818 | 17229380 | 26 | 7.00E-12 | Nostoc sp. PCC 7120 | hypothetical protein all1888 [Nostoc sp. PCC 7120] pir AB2042 hypothetical protein all1888 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73587.1 all1888 [Nostoc sp. PCC 7120] | | | |
| 25819, 25820 | 54294157 | 36 | 3.00E-13 | Legionella pneumophila str. Lens | hypothetical protein lpi1221 [Legionella pneumophila str. Lens] emb CAH15460.1 hypothetical protein [Legionella pneumophila str. Lens] | | | |
| 25821, 25822 | 48855642 | 36 | 4.00E-12 | Cytophaga hutchinsonii | COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 25823, 25824 | 29349999 | 41 | 2.00E-41 | Bacteroides thetaiotaomicron VPI-5482 | transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16] dbj BAD62945.1 transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16] | | | |
| 25825, 25826 | 56962183 | 27 | 2.00E-12 | Bacillus clausii KSM-K16 | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---------------------------------------|---|--|----|----------|----------|
| 25829, | 48853435 | 67 | 3.00E-60 | Cytophaga hutchinsonii | COG1088: dTDP-D-glucose 4,6-dehydratase [Cytophaga hutchinsonii] | | | | 4.2.1.46 |
| 25830 | | | | Methylobacillus | COG2010: Cytochrome c, mono- and diheme variants [Methylobacillus flagellatus KT] | | | | 1.7.99.3 |
| 2583, | 53759377 | 34 | 7.00E-14 | flagellatus KT | | | | | |
| 2584 | | | | Thiobacillus denitrificans ATCC 25259 | COG0189: Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase) [Thiobacillus denitrificans ATCC 25259] | | | | |
| 25835, | 52008037 | 44 | 7.00E-18 | | ribosomal protein S6 modification protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_122785.1 hypothetical protein lpp0446 [Legionella pneumophila str. Paris] gb AAU26476.1 ribosomal protein S6 modification protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH11594.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | |
| 25837, | 52840624 | 36 | 2.00E-11 | Philadelphia 1 | hypothetical protein, predicted Glutamate--cysteine ligase [Azoarcus sp. EbN1] emb CAI10097.1 hypothetical protein, predicted Glutamate--cysteine ligase [Azoarcus sp. EbN1] | | | | |
| 25839, | 56479409 | 48 | 4.00E-64 | Azoarcus sp. EbN1 | putative nucleoside-diphosphate sugar epimerases/dehydratase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75705.1 putative nucleoside-diphosphate sugar epimerases/dehydratase [Bacteroides thetaiotaomicron VPI-5482] | Clostridium tetani E88, section 8 of 10 of the complete genome | 84 | 4.00E-17 | 4.2.1.- |
| 25841, | 29346008 | 60 | 2.00E-74 | VPI-5482 | hypothetical protein Chut02003040 [Cytophaga hutchinsonii] | | | | |
| 25843, | 48854367 | 58 | 2.00E-69 | Cytophaga hutchinsonii | COG0212: 5-formyltetrahydrofolate cyclo-ligase [Cytophaga hutchinsonii] | | | | 6.3.3.2 |
| 25844 | | | | Cytophaga hutchinsonii | COG1459: Type II secretory pathway, component PulF [Cytophaga hutchinsonii] | | | | |
| 25845, | 48856113 | 33 | 1.00E-20 | | COG1217: Predicted membrane GTPase involved in stress response [Cytophaga hutchinsonii] | | | | |
| 25849, | 48855359 | 38 | 2.00E-32 | Cytophaga hutchinsonii | COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii] | | | | |
| 25850 | | | | Cytophaga hutchinsonii | hypothetical protein EF0112 [Enterococcus faecalis V583] gb AAO79987.1 conserved domain protein [Enterococcus faecalis V583] | | | | |
| 2585, | 48854524 | 62 | 2.00E-80 | Cytophaga hutchinsonii | hypothetical protein Chut02002154 [Cytophaga hutchinsonii] | | | | |
| 25851, | 48856245 | 53 | 6.00E-60 | Cytophaga hutchinsonii | putative sun protein [Bdellovibrio bacteriovorus HD100] emb CAE79023.1 putative sun protein [Bdellovibrio bacteriovorus HD100] | | | | 2.1.1.- |
| 25852 | | | | Enterococcus faecalis V583 | COG2374: Predicted extracellular nuclease [Exiguobacterium sp. 255-15] | | | | |
| 25855, | 29374763 | 29 | 8.00E-10 | faecalis V583 | | | | | |
| 25856 | | | | Cytophaga hutchinsonii | | | | | |
| 25859, | 48855090 | 34 | 1.00E-27 | | | | | | |
| 25860 | | | | Bdellovibrio bacteriovorus HD100 | | | | | |
| 25861, | 42522650 | 53 | 6.00E-43 | | | | | | |
| 25862 | | | | Exiguobacterium | | | | | |
| 25863, | 46113550 | 36 | 5.00E-07 | sp. 255-15 | | | | | |
| 25864 | | | | | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|--|---|--|--|---------------|
| 25865, 25866 | 11279060 | 44 | 1.00E-35 | Imported | cell wall lipoprotein ewlA [imported] - Erysipelothrix rhusiopathiae gb AAB01156.1 EwIA | | | |
| 2587, 2588 | 42523429 | 72 | 2.00E-94 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd1952 [Bdellovibrio bacteriovorus HD100] emb CAE79802.1 mp [Bdellovibrio bacteriovorus HD100] | | | 6.3.2.- |
| 25871, 25872 | 51598164 | 67 | 6.00E-87 | Yersinia pseudotuberculosis IP 32953 | possible type I restriction enzyme (restriction subunit) [Yersinia pseudotuberculosis IP 32953] emb CAH23117.1 possible type I restriction enzyme (restriction subunit) [Yersinia pseudotuberculosis IP 32953] | | | 3.1.21.3 |
| 25873, 25874 | 29348700 | 29 | 1.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3291 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78397.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482] | | | |
| 25875, 25876 | 48855613 | 34 | 4.00E-14 | Cytophaga hutchinsonii | COG0308: Aminopeptidase N [Cytophaga hutchinsonii] | | | |
| 25877, 25878 | 48853831 | 50 | 8.00E-68 | Cytophaga hutchinsonii | COG0527: Aspartokinases [Cytophaga hutchinsonii] | | | 2.7.2.4 |
| 25881, 25882 | 48855337 | 51 | 4.00E-64 | Cytophaga hutchinsonii | COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii] | | | |
| 25883, 25884 | 31195677 | 61 | 2.00E-82 | Anopheles gambiae | ENSANGP00000000375 [Anopheles gambiae] | | | 6.1.1.18 |
| 25887, 25888 | 21231990 | 61 | 4.00E-58 | Xanthomonas campestris pv. campestris str. ATCC 33913 | hypothetical protein XCC2559 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM41831.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | 3.6.1.13 |
| 2589, 25891 | 28375463 | 36 | 5.00E-55 | Cytophaga hutchinsonii | SMC protein [Cytophaga hutchinsonii] ref ZP_00308092.1 COG1196: Chromosome segregation ATPases [Cytophaga hutchinsonii] | | | |
| 25892, 25893 | 29345486 | 50 | 1.00E-57 | Bacteroides thetaiotaomicron VPI-5482 | transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75183.1 transposase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 25894, 25899 | 48854473 | 45 | 3.00E-40 | Cytophaga hutchinsonii | COG1648: Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain) [Cytophaga hutchinsonii] | | | 2.1.1.10 7 |
| 25900, 25901 | 48856102 | 38 | 4.00E-18 | Cytophaga hutchinsonii | COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 25902, 25903 | 32474367 | 53 | 2.00E-32 | Rhodopirella baltica SH 1 | probable secreted glycosyl hydrolase [Rhodopirella baltica SH 1] emb CAD74907.1 probable secreted glycosyl hydrolase [Pirella sp.] | | | |
| 25904, 25905 | 57236797 | 47 | 2.00E-34 | Flavobacterium johnsoniae | SprA [Flavobacterium johnsoniae] | | | |
| 25906, 25907 | 31790365 | 35 | 2.00E-33 | uncultured Acidobacteria bacterium | hypothetical protein [uncultured Acidobacteria bacterium] | | | |

| | | | | | | | | |
|--------|----------|----|----------|---------------------------------|--|--|----|----------|
| 2591, | 29349999 | 25 | 5.00E-16 | Bacteroides thetaiotaomicron | putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 2592 | AAB1851 | | | | | | | |
| 25911, | 5 | 41 | 1.00E-36 | | Desc:Amino acid sequence of prolyl-tripeptidyl peptidase DPP. | | | 3.4.14.5 |
| 25912 | | | | | Org:Porphyromonas gingivalis | | | |
| 25913, | 55819125 | 33 | 4.00E-07 | Mimivirus | HNH endonuclease [Mimivirus] gb AAV50519.1 HNH endonuclease | | | |
| 25914 | | | | | [Mimivirus] | | | |
| 25917, | | | | | tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | |
| 25918 | 53712631 | 33 | 7.00E-37 | Bacteroides fragilis YCH46 | dbj BAD48089.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | |
| 25919, | | | | | COG0286: Type I restriction-modification system methyltransferase subunit | | | |
| 25920 | 46320397 | 32 | 1.00E-14 | Burkholderia cepacia R1808 | [Burkholderia cepacia R1808] | | | |
| 25921, | | | | | tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | |
| 25922 | 53712631 | 42 | 6.00E-52 | Bacteroides fragilis YCH46 | dbj BAD48089.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | |
| 25923, | | | | | | | | 2.4.1.15 |
| 25924 | 48854183 | 52 | 4.00E-28 | Cytophaga hutchinsonii | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | 1 |
| 25927, | | | | | COG4277: Predicted DNA-binding protein with the Helix-hairpin-helix motif | | | |
| 25928 | 48855675 | 86 | 1.00E-84 | Cytophaga hutchinsonii | [Cytophaga hutchinsonii] | | 94 | 7.00E-12 |
| 25929, | | | | | | | | |
| 25930 | 41690267 | 77 | 9.00E-29 | Psychrobacter sp. 273-4 | hypothetical protein Psyc03000442 [Psychrobacter.sp. 273-4] | | | |
| 2593, | | | | | preprotein translocase, YajC subunit [Porphyromonas gingivalis W83] | | | |
| 25931, | 34396613 | 34 | 2.00E-13 | Porphyromonas gingivalis W83 | ref NP_904780.1 preprotein translocase, YajC subunit [Porphyromonas gingivalis W83] | | | |
| 25932 | 24374604 | 32 | 8.00E-30 | Shewanella oneidensis MR-1 | sensory box protein [Shewanella oneidensis MR-1] gb AAN56091.1 sensory box protein [Shewanella oneidensis MR-1] | | | 2.7.3.- |
| 25933, | | | | | helicase [Shewanella oneidensis MR-1] gb AAN53453.1 helicase | | | |
| 25934 | 24371966 | 48 | 2.00E-38 | Shewanella oneidensis MR-1 | [Shewanella oneidensis MR-1] | | | |
| 25935, | | | | | Amidohydrolase family enzyme [Idiomarina loihiensis L2TR] gb AAV82933.1 | | | |
| 25936 | 56461201 | 63 | 2.00E-87 | Idiomarina loihiensis L2TR | Amidohydrolase family enzyme [Idiomarina loihiensis L2TR] | | | |
| 25937, | 53610376 | 50 | 6.00E-36 | Azotobacter vinelandii | COG1262: Uncharacterized conserved protein [Azotobacter vinelandii] | | | |
| 25939, | | | | | | | | |
| 25940 | 48854843 | 42 | 8.00E-49 | Cytophaga hutchinsonii | COG0196: FAD synthase [Cytophaga hutchinsonii] | | | 2.7.1.26 |
| 25941, | | | | | | | | |
| 25942 | 48854067 | 30 | 1.00E-12 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |

| | | | | | | | | | |
|-----------------|----------|----|-----------|---|--|---|----|----------|----------|
| 25943, 25944 | 29346245 | 70 | 6.00E-55 | Bacteroides thetaiotaomicron VPI-5482 | tRNA-guanine transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75942.1 tRNA-guanine transglycosylase [Bacteroides thetaiotaomicron VPI-5482] | Bacteroides thetaiotaomicron VPI-5482, section 4 of 21 of the complete genome | 91 | 1.00E-09 | 2.4.2.29 |
| 25945, 25946 | 53711597 | 53 | 2.00E-55 | Bacteroides fragilis YCH46 | UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Bacteroides fragilis YCH46] dbj BAD47055.1 UDP-N-acetylglucosamine-N- acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N- acetylglucosamine transferase [Bacteroides fragilis YCH46] | | | 2.4.1.- | |
| 25947, 25948 | 22652003 | 43 | 2.00E-15 | Synechococcus sp. PCC 7002 | hypothetical protein [Synechococcus sp. PCC 7002] | | | | |
| 25949, 25950 | 28898510 | 63 | 2.00E-68 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VP1736 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC59999.1 conserved hypothetical protein [Vibrio parahaemolyticus] hypothetical cell division control protein [Sulfolobus tokodaii str. 7] dbj BAB67696.1 700aa long hypothetical cell division control protein [Sulfolobus tokodaii str. 7] | | | 3.1.6.- | |
| 25951, 25952 | 15922918 | 36 | 4.00E-26 | Sulfolobus tokodaii str. 7 | | Photobacterium profundum SS9 chromosome 2; segment 3/7 | 83 | 2.00E-16 | 2.7.1.- |
| 25953, 25954 | 54302486 | 70 | 1.00E-102 | Photobacterium profundum SS9 | hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1 hypothetical maturase [Photobacterium profundum] type I site-specific deoxyribonuclease [Methanosarcina acetivorans C2A] gb AAM05520.1 type I site-specific deoxyribonuclease [Methanosarcina acetivorans str. C2A] | | | 3.1.21.3 | |
| 25955, 25956 | 20090965 | 61 | 9.00E-32 | Methanosarcina acetivorans C2A | | | | | 3.1.21.3 |
| 25957, 25958 | 9789464 | 41 | 1.00E-19 | Lactococcus lactis subsp. lactis | HsdS [Lactococcus lactis subsp. lactis] ref NP_862616.1 HsdS [Lactococcus lactis subsp. lactis] gb AAF69139.1 HsdS [Lactococcus lactis] type I site-specific deoxyribonuclease [Methanosarcina acetivorans C2A] gb AAM05518.1 type I site-specific deoxyribonuclease [Methanosarcina acetivorans str. C2A] | | | 3.1.21.3 | |
| 25959, 25960 | 20090963 | 56 | 2.00E-25 | Methanosarcina acetivorans C2A | | | | | 3.1.21.3 |
| 25967, 25968 | 53713424 | 28 | 7.00E-11 | Bacteroides fragilis YCH46 | ATP-dependent helicase [Bacteroides fragilis YCH46] dbj BAD48882.1 ATP- dependent helicase [Bacteroides fragilis YCH46] tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] dbj BAD48089.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | | |
| 25969, 25970 | 53712631 | 37 | 6.00E-30 | Bacteroides fragilis YCH46 | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---------------------------------------|---|--|--|----------------------|----------|
| 2597, 2598 | 13508374 | 32 | 6.00E-09 | Mycoplasma pneumoniae M129 | hypothetical protein MPN635 [Mycoplasma pneumoniae M129] gb AA895855.1 conserved hypothetical protein [Mycoplasma pneumoniae M129] pir S73533 hypothetical protein E30_orf352 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75162 YG35_MYCPN Hypothetical protein MPN635 (E30_orf352) | | | | |
| 25971, 25972 | 53713920 | 49 | 2.00E-55 | Bacteroides fragilis YCH46 | putative ABC transporter ATP-binding protein or permease protein [Bacteroides fragilis YCH46] dbj BAD49378.1 putative ABC transporter ATP-binding protein or permease protein [Bacteroides fragilis YCH46] | | | | |
| 25973, 25974 | 29348441 | 32 | 4.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | conserved hypothetical protein, with a weak acyltransferase domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO78138.1 conserved hypothetical protein, with a weak acyltransferase domain [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 25977, 25978 | 29345890 | 56 | 4.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.--- |
| 25983, 25984 | 48853718 | 45 | 5.00E-66 | Cytophaga hutchinsonii | COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii] | | | | |
| 25985, 25986 | 38174845 | 36 | 3.00E-09 | Melittangium lichenicola | hypothetical protein [Melittangium lichenicola] | | | | |
| 25987, 25988 | 53757541 | 52 | 1.00E-43 | Methylococcus capsulatus str. Bath | type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath] ref YP_114328.1 type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath] | | | | 3.1.21.3 |
| 25989, 25990 | 34396756 | 56 | 3.00E-26 | Porphyromonas gingivalis W83 | (thiamine monophosphate kinase [Porphyromonas gingivalis W83] ref NP_904922.1 thiamine monophosphate kinase [Porphyromonas gingivalis W83]) | | | | 2.7.4.16 |
| 2599, 2600 | 53795689 | 28 | 1.00E-17 | Chloroflexus aurantiacus | COG1205: Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster [Chloroflexus aurantiacus] | | | | |
| 25991, 25992 | 42630866 | 35 | 4.00E-18 | Haemophilus influenzae R2866 | COG0457: FOG: TPR repeat [Haemophilus influenzae R2866] | | | | |
| 25993, 25994 | 4184091 | 23 | 5.00E-12 | Bacteroides fragilis | BfmB [Bacteroides fragilis] | | | | |
| 25995, 25996 | 34397651 | 69 | 8.00E-70 | Porphyromonas gingivalis W83 | DNA gyrase, B subunit [Porphyromonas gingivalis W83] ref NP_905814.1 DNA gyrase, B subunit [Porphyromonas gingivalis W83] | | | | |
| 25997, 25998 | 29349537 | 35 | 1.00E-08 | Bacteroides thetaiotaomicron VPI-5482 | outer membrane assembly protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79234.1 outer membrane assembly protein [Bacteroides thetaiotaomicron VPI-5482] | | | 82 2.00E-36 5.99.1.3 | |

| | | | | | | | | |
|--------|----------|----|----------|---|--|--|--|----------|
| 26001, | 48855613 | 36 | 7.00E-24 | Cytophaga hutchinsonii | COG0308: Aminopeptidase N [Cytophaga hutchinsonii] | | | |
| 26002, | 48855613 | 36 | 7.00E-24 | Cytophaga hutchinsonii | COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] | | | |
| 26005, | 48855423 | 28 | 3.00E-16 | Cytophaga hutchinsonii | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | |
| 26006 | | | | | COG0177: Predicted EndoIII-related endonuclease [Microbulbifer degradans] | | | 4.2.99.1 |
| 26007, | 48855521 | 26 | 4.00E-13 | Cytophaga hutchinsonii | | | | 8 |
| 26008 | | | | Microbulbifer | | | | |
| 26009, | 48861416 | 71 | 2.00E-60 | degradans 2-40 | Carboxyl-terminal protease, periplasmic [Idiomarina loihiensis L2TR] | | | 3.4.21.- |
| 26010 | | | | | | | | |
| 26011, | 56460382 | 54 | 9.00E-61 | Idiomarina | | | | |
| 26012 | | | | loihiensis L2TR | | | | |
| 26017, | 46316058 | 49 | 2.00E-32 | Burkholderia cepacia R18194 | COG3265: Glucanase kinase [Burkholderia cepacia R18194] | | | 2.7.1.12 |
| 26018 | | | | | | | | |
| 26019, | | | | Bacteroides | hypothetical protein BT2390 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 26020 | 29347800 | 56 | 2.00E-65 | thetaitaomicron VPI-5482 | gb AAO77497.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 26021, | | | | | | | | |
| 26022 | 53713020 | 45 | 5.00E-32 | Bacteroides fragilis YCH46 | slalate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAC56897.1 | | | |
| 26023, | | | | | slalate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAD48478.1 | | | 3.1.1.47 |
| 26024 | 48854977 | 60 | 1.00E-60 | Cytophaga hutchinsonii | COG0685: 5,10-methylenetetrahydrofolate reductase [Cytophaga hutchinsonii] | | | 1.7.99.5 |
| | | | | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | hypothetical protein FN0185 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94391.1 Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | |
| 26029, | | | | | | | | |
| 26030 | 19703530 | 43 | 2.00E-30 | Thermococcus kodakaraensis | predicted ATP-dependent endonuclease, OLD family [Thermococcus kodakaraensis] ref YP_183808.1 predicted ATP-dependent endonuclease, OLD family [Thermococcus kodakaraensis] | | | |
| 26031, | 57159654 | 27 | 1.00E-08 | kodakaraensis | | | | |
| 26032 | | | | | | | | |
| | | | | | | | | |
| 26033, | | | | | type I restriction-modification enzyme 1, S subunit [Methanocaldococcus jannaschii DSM 2661] gb AAB99219.1 type I restriction-modification enzyme 1, S subunit [Methanocaldococcus jannaschii DSM 2661] plr JAG4452 type I restriction-modification enzyme, S subunit homolog - Methanocaldococcus jannaschii sp Q58615 YC18_METJ.A Hypothetical protein MJ1218 | | | 3.1.21.3 |
| 26034 | 15669403 | 28 | 8.00E-13 | 2661 | | | | |
| 26035, | | | | Pseudomonas fluorescens PfO-1 | COG1368: Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily [Pseudomonas fluorescens PfO-1] | | | |
| 26036 | 48730332 | 34 | 1.00E-14 | Bacteroides thetaiotaomicron | hypothetical protein BT2213 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 26041, | | | | | gb AAO77320.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 26042 | 29347623 | 26 | 4.00E-13 | VPI-5482 | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|--|--|--|--|----------|
| 26043, | 45857883 | 37 | 9.00E-48 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAST0606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | 2.7.3.- |
| 26044 | | | | Fiocruz L1-130 | | | | | |
| 26045, | | | | Bacteroides thetaiotaomicron | hypothetical protein BT0761 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75868.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26046 | 29346171 | 29 | 4.00E-28 | VPI-5482 | | | | | |
| 26051, | | | | Bacteroides fragilis | hypothetical protein BF2022 [Bacteroides fragilis YCH46] dbj BAD48769.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | 3.4.13.9 |
| 26052 | 53713311 | 49 | 6.00E-44 | YCH46 | | | | | |
| 26053, | | | | Borrelia burgdorferi | hypothetical protein BB0756 [Borrelia burgdorferi B31] gb AAC67104.1 B. burgdorferi predicted coding region BB0756 [Borrelia burgdorferi B31] | | | | |
| 26054 | 15595101 | 25 | 1.00E-12 | B31 | pir C70194 hypothetical protein BB0756 - Lyme disease spirochete | | | | |
| 26055, | | | | Bacteroides thetaiotaomicron | ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76349.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26056 | 29346652 | 68 | 2.00E-72 | VPI-5482 | | | | | |
| 26057, | | | | Silicibacter pomeroyi DSS-3 | conserved hypothetical protein [Silicibacter pomeroyi DSS-3] ref YP_168196.1 hypothetical protein SPO2990 [Silicibacter pomeroyi DSS-3] | | | | |
| 26058 | 56679562 | 32 | 3.00E-17 | pomeroyi DSS-3 | | | | | |
| 26059, | | | | Rhodopirellula | hypothetical protein RB9659 [Rhodopirellula baltica SH 1] emb CAD76391.1 conserved hypothetical protein [Pirellula sp.] | | | | 2.4.1.18 |
| 26060 | 32476012 | 55 | 2.00E-36 | baltica SH 1 | | | | | 2 |
| 26063, | | | | Cytophaga hutchinsonii | COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii] | | | | |
| 26064 | 48855019 | 48 | 2.00E-65 | | | | | | |
| 26067, | | | | Pseudomonas syringae pv. syringae B728a | COG0463: Glycosyltransferases involved in cell wall biogenesis [Pseudomonas syringae pv. syringae B728a] | | | | |
| 26068 | 23472289 | 43 | 7.00E-20 | | | | | | |
| 26071, | | | | Bacteroides fragilis | putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD50166.1 putative glycosyltransferase [Bacteroides fragilis YCH46] | | | | |
| 26072 | 53714708 | 32 | 5.00E-28 | YCH46 | | | | | |
| 26077, | | | | Dechloromonas aromatica RCB | COG3385: FOG; Transposase and inactivated derivatives [Dechloromonas aromatica RCB] | | | | |
| 26078 | 53730535 | 57 | 5.00E-36 | | | | | | |
| 26085, | | | | Rhodopseudomonas palustris CGA009 | possible peptidase [Rhodopseudomonas palustris CGA009] emb CAE27336.1 possible peptidase [Rhodopseudomonas palustris CGA009] | | | | 3.4.21.- |
| 26086 | 39934964 | 25 | 1.00E-08 | s palustris CGA009 | | | | | |
| 26087, | | | | Actinobacillus pleuropneumoniae serovar 1 | COG3265: Gluconate kinase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | | 2.7.1.12 |
| 26088 | 53728938 | 71 | 6.00E-35 | | | | | | |

| | | | | | | | | | |
|-----------------------------------|----------------------|----------|----------------------|--|---|---|----|----------|----------|
| 26089, 26090, 2609, 2610 | 15894619 48854018 | 37 62 | 5.00E-14 2.00E-85 | Clostridium acetobutylicum ATCC 824 Cytophaga hutchinsonii | Transcriptional regulator of the LacI family [Clostridium acetobutylicum ATCC 824] gb AAK79308.1 Transcriptional regulator of the LacI family [Clostridium acetobutylicum ATCC 824] pir A97065 transcription regulator of the LacI family [imported] - Clostridium acetobutylicum | | | | |
| 26091, 26092 | 51243929 | 54 | 2.00E-64 | Desulfotalea psychrophila LSV54 | COG0423: Glycyl-tRNA synthetase (class I) [Cytophaga hutchinsonii] hypothetical protein DP0077 [Desulfotalea psychrophila LSV54] emb CAG34806.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | | 6.1.1.14 |
| 26093, 26094 | 29349716 | 47 | 5.00E-19 | Bacteroides thetaiotaomicron VPI-5482 | pantoate--beta-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79413.1 pantoate--beta-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] | | | | 1.6.5.3 |
| 26095, 26096 | 15895943 | 49 | 2.00E-84 | Clostridium acetobutylicum ATCC 824 | Trehalose/maltose hydrolase (phosphorylase) [Clostridium acetobutylicum ATCC 824] gb AAK80632.1 Trehalose/maltose hydrolase (phosphorylase) [Clostridium acetobutylicum ATCC 824] pir E97230 trehalose/maltose hydrolase (phosphorylase) [imported] - Clostridium acetobutylicum | Clostridium acetobutylicum ATCC 824 section 254 of 356 of the complete genome | 86 | 5.00E-11 | 2.4.1.8 |
| 261, 262 | 28852364 | 66 | 2.00E-78 | Pseudomonas syringae pv. tomato str. DC3000 | aminotransferase, DegT/DnrJ/EryC1/StrS family [Pseudomonas syringae pv. tomato str. DC3000] ref NP_791743.1 aminotransferase, DegT/DnrJ/EryC1/StrS family [Pseudomonas syringae pv. tomato str. DC3000] | | | | |
| 26101, 26102 | 29346728 | 39 | 7.00E-28 | Bacteroides thetaiotaomicron VPI-5482 | signaling protein without kinase domain [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76425.1 signaling protein without kinase domain [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |
| 26103, 26104 | 29349375 | 38 | 7.00E-19 | Bacteroides thetaiotaomicron VPI-5482 | putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79072.1 putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI- 5482] | | | | |
| 26109, 26110 | 53712202 | 56 | 2.00E-66 | Bacteroides fragilis YCH46 | orotidine 5'-phosphate decarboxylase [Bacteroides fragilis YCH46] dbj BAD47660.1 orotidine 5'-phosphate decarboxylase [Bacteroides fragilis YCH46] | | | | 4.1.1.23 |
| 2611, 2612 | 1208896 | 37 | 1.00E-31 | Anaerocellum thermophilum | hypothetical protein [Anaerocellum thermophilum] | | | | 5.3.1.9 |
| 26111, 26112 | 48848828 | 70 | 2.00E-36 | Novosphingobium aromaticivorans DSM 12444 | COG5394: Uncharacterized protein conserved in bacteria [Novosphingobium aromaticivorans DSM 12444] | | | | |
| 26115, 26116 | 28898411 | 25 | 6.00E-12 | Vibrio parahaemolyticus RIMD 2210633 | putative GGDEF family protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC59900.1 putative GGDEF family protein [Vibrio parahaemolyticus] | | | | 4.6.1.2 |
| 26117, 26118 | 48853831 | 43 | 1.00E-54 | Cytophaga hutchinsonii | COG0527: Aspartokinases [Cytophaga hutchinsonii] | | | | 2.7.2.4 |

| | | | | | | | | | |
|--------|----------|----|-----------|--------------------------------------|---|--|--|--|----------|
| 26119, | 53714264 | 39 | 1.00E-33 | Bacteroides fragilis YCH46 | folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 | | | | 6.3.2.17 |
| 26120 | | | | | folypolyglutamate synthase [Bacteroides fragilis YCH46] | | | | |
| 26123, | | | | | hypothetical protein CO0341 [Caulobacter crescentus CB15] | | | | |
| 26124 | 16124596 | 32 | 7.00E-19 | Caulobacter crescentus CB15 | gb AAK22328.1 hypothetical protein [Caulobacter crescentus CB15] | | | | |
| 26125, | | | | | pir D87291 hypothetical protein CO0341 [imported] - Caulobacter crescentus | | | | |
| 26126 | 34396714 | 37 | 3.00E-37 | Porphyromonas gingivalis W83 | htrA protein [Porphyromonas gingivalis W83] ref NP_904880.1 htrA protein [Porphyromonas gingivalis W83] | | | | 3.4.21.- |
| 26127, | | | | | GldI [Flavobacterium johnsoniae] | | | | 5.2.1.8 |
| 26128 | 38195402 | 42 | 2.00E-34 | Flavobacterium johnsoniae | COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii] | | | | 2.3.2.- |
| 26129, | | | | | Geobacter sulfurreducens PCA | | | | |
| 26130 | 48854578 | 45 | 2.00E-61 | Geobacter sulfurreducens PCA | GTP pyrophosphokinase [Geobacter sulfurreducens PCA] gb AAR35612.1 | | | | 2.7.6.5 |
| 2613, | 39997334 | 62 | 1.00E-122 | Flavobacterium johnsoniae | GldB [Flavobacterium johnsoniae] | | | | |
| 26133, | 5360188 | 38 | 6.00E-32 | Trichinella pseudospiralis | unknown [Trichinella pseudospiralis] | | | | |
| 26135, | 3329480 | 40 | 7.00E-21 | Cytophaga hutchinsonii | COG2911: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 26136 | | | | | COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Psychrobacter sp. 273-4] | | | | 3.1.21.3 |
| 26137, | 48855182 | 33 | 2.00E-10 | Psychrobacter sp. 273-4 | predicted ABC-type Fe3+-hydroxamate transport system, periplasmic component [Azoarcus sp. EbN1] emb CAI08173.1 predicted ABC-type Fe3+-hydroxamate transport system, periplasmic component [Azoarcus sp. EbN1] | | | | |
| 26141, | 52853569 | 93 | 1.00E-100 | Azoarcus sp. EbN1 | COG0216: Protein chain release factor A [Cytophaga hutchinsonii] | | | | |
| 26142 | | | | | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | | |
| 26145, | | | | | signal peptidase I [Bacteroides fragilis YCH46] dbj BAD46930.1 signal peptidase I [Bacteroides fragilis YCH46] | | | | 2.1.1.- |
| 26146 | 56477485 | 35 | 2.00E-12 | Cytophaga hutchinsonii | hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1 | | | | |
| 26147, | | | | | hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 26148 | 48854332 | 60 | 6.00E-42 | Bacteroides fragilis YCH46 | two-component system response regulator protein [Bacteroides fragilis YCH46] | | | | |
| 2615, | | | | | thetaiotaomicon VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetaiotaomicon VPI-5482] | | | | |
| 2615, | 48854899 | 55 | 2.00E-35 | Cytophaga hutchinsonii | | | | | |
| 2616 | | | | | | | | | |
| 26153, | 53711472 | 30 | 1.00E-15 | Bacteroides fragilis YCH46 | | | | | |
| 26154 | | | | | | | | | |
| 26155, | 53712193 | 28 | 4.00E-15 | Bacteroides fragilis YCH46 | | | | | |
| 26156 | | | | | | | | | |
| 26157, | | | | | | | | | |
| 26158 | 29349974 | 33 | 4.00E-23 | Bacteroides thetaiotaomicon VPI-5482 | | | | | |

| | | | | | | | | |
|--------|----------|----|-----------|---|--|--|----|----------|
| 26159, | 48855208 | 39 | 4.00E-22 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | |
| 26160 | | | | Flavobacterium | | | | |
| 26161, | 14531035 | 45 | 8.00E-22 | johnsoniae | gliding motility protein GldG [Flavobacterium johnsoniae] | | | |
| 26162 | | | | | | | | |
| 26163, | 41688937 | 92 | 1.00E-146 | Psychrobacter sp. | COG3328: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] ref ZP_00147021.1 COG3328: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] | Desc:E. coli CFT073 genomic sequence #251. | 86 | 6.00E-07 |
| 26164 | | | | Shewanella | hypothetical protein S00366 [Shewanella oneidensis MR-1] gb AA53451.1 | Org:Escherichia coli | | |
| 26165, | 24371964 | 37 | 4.00E-26 | oneidensis MR-1 | hypothetical protein [Shewanella oneidensis MR-1] | | | |
| 26166 | | | | Cytophaga | | | | |
| 26167, | 48855619 | 27 | 2.00E-07 | hutchinsonii | COG1587: Uroporphyrinogen-III synthase [Cytophaga hutchinsonii] | | | |
| 26168 | | | | Bacteroides fragilis | DNA primase [Bacteroides fragilis YCH46] dbj BAD50689.1 DNA primase [Bacteroides fragilis YCH46] | | | 2.7.7.- |
| 2617, | 53715231 | 36 | 4.00E-53 | YCH46 | | | | |
| 2618 | | | | Cytophaga | | | | |
| 26177, | 48853367 | 29 | 6.00E-09 | hutchinsonii | hypothetical protein Chut02003866 [Cytophaga hutchinsonii] | | | |
| 26178 | | | | | | Desc:Streptococcus polynucleotide SEQ ID NO 4279. | | |
| 26181, | 29349217 | 56 | 1.00E-58 | Bacteroides thetaiotaomicron | ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | Org:Streptococcus pyogenes | 90 | 5.00E-07 |
| 26182 | | | | VPI-5482 | | Xanthomonas campestris pv. campestris str. ATCC 33913, section 312 of 460 of the complete genome | | |
| 26183, | | | | Desulfovibrio vulgaris subsp. vulgaris str. | type I restriction-modification system, M subunit [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 26184 | 46580119 | 74 | 1.00E-114 | Hildenborough | | | | |
| 26185, | | | | Cytophaga | COG3182: Uncharacterized iron-regulated membrane protein [Cytophaga hutchinsonii] | | | |
| 26186 | 48855705 | 37 | 7.00E-17 | hutchinsonii | | | | |
| 26187, | | | | Cytophaga | COG3182: Uncharacterized iron-regulated membrane protein [Cytophaga hutchinsonii] | | | 1.8.1.2 |
| 26188 | 48855705 | 45 | 3.00E-16 | hutchinsonii | | | | |
| 26189, | | | | Bacteroides fragilis | hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 26190 | 53712708 | 35 | 3.00E-34 | YCH46 | | | | |
| 2619, | | | | Cytophaga | | | | |
| 2620 | 48855421 | 33 | 5.00E-17 | hutchinsonii | COG0210: Superfamily I DNA and RNA helicases [Cytophaga hutchinsonii] | | | |
| 26191, | | | | Cytophaga | | | | |
| 26192 | 48855274 | 44 | 6.00E-46 | hutchinsonii | COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii] | | | 2.7.7.- |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|--|---------------|
| 26193, | 29348750 | 38 | 6.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3341 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78447.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26194 | | | | Trichinella | unknown [Trichinella pseudospiralis] | | | | |
| 26195, | 3329480 | 31 | 2.00E-10 | pseudospiralis | COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii] | | | | |
| 26196 | | | | Cytophaga hutchinsonii | | | | | |
| 26201, | 48855337 | 59 | 4.00E-44 | Desulfovibrio | COG3004: Na ⁺ /H ⁺ antiporter [Desulfovibrio desulfuricans G20] | | | | 3.4E-5 |
| 26202, | 23473914 | 54 | 4.00E-42 | desulfuricans G20 | | | | | |
| 26205, | | | | Cytophaga hutchinsonii | hypothetical protein Chut02003091 [Cytophaga hutchinsonii] | | | | |
| 26206 | 48854003 | 42 | 5.00E-29 | hutchinsonii | | | | | |
| 26207, | | | | Cytophaga | hypothetical protein Chut02003091 [Cytophaga hutchinsonii] | | | | |
| 26208 | 48854003 | 27 | 6.00E-20 | hutchinsonii | COG0685: 5,10-methylenetetrahydrofolate reductase [Cytophaga hutchinsonii] | | | | 1.5.1.20 |
| 26209, | | | | Cytophaga | | | | | |
| 26210 | 48854977 | 58 | 6.00E-44 | hutchinsonii | | | | | |
| 26211, | | | | Bacteroides fragilis | hypothetical protein BF3300 [Bacteroides fragilis YCH46] db BAD50044.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 26212 | | | | YCH46 | | | | | |
| 26215, | | | | Anopheles | ENSANGP00000000474 [Anopheles gambiae] | | | | |
| 26216 | 53714586 | 39 | 2.00E-20 | gambiae | | | | | |
| 26217, | 31195541 | 61 | 6.00E-30 | | | | | | |
| 26218 | | | | Bacteroides fragilis | excinuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD50064.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46] | | | | 3.4.24.5 7 |
| 26219, | | | | YCH46 | | | | | |
| 26220 | 53714606 | 64 | 2.00E-68 | Riemerella | CAMP factor [Riemerella anatipestifer] | | | | |
| 26221, | | | | anatipestifer | COG0723: Deacetylases, including yeast histone deacetylase and acetoacetyl utilization protein [Cytophaga hutchinsonii] | | | | |
| 26222 | 11692013 | 66 | 7.00E-63 | Cytophaga | beta 1,4 glucosyltransferase [Aquifex aeolicus VF5] gb AAC07593.1 beta 1,4 glucosyltransferase - Aquifex aeolicus | | | | |
| 26225, | 48855767 | 57 | 6.00E-37 | hutchinsonii | small heat shock protein (hsp20-1) [Archaeoglobus fulgidus DSM 4304] putative translation factor [Bacteroides fragilis YCH46] db BAD50847.1 | | | | 2.--- |
| 26226 | | | | Aquifex aeolicus | | | | | |
| 26229, | 15606814 | 37 | 2.00E-21 | VF5 | | | | | |
| 26230 | | | | Archaeoglobus | | | | | |
| 2623, | | | | fulgidus DSM 4304 | | | | | |
| 2624 | 11498894 | 48 | 1.00E-20 | Bacteroides fragilis | | | | | |
| 26231, | | | | YCH46 | | | | | |
| 26232 | 53715189 | 42 | 5.00E-24 | Crocospaera | | | | | |
| 26233, | 45525072 | 46 | 6.00E-43 | watsonii WH 8501 | | | | | |
| 26234 | | | | | | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|--|----------|
| 26235, | 29348887 | 32 | 5.00E-23 | Bacteroides thetaiotaomicron VPI-5482 | integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78584.1 integrase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26236, | 48855612 | 34 | 4.00E-36 | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | | |
| 26243, | 24375180 | 30 | 2.00E-10 | Shewanella oneidensis MR-1 | hypothetical protein SO3682 [Shewanella oneidensis MR-1] gb AAN56667.1 hypothetical protein [Shewanella oneidensis MR-1] | | | | |
| 26244, | | | | | | | | | |
| 26245, | | | | | | | | | |
| 26246, | | | | | | | | | |
| 26247, | | | | | | | | | |
| 26248, | 15842808 | 23 | 1.00E-07 | Thermotoga maritima MSB8 | hypothetical protein TM0033 [Thermotoga maritima MSB8] gb AAD35127.1 hypothetical protein TM0033 [Thermotoga maritima MSB8] pir F72424 | | | | |
| 26249, | | | | | | | | | |
| 26250, | 42527168 | 33 | 2.00E-15 | Treponema denticola ATCC 35405 | hypothetical protein - Thermotoga maritima (strain MSB8) hypothetical protein TDE1661 [Treponema denticola ATCC 35405] gb AAS12177.1 conserved hypothetical protein [Treponema denticola ATCC 35405] | | | | |
| 2625, | | | | | | | | | |
| 2626, | 21244775 | 38 | 1.00E-51 | Xanthomonas axonopodis pv. citri str. 306 | beta-xylosidase [Xanthomonas axonopodis pv. citri str. 306] gb AAM38893.1 beta-xylosidase [Xanthomonas axonopodis pv. citri str. 306] | | | | 3.2.1.37 |
| 26253, | | | | | | | | | |
| 26254, | 33861696 | 36 | 2.00E-29 | Prochlorococcus marinus subsp. pastoris str. CCMP1986 | DNA polymerase I [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19599.1 DNA polymerase I [Prochlorococcus marinus subsp. pastoris str. CCMP1986] | | | | 2.7.7.7 |
| 26255, | | | | | | | | | |
| 26256, | 29346867 | 34 | 5.00E-30 | Bacteroides thetaiotaomicron VPI-5482 | two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO78564.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26259, | | | | | | | | | |
| 26260, | 48853613 | 41 | 2.00E-20 | Cytophaga hutchinsonii | COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii] | | | | |
| 26261, | | | | | | | | | |
| 26262, | 29345596 | 39 | 2.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | thiol:disulfide interchange protein dsbD precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO75293.1 thiol:disulfide interchange protein dsbD precursor [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26263, | | | | | | | | | |
| 26264, | 54302756 | 39 | 2.00E-13 | Photobacterium profundum SS9 | hypothetical protein PBPR81077 [Photobacterium profundum SS9] emb CAG22949.1 conserved hypothetical protein [Photobacterium profundum] | | | | |
| 26267, | | | | | | | | | |
| 26268, | 53714565 | 28 | 4.00E-19 | Bacteroides fragilis YCH46 | hypothetical protein BF3279 [Bacteroides fragilis YCH46] dbj BAD50023.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 26269, | | | | | | | | | |
| 26270, | 48855808 | 43 | 9.00E-24 | Cytophaga hutchinsonii | COG0694: Thioredoxin-like proteins and domains [Cytophaga hutchinsonii] | | | | |
| 26271, | | | | | | | | | |
| 26272, | 52841852 | 49 | 4.00E-28 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | alpha/beta hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27704.1 alpha/beta hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | |

| | | | | | | | | | |
|--------------|----------|----|-----------|--|--|---|----|----------|----------|
| 26273, 26274 | 41690505 | 76 | 4.00E-28 | Psychrobacter sp. 273-4 | COG1826: Sec-independent protein secretion pathway components [Psychrobacter sp. 273-4] | | | | |
| 26275, 26276 | 53714594 | 41 | 5.00E-17 | Bacteroides fragilis YCH46 | LacI family transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD50052.1 LacI family transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 26277, 26278 | 53711667 | 61 | 6.00E-50 | Bacteroides fragilis YCH46 | hypothetical protein BF0376 [Bacteroides fragilis YCH46] dbj BAD47125.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 26279, 26280 | 31790365 | 43 | 1.00E-25 | uncultured Acidobacteria bacterium | hypothetical protein [uncultured Acidobacteria bacterium] | | | | |
| 26281, 26282 | 15807914 | 32 | 1.00E-24 | Deinococcus radiodurans R1 | acyl-CoA dehydrogenase, putative [Deinococcus radiodurans R1] gb AAF12388.1 acyl-CoA dehydrogenase, putative [Deinococcus radiodurans] pir C75578 probable acyl-CoA dehydrogenase - Deinococcus radiodurans (strain R1) | | | | 1.3.99.2 |
| 26283, 26284 | 53691838 | 31 | 8.00E-32 | Desulfovibrio desulfuricans G20 | COG0642: Signal transduction histidine kinase [Desulfovibrio desulfuricans G20] | | | | 2.7.3.- |
| | | | | | | Escherichia coli EcoE type I restriction-modification enzyme R subunit (hsdR) and EcoE type I restriction modification enzyme M subunit (hsdM) genes, complete cds; and hsdS gene, partial sequence | 78 | 7.00E-16 | 2.1.1.72 |
| 26285, 26286 | 54308990 | 83 | 1.00E-119 | Photobacterium profundum SS9 | putative type I restriction enzyme EcoEI Mprotein [Photobacterium profundum SS9] emb CAG20208.1 putative type I restriction enzyme EcoEI Mprotein [Photobacterium profundum] | | | | |
| 26289, 26290 | 48855629 | 42 | 9.00E-21 | Cytophaga hutchinsonii | COG0356: F0F1-type ATP synthase, subunit a [Cytophaga hutchinsonii] | | | | |
| | | | | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC11677 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_712440.1 hypothetical protein LA2259 [Leptospira interrogans serovar Lai str. 56601] gb AAN49458.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS70268.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 26293, 26294 | 45657545 | 44 | 2.00E-29 | | | | | | |
| 26295, 26296 | 48854664 | 41 | 1.00E-42 | Cytophaga hutchinsonii | COG2217: Cation transport ATPase [Cytophaga hutchinsonii] | | | | 3.6.1.- |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|----------|--|--|
| 26333, 26334 | 32477073 | 28 | 1.00E-16 | Rhodopirellula baltica SH 1 | similar to preprotein translocase SecA chain [Rhodopirellula baltica SH 1 emb]CAD79222.1] similar to preprotein translocase SecA chain [Pirellula sp.] | | | |
| 26335, 26336 | 20807328 | 32 | 2.00E-09 | Thermoanaerobact er tengcongensis MB4 | transposase [Thermoanaerobacter tengcongensis MB4] transposase [Thermoanaerobacter tengcongensis MB4] | | | |
| 26339, 26340 | 506709 | 39 | 1.00E-34 | Staphylococcus aureus | type 1 capsule synthesis gene; CapM [Staphylococcus aureus] sp[P39862]CAPM_STAAU Capsular polysaccharide biosynthesis glycosyl transferase capM | 2.4.1.- | | |
| 26347, 26348 | 57636503 | 44 | 1.00E-13 | Staphylococcus epidermidis RP62A | rhodanese-like domain protein [Staphylococcus epidermidis RP62A] ref YP_189979.1 rhodanese-like domain protein [Staphylococcus epidermidis RP62A] | 1.6.- | | |
| 26349, 26350 | 48855702 | 40 | 3.00E-32 | Cytophaga hutchinsonii | COG3279: Response regulator of the LytR/AlgR family [Cytophaga hutchinsonii] | | | |
| 2635, 2636 | 45250014 | 34 | 6.00E-07 | Aneurinibacillus thermoaerophilus | putative transposase [Aneurinibacillus thermoaerophilus] | | | |
| 26351, 26352 | 29349257 | 34 | 8.00E-30 | Bacteroides thetataotomicon VPI-5482 | hypothetical protein BT3849 [Bacteroides thetataotomicon VPI-5482] gb AAO78954.1 conserved hypothetical protein [Bacteroides thetataotomicon VPI-5482] | | | |
| 26353, 26354 | 29346745 | 57 | 1.00E-55 | Bacteroides thetataotomicon VPI-5482 | folypolyglutamate synthase [Bacteroides thetataotomicon VPI-5482] gb AAO76442.1 folypolyglutamate synthase [Bacteroides thetataotomicon VPI-5482] | 6.3.2.17 | | |
| 26355, 26356 | 48831629 | 39 | 2.00E-29 | Magnetococcus sp. MC-1 | COG0248: Exopolyphosphatase [Magnetococcus sp. MC-1] polyphosphate kinase [Vibrio parahaemolyticus RIMD 2210633] db BAC58836.1 polyphosphate kinase [Vibrio parahaemolyticus] | 3.6.1.11 | | |
| 26357, 26358 | 28997347 | 51 | 9.00E-72 | Vibrio parahaemolyticus RIMD 2210633 | sp Q87S51 PPK_VIBPA Polyphosphate kinase (Polyphosphoric acid kinase) (ATP-polyphosphate phosphotransferase) | 2.7.4.1 | | |
| 26359, 26360 | 16119697 | 43 | 4.00E-39 | Agrobacterium tumefaciens str. C58 | hypothetical protein AGR_pAT_692 [Agrobacterium tumefaciens str. C58] gb AAK90844.1 AGR_pAT_692p [Agrobacterium tumefaciens str. C58] sp Q8UUK7 DP42_AGR15 DNA polymerase IV 2 (Pol IV 2) | 2.7.7.7 | | |
| 26361, 26362 | 45858436 | 29 | 3.00E-13 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711250.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AAN48268.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AAS71159.1 alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|---|----|----------|----------|
| 26297, | 29350005 | 63 | 2.00E-82 | Bacteroides thetataoiaomicon VPI-5482 | endopeptidase Cip ATP-binding chain B [Bacteroides thetataoiaomicon VPI-5482] sp Q89Y3 CLPB_BACTN_Chaperone clpB gb AAO79702.1 | Desc:Staphylococcus aureus DNA for cellular proliferation protein #1366. Org:Staphylococcus aureus | 85 | 1.00E-32 | |
| 26298 | | | | | endopeptidase Cip ATP-binding chain B [Bacteroides thetataoiaomicon VPI-5482] | | | | |
| 26301, | 48854653 | 60 | 4.00E-86 | Cytophaga hutchinsonii | COG0635: Coproporphyrinogen III oxidase and related Fe-S oxidoreductases [Cytophaga hutchinsonii] | | | | 1.00E-32 |
| 26302 | | | | | nitrogen fixation specific regulatory protein NifA [Chlorobium tepidum TLS] | | | | |
| 26303, | | | | | gb AAAM72756.1 nitrogen fixation specific regulatory protein NifA [Chlorobium tepidum TLS] | | | | |
| 26304 | 21674349 | 55 | 1.00E-33 | Chlorobium tepidum TLS | putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47143.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] | | | | |
| 26305, | 53711685 | 32 | 3.00E-09 | Bacteroides fragilis YCH46 | membrane-bound lytic murein transglycosylase D [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231868.1 membrane-bound lytic murein transglycosylase D [Vibrio cholerae O1 biovar eltor str. N16961] p B82102 | | | | |
| 26307, | | | | | membrane-bound lytic murein transglycosylase D VC2237 [Imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | 3.2.1.- |
| 26308 | 9656796 | 31 | 9.00E-21 | Vibrio cholerae O1 biovar eltor str. N16961 | molybdopterin biosynthesis protein moeB [Clostridium tetani E88] | | | | |
| 26309, | | | | | gb AAO36281.1 molybdopterin biosynthesis protein moeB [Clostridium tetani E88] | | | | |
| 26310 | 28211400 | 32 | 3.00E-07 | Clostridium tetani E88 | hypothetical protein Chut02000044 [Cytophaga hutchinsonii] | | | | |
| 2631, | 48856332 | 67 | 8.00E-38 | Cytophaga hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 26313, | | | | | | | | | |
| 26314 | 48856112 | 32 | 2.00E-17 | Cytophaga hutchinsonii | COG1946: Acyl-CoA thioesterase [Pseudomonas syringae pv. syringae B728a] | | | | 3.1.2.- |
| 26319, | | | | | | | | | |
| 26320 | 46188140 | 39 | 1.00E-24 | Pseudomonas syringae pv. syringae B728a | formyltetrahydrofolate deformylase [Bacteroides thetataoiaomicon VPI-5482] | | | | |
| 26321, | | | | | gb AAO76488.1 formyltetrahydrofolate deformylase [Bacteroides thetataoiaomicon VPI-5482] | | | | 3.5.1.10 |
| 26322 | 29346791 | 50 | 5.00E-53 | Bacteroides thetataoiaomicon VPI-5482 | putative hemolysin [Vibrio parahaemolyticus RIMD 2210633] | | | | |
| 26323, | | | | | dbj BAC58635.1 putative hemolysin [Vibrio parahaemolyticus] | | | | |
| 26324 | 28897146 | 43 | 1.00E-44 | Vibrio parahaemolyticus RIMD 2210633 | GldH [Flavobacterium columnare] | | | | |
| 26327, | | | | | | | | | |
| 26328 | 55540762 | 49 | 3.00E-34 | Flavobacterium columnare | COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 2633, | | | | | | | | | |
| 2634 | 48856489 | 44 | 2.00E-61 | Cytophaga hutchinsonii | | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|----------|----|---|--|--|--|--|---------|
| 26363, 26364 | 48846331 | 36 | 7.00E-30 | 15 | Geobacter metallireducens GS | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | | 2.7.3.- |
| 26365, 26366 | 48855464 | 38 | 7.00E-24 | | Cytophaga hutchinsonii | COG1999: Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems [Cytophaga hutchinsonii] | | | | |
| 26367, 26368 | 48854312 | 41 | 1.00E-23 | | Cytophaga hutchinsonii | COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii] | | | | |
| | | | | | | Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930575.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930493.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930331.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928792.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928083.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_927821.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16814.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15731.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15843.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15473.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE13790.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE13033.1 Transposase, IS630 | | | | |
| 2637, 2638 | 37528266 | 27 | 6.00E-11 | | Photorhabdus luminescens subsp. laumondii TTO1 | hypothetical protein BF0706 [Bacteroides fragilis YCH46] db BAD47453.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | 3.1.- |
| 26371, 26372 | 53711995 | 47 | 2.00E-16 | | Bacteroides fragilis YCH46 | GGDEF domain protein [Shewanella oneidensis MR-1] gb AAN55538.1 | | | | |
| 26373, 26374 | 24374051 | 45 | 9.00E-54 | | Shewanella oneidensis MR-1 | GGDEF domain protein [Shewanella oneidensis MR-1] | | | | |
| 26375, 26376 | 5006988 | 34 | 3.00E-31 | | Klebsiella pneumoniae | putative glycosyltransferase [Klebsiella pneumoniae] | | | | |
| 26377, 26378 | 23005587 | 32 | 2.00E-09 | | Magnetospirillum magnetotacticum MS-1 | COG1112: Superfamily I DNA and RNA helicases and helicase subunits [Magnetospirillum magnetotacticum MS-1] | | | | |
| 26379, 26380 | 48854362 | 23 | 1.00E-17 | | Cytophaga hutchinsonii | COG1033: Predicted exporters of the RND superfamily [Cytophaga hutchinsonii] | | | | |
| 26381, 26382 | 48853518 | 41 | 1.00E-43 | | Cytophaga hutchinsonii | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|---|----------------------------------|----------------|----------------------------------|--|--|----|----------|----------|---------------|
| 26385, 26386, 26387, 26388, 26389, 26390 | 54295786 48853586 14518365 | 41 48 42 | 4.00E-44 3.00E-55 9.00E-42 | Legionella pneumophila str. Lens Cytophaga hutchinsonii Microscilla sp. PRE1 | hypothetical protein lp2876 [Legionella pneumophila str. Lens] emb CAH17120.1 hypothetical protein [Legionella pneumophila str. Lens] COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga hutchinsonii] putative transposase [Microscilla sp. PRE1] gb AAK62882.1 MS160, putative transposase [Microscilla sp. PRE1] radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195] gb AAW39435.1 radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195] | | | | 3.4.21.5 3 |
| 26391, 26392, 26393, 26394 | 57233930 28829330 | 43 38 | 1.00E-18 1.00E-26 | Dehalococcoides ethenogenes 195 Dictyostelium discoideum | hypothetical protein [Dictyostelium discoideum] hypothetical protein, predicted Glutamate-cysteine ligase [Azoarcus sp. EbN1] emb CAI10097.1 hypothetical protein, predicted Glutamate-cysteine ligase [Azoarcus sp. EbN1] COG0732: Restriction endonuclease S subunits [Desulfovibrio desulfuricans G20] | | | | 5.2.1.8 |
| 26395, 26396, 26397, 26398 | 56479409 53690939 | 50 41 | 5.00E-48 4.00E-22 | Azoarcus sp. EbN1 Desulfovibrio desulfuricans G20 | | | | | 3.1.21.3 |
| 26399, 26400 | 48895665 | 68 | 6.00E-61 | Trichodesmium erythraeum IMS101 | COG0286: Type I restriction-modification system methyltransferase subunit [Trichodesmium erythraeum IMS101] XANTHINE DEHYDROGENASE [Brucella melitensis 16M] gb AAL52756.1 XANTHINE DEHYDROGENASE [Brucella melitensis 16M] pir AI3448 xanthine dehydrogenase (EC 1.1.1.204) [Imported] - Brucella melitensis (strain 16M) | 86 | 2.00E-08 | 2.1.1.72 | |
| 26401, 26402 | 17987858 | 37 | 8.00E-40 | Brucella melitensis 16M | | | | | 1.1.1.20 4 |
| 26403, 26404, 26405, 26406 | 48859543 37962765 | 36 43 | 3.00E-40 5.00E-10 | Clostridium thermocellum ATCC 27405 Salmonella typhimurium | COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] hypothetical protein [Salmonella typhimurium] | | | | 2.7.3.- |
| 26407, 26408, 26409, 26410 | 53712444 48854999 | 31 46 | 2.00E-09 1.00E-24 | Bacteroides fragilis YCH46 Cytophaga hutchinsonii | hypothetical protein BF1152 [Bacteroides fragilis YCH46] db BAD47902.1 conserved hypothetical protein [Bacteroides fragilis YCH46] COG1832: Predicted CoA-binding protein [Cytophaga hutchinsonii] COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga hutchinsonii] | | | | 3.4.21.5 3 |
| 2641, 2642 | 48853586 | 55 | 2.00E-86 | Cytophaga hutchinsonii | | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|---------------------------------------|---|--|--|--|----------|
| 26419, | 48856761 | 36 | 2.00E-38 | Cytophaga hutchinsonii | COG0550: Topoisomerase IA [Cytophaga hutchinsonii] | | | | 5.99.1.2 |
| 26420 | | | | | putative UDP-glucose-6 dehydrogenase [Bacteroides fragilis YCH46] | | | | |
| 26421, | | | | Bacteroides fragilis YCH46 | dbj BAD48192.1 putative UDP-glucose-6 dehydrogenase [Bacteroides fragilis YCH46] | | | | 1.1.1.- |
| 26422 | 53712734 | 53 | 6.00E-35 | | | | | | |
| 26423, | | | | Bacteroides thetaiotaomicron VPI-5482 | thiol:disulfide interchange protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26424 | 29346702 | 36 | 4.00E-26 | | gb AAO76399.1 thiol:disulfide interchange protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26425, | | | | Cytophaga hutchinsonii | COG1459: Type II secretory pathway, component PulF [Cytophaga hutchinsonii] | | | | |
| 26426 | 48855359 | 37 | 2.00E-57 | | | | | | |
| 26427, | | | | Bacteroides thetaiotaomicron VPI-5482 | Integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78584.1 | | | | |
| 26428 | 29348887 | 35 | 1.00E-22 | | Integrase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26429, | ABP3863 | | | | Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID | | | | 1.1.99.1 |
| 26430 | 5 | 53 | 2.00E-62 | | NO:3480. Org:Staphylococcus epidermidis | | | | 6 |
| 2643, | | | | Psychrobacter sp. | COG0367: Asparagine synthase (glutamine-hydrolyzing) [Psychrobacter sp. | | | | 6.3.5.4 |
| 2644 | 52853615 | 48 | 1.00E-58 | | 273-4] | | | | |
| 26433, | | | | Clostridium thermocellum | COG0642: Signal transduction histidine kinase [Clostridium thermocellum | | | | 2.7.3.- |
| 26434 | 48859543 | 41 | 7.00E-42 | | ATCC 27405] | | | | |
| 26435, | | | | Bacteroides fragilis YCH46 | putative aminotransferase [Bacteroides fragilis YCH46] dbj BAD47862.1 | | | | |
| 26436 | 53712404 | 55 | 1.00E-50 | | putative aminotransferase [Bacteroides fragilis YCH46] | | | | |
| 26437, | | | | Thermoanaerobacter tengcongensis MB4 | predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4] | | | | |
| 26438 | 20806598 | 38 | 2.00E-33 | | gb AAM23373.1 predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4] | | | | |
| 26439, | | | | Nostoc punctiforme PCC 73102 | COG5278: Predicted periplasmic ligand-binding sensor domain [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 26440 | 23128582 | 39 | 2.00E-39 | | transcriptional repressor of sporulation and degradative enzymes production [Geobacillus kaustophilus HTA426] dbj BAD75024.1 transcriptional repressor of sporulation and degradative enzymes production [Geobacillus kaustophilus HTA426] | | | | |
| 26445, | | | | Geobacillus kaustophilus HTA426 | kaustophilus HTA426] | | | | |
| 26446 | 56419274 | 45 | 5.00E-11 | | COG0451: Nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii] | | | | 5.1.3.20 |
| 2645, | | | | Cytophaga hutchinsonii | Desc:Porphyromonas gingivalis protein PG111. Org:Porphyromonas gingivalis | | | | |
| 2646 | 48855023 | 61 | 8.00E-33 | | | | | | |
| 26453, | AA3433 | | | | | | | | |
| 26454 | 1 | 39 | 4.00E-32 | | | | | | |
| 26455, | | | | Mesorhizobium sp. BNC1 | COG0419: ATPase involved in DNA repair [Mesorhizobium sp. BNC1] | | | | |
| 26456 | 45680928 | 25 | 1.00E-12 | | HrgA protein [Campylobacter jejuni RM1221] gb AAW36198.1 HrgA protein | | | | |
| 26457, | | | | Campylobacter jejuni RM1221 | [Campylobacter jejuni RM1221] | | | | |
| 26458 | 57238615 | 33 | 4.00E-25] | | | | | | |

| | | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|--|----------|
| 26461, 26462 | 55378462 | 38 | 6.00E-18 | Haloarcula marismortui ATCC 43049 | sulfatase [Haloarcula marismortui ATCC 43049] gblAAV46606.1] sulfatase [Haloarcula marismortui ATCC 43049] | | | | |
| 26463, 26464 | 16124596 | 35 | 6.00E-35 | Caulobacter crescentus CB15 | hypothetical protein CC0341 [Caulobacter crescentus CB15] gblAAK22328.1] hypothetical protein [Caulobacter crescentus CB15] pir[D87291 hypothetical protein CC0341 [imported] - Caulobacter crescentus | | | | 3.2.1.41 |
| 26467, 26468 | 48855923 | 41 | 3.00E-41 | Cytophaga hutchinsonii | COG2812: DNA polymerase III, gamma/tau subunits [Cytophaga hutchinsonii] | | | | 2.7.7.7 |
| 26469, 26470 | 50235077 | 46 | 2.00E-51 | Riemerella anatipestifer | OmpA [Riemerella anatipestifer] | | | | |
| 2647, 2648 | 56677853 | 36 | 4.00E-25 | Silicibacter pomeroi DSS-3 | conserved domain protein [Silicibacter pomeroi DSS-3] ref[YP_166471.1] hypothetical protein SPO1224 [Silicibacter pomeroi DSS-3] | | | | |
| 26471, 26472 | 48854902 | 36 | 8.00E-35 | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | | |
| 26473, 26474 | 48856112 | 33 | 3.00E-20 | Cytophaga hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 26475, 26476 | 48732855 | 43 | 5.00E-43 | Pseudomonas fluorescens PfO-1 | COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Pseudomonas fluorescens PfO-1] | | | | |
| 26477, 26478 | 48859543 | 41 | 6.00E-19 | Clostridium thermocellum ATCC 27405 | COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | | 2.7.3.- |
| 26485, 26486 | 48855760 | 64 | 2.00E-76 | Cytophaga hutchinsonii | COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii] | | | | 3.2.1.4 |
| 26489, 26490 | 29346495 | 39 | 1.00E-07 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1085 [Bacteroides thetaiotaomicron VPI-5482] gblAAO76192.1] hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482] | | | | |
| 2649, 2650 | 48856049 | 44 | 7.00E-32 | Cytophaga hutchinsonii | hypothetical protein Chut02001282 [Cytophaga hutchinsonii] | | | | |
| 26491, 26492 | 96583390 | 40 | 2.00E-07 | Vibrio cholerae O1 biovar eltor str. N16961 | transcriptional regulator, LuxR family [Vibrio cholerae O1 biovar eltor str. N16961] ref[NP_233336.1] transcriptional regulator, LuxR family [Vibrio cholerae O1 biovar eltor str. N16961] pir[H82395 transcription regulator LuxR family VCA0952 [imported] - Vibrio cholerae (strain N16961 serogroup O1)] | | | | |
| 26493, 26494 | 21245070 | 31 | 2.00E-15 | Xanthomonas axonopodis pv. citri str. 306 | hypothetical protein XAC4358 [Xanthomonas axonopodis pv. citri str. 306] gblAAM39188.1] conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] | | | | 2.7.3.- |

| | | | | | | | | | | |
|---------------------------|----------------------|----------|----------------------|--------------------------------------|---|---|--|--|----|----------------|
| 26495, 26496 | 16080603 | 39 | 1.00E-20 | 168 | Bacillus subtilis subsp. subtilis str. | two-component sensor histidine kinase [Bacillus subtilis subsp. subtilis str. 168] emb CAB15567.1 two-component sensor histidine kinase [Bacillus subtilis subsp. subtilis str. 168] pir RGBSDS degradative enzyme regulator / competence regulator degS - Bacillus subtilis gb AAC44937.1 histidine kinase sp P13799 DEGS_BACSU Sensor protein degS gb AAA22734.1 transcriptional activator protein gb AAA22732.1 degS protein | | | | 2.7.3.- |
| 265, 266 | 48862089 | 50 | 8.00E-64 | degradans 2-40 | Microbulbifer | hypothetical protein Mdeg02002723 [Microbulbifer degradans 2-40] | | | | |
| 26501, 26502 | 24374891 | 52 | 2.00E-36 | oneidensis MR-1 | Shewanella | hypothetical protein SO3380 [Shewanella oneidensis MR-1] gb AAN56378.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | | |
| 26507, 26508 | 17227649 | 43 | 3.00E-40 | 7120 | Nostoc sp. PCC | penicillin-binding protein [Nostoc sp. PCC 7120] pir AI1825 penicillin-binding protein [imported] - Nostoc sp. (strain PCC 7120) dbj BAB77677.1 penicillin-binding protein [Nostoc sp. PCC 7120] | | | | 3.5.2.6 |
| 2651, 2652 | 48854173 | 24 | 7.00E-09 | hutchinsonii | Cytophaga | hypothetical protein Chut02002840 [Cytophaga hutchinsonii] | | | | 3.2.1.13 |
| 26512, 26513, 26514 | 18086516 48856843 | 36 55 | 8.00E-28 8.00E-37 | Cellvibrio japonicus hutchinsonii | Cytophaga | alpha-glucuronidase [Cellvibrio japonicus] COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Cytophaga hutchinsonii] | | | | 6.2.1.1 |
| 26515, 26516 | 56461030 | 51 | 4.00E-25 | Idiomarina loihensis L2TR | Idiomarina | Zn-dependent aminopeptidase [Idiomarina loihensis L2TR] gb AAV82762.1 Zn-dependent aminopeptidase [Idiomarina loihensis L2TR] | | | | |
| 26517, 26518 | 31195879 | 54 | 1.00E-29 | Anopheles gambiae | Anopheles | ENSANGP00000000448 [Anopheles gambiae] | | | | 2.1.1.34 |
| 26521, 26522 | 48856383 | 40 | 1.00E-31 | hutchinsonii | Cytophaga | COG0044: Dihydroorotase and related cyclic amidohydrolases [Cytophaga hutchinsonii] | | | | 3.5.2.3 |
| 26523, 26524 | 29609430 | 62 | 3.00E-79 | Streptomyces avermitilis MA-4680 | Streptomyces | putative sugar ABC transporter ATP-binding protein [Streptomyces avermitilis MA-4680] ref NP_826945.1 putative sugar ABC transporter ATP-binding protein [Streptomyces avermitilis MA-4680] | Streptomyces avermitilis genomic DNA, complete genome, section 24/30 | | 90 | 2.00E-09 1.8.- |
| 26525, 26526 | 53715357 | 28 | 1.00E-21 | YCH46 | Bacteroides fragilis | hypothetical protein BF4073 [Bacteroides fragilis YCH46] dbj BAD50815.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 26527, 26528 | 48855642 | 34 | 6.00E-40 | hutchinsonii | Cytophaga | COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] Uncharacterized conserved secreted protein [Idiomarina loihensis L2TR] | | | | 5.2.1.8 |
| 26529, 26530 | 56459960 | 34 | 3.00E-09 | Idiomarina loihensis L2TR | Idiomarina | Uncharacterized conserved secreted protein [Idiomarina loihensis L2TR] | | | | |

| | | | | | | | | |
|--------|----------|----|-----------|---|---|--|--|----------|
| 2653, | 48856392 | 48 | 1.00E-18 | Cytophaga hutchinsonii | COG0419: ATPase Involved in DNA repair [Cytophaga hutchinsonii] | | | |
| 2654 | | | | Rubrivivax | COG1988: Predicted membrane-bound metal-dependent hydrolases | | | |
| 26531, | | | | gelatinosus PM1 | [Rubrivivax gelatinosus PM1] | | | |
| 26532 | 47575209 | 31 | 2.00E-21 | Cytophaga hutchinsonii | COG0265: Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain [Cytophaga hutchinsonii] | | | 3.4.21.- |
| 26533, | | | | Cytophaga hutchinsonii | COG0602: Organic radical activating enzymes [Cytophaga hutchinsonii] | | | |
| 26534 | 48853851 | 29 | 6.00E-11 | Cytophaga hutchinsonii | methionyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD51240.1 | | | 6.1.1.10 |
| 26535, | | | | Cytophaga hutchinsonii | methionyl-tRNA synthetase [Bacteroides fragilis YCH46] | | | |
| 26536 | 48856308 | 49 | 3.00E-30 | Cytophaga hutchinsonii | COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii] | | | 3.1.- |
| 26537, | | | | Bacteroides fragilis YCH46 | DNA processing protein DprA, putative [Porphyromonas gingivalis W83] | | | |
| 26538 | 53715782 | 69 | 1.00E-102 | Cytophaga hutchinsonii | ref NP_904614.1 DNA processing protein DprA, putative [Porphyromonas gingivalis W83] | | | |
| 26541, | | | | Cytophaga hutchinsonii | COG0147: Anthranilate/para-aminobenzoate synthetases component I [Cytophaga hutchinsonii] | | | 4.1.3.- |
| 26542 | 48855589 | 44 | 2.00E-16 | Cytophaga hutchinsonii | ENSANGP00000000452 [Anopheles gambiae] | | | |
| 26545, | | | | Porphyromonas gingivalis W83 | Desc:Porphyromonas gingivalis protein PG48. Org:Porphyromonas gingivalis | | | |
| 26546 | 34396447 | 43 | 4.00E-60 | Cytophaga hutchinsonii | DNA gyrase A subunit [Bacteroides fragilis YCH46] dbj BAD49160.1 DNA gyrase A subunit [Bacteroides fragilis YCH46] | | | 5.99.1.3 |
| 26547, | | | | Cytophaga hutchinsonii | ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] | | | |
| 26548 | 48856398 | 53 | 5.00E-41 | Anopheles gambiae | ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] | | | |
| 26549, | | | | Anopheles gambiae | ENSANGP000000002020 [Anopheles gambiae] | | | |
| 26550 | 31195945 | 40 | 3.00E-26 | Anopheles gambiae | COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] | | | 2.7.7.24 |
| 26551, | AAV3438 | | | Anopheles gambiae | COG0644: Dehydrogenases (flavoproteins) [Cytophaga hutchinsonii] | | | 1.- |
| 26552 | 2 | 37 | 5.00E-25 | Anopheles gambiae | COG1741: Pirin-related protein [Cytophaga hutchinsonii] | | | |
| 26553, | | | | Bacteroides fragilis YCH46 | ferrochelatase [Pseudomonas syringae pv. tomato str. DC3000] | | | |
| 26554 | 53713702 | 52 | 1.00E-78 | Bacteroides fragilis YCH46 | ref NP_790962.1 ferrochelatase [Pseudomonas syringae pv. tomato str. DC3000] sp Q888A2 HEMZ_PSESM Ferrochelatase (Protoheme ferro-lyase) (Heme synthetase) | | | 4.99.1.1 |
| 26555, | | | | Bacteroides fragilis YCH46 | | | | |
| 26556 | 53715217 | 46 | 2.00E-50 | Anopheles gambiae | | | | |
| 26557, | | | | Anopheles gambiae | | | | |
| 26558 | 31194819 | 41 | 6.00E-52 | Cytophaga hutchinsonii | | | | |
| 26559, | | | | Cytophaga hutchinsonii | | | | |
| 26560 | 48853434 | 68 | 2.00E-83 | Cytophaga hutchinsonii | | | | |
| 26563, | | | | Cytophaga hutchinsonii | | | | |
| 26564 | 48853677 | 52 | 4.00E-58 | Cytophaga hutchinsonii | | | | |
| 26565, | | | | Cytophaga hutchinsonii | | | | |
| 26566 | 48856673 | 65 | 2.00E-65 | Cytophaga hutchinsonii | | | | |
| 26567, | | | | Pseudomonas syringae pv. tomato str. DC3000 | | | | |
| 26568 | 28851580 | 55 | 8.00E-23 | Pseudomonas syringae pv. tomato str. DC3000 | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|--|--|--|---------------|
| 26569, 26570 | 29346615 | 69 | 1.00E-68 | Bacteroides thetaiotaomicron VPI-5482 | putative ATPase, AAA family [Bacteroides thetaiotaomicron VPI-5482] gb AAO76312.1 putative ATPase, AAA family [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.7.7 |
| 26573, 26574 | 45659189 | 43 | 1.00E-57 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gb AA51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gb AA51417.1 sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | 2.7.7.4 |
| 26575, 26576 | 53759913 | 38 | 4.00E-34 | Methylobacillus flagellatus KT | COG0232: dGTP triphosphohydrolase [Methylobacillus flagellatus KT] | | | 3.1.5.1 |
| 26577, 26578 | 53765021 | 44 | 8.00E-41 | Anabaena variabilis ATCC 29413 | COG0732: Restriction endonuclease S subunits [Anabaena variabilis ATCC 29413] | | | 3.1.21.3 |
| 26579, 26580 | 48856952 | 50 | 6.00E-67 | Cytophaga hutchinsonii | COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii] | | | 4.1.3.27 |
| 26581, 26582 | 39545768 | 24 | 2.00E-09 | Aeromonas hydrophila | putative ADP-heptose:LPS [Aeromonas hydrophila] | | | |
| 26583, 26584 | 34398084 | 60 | 5.00E-39 | Porphyromonas gingivalis W83 | conserved hypothetical protein TIGR00250 [Porphyromonas gingivalis W83] ref NP_906245.1 conserved hypothetical protein TIGR00250 [Porphyromonas gingivalis W83] | | | |
| 26589, 26590 | 32477598 | 47 | 3.00E-35 | Rhodopirella baltica SH 1 | hypothetical protein RB12586 [Rhodopirella baltica SH 1] emb CAD77669.1 hypothetical protein [Pirellula sp.] | | | |
| 2659, 2660 | 15076967 | 50 | 2.00E-23 | Myxococcus xanthus | response regulator HsfA [Myxococcus xanthus] | | | 2.7.-- |
| 26595, 26596 | 53711678 | 34 | 1.00E-09 | Bacteroides fragilis YCH46 | putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47136.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] | | | |
| 26601, 26602 | 54024396 | 47 | 8.00E-07 | Nocardia farcinica IFM 10152 | putative peptidase [Nocardia farcinica IFM 10152] dbj BAD57274.1 putative peptidase [Nocardia farcinica IFM 10152] | | | 3.4.17.1 1 |
| 26605, 26606 | 53711487 | 66 | 2.00E-68 | Bacteroides fragilis YCH46 | cysteinyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD46945.1 cysteinyl-tRNA synthetase [Bacteroides fragilis YCH46] | | | 6.1.1.16 |
| 2661, 2662 | 48853597 | 56 | 2.00E-67 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | 2.4.1.83 |
| 26611, 26612 | ABG3170 | 7 | 5.00E-14 | | Desc:Beta 1,3-galactose transferase protein #6. Org:Streptococcus agalactiae | | | 2.-- |
| 26613, 26614 | 17940055 | 31 | 1.00E-23 | Leptospira interrogans | unknown [Leptospira interrogans] | | | 2.4.-- |

| | | | | | | | | | |
|--------|----------|----|----------|--|---|--|--|--|----------|
| 26615, | 48853782 | 54 | 4.00E-29 | Cytophaga hutchinsonii | COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Cytophaga hutchinsonii] | | | | 2.7.7.7 |
| 26616 | | | | | | | | | |
| 26617, | 48854964 | 50 | 2.00E-26 | Cytophaga hutchinsonii | COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | | |
| 26618 | | | | | | | | | |
| 26621, | | | | | DNA polymerase III, gamma and tau subunits [Porphyromonas gingivalis W83] ref[NP_905573.1] DNA polymerase III, gamma and tau subunits [Porphyromonas gingivalis W83] | | | | |
| 26622 | 34397409 | 28 | 2.00E-07 | Porphyromonas gingivalis W83 | | | | | |
| 26623, | | | | | cytosine deaminase [Chlorobium tepidum TLS] gb AAM71830.1 cytosine deaminase [Chlorobium tepidum TLS] | | | | 3.5.4.1 |
| 26624 | 21673423 | 62 | 2.00E-46 | Chlorobium tepidum TLS | | | | | |
| 26627, | | | | | | | | | |
| 26628 | 48856903 | 32 | 1.00E-35 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | | |
| | | | | | | | | | |
| 26631, | | | | | NRF1 PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09530.1 | | | | |
| 26632 | 34556815 | 31 | 6.00E-34 | Wolinella succinogenes DSM 1740 | NRF1 PROTEIN [Wolinella succinogenes] | | | | |
| 26633, | | | | | | | | | |
| 26634 | 48854753 | 40 | 7.00E-13 | Cytophaga hutchinsonii | COG1078: HD superfamily phosphohydrolases [Cytophaga hutchinsonii] | | | | |
| | | | | | | | | | |
| 26635, | | | | | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Bacteroides fragilis YCH46] dbj BAD47688.1 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Bacteroides fragilis YCH46] | | | | 2.3.1.- |
| 26636 | 53712200 | 51 | 4.00E-36 | 3-hydroxymyristoyl | | | | | |
| 26639, | | | | | | | | | |
| 26640 | 48856260 | 29 | 5.00E-19 | Cytophaga hutchinsonii | COG0489: ATPases involved in chromosome partitioning [Cytophaga hutchinsonii] | | | | |
| 26641, | | | | | | | | | |
| 26642 | AAR5666 | 7 | | | Desc:Bacteroides fragilis RprX regulatory response protein. Org:Bacteroides fragilis | | | | 2.7.3.- |
| | | 38 | 8.00E-37 | | | | | | |
| 26643, | | | | | | | | | |
| 26644 | 48854369 | 45 | 7.00E-21 | Cytophaga hutchinsonii | COG0608: Single-stranded DNA-specific exonuclease [Cytophaga hutchinsonii] | | | | 3.1.- |
| 26645, | | | | | | | | | |
| 26646 | 57167881 | 32 | 2.00E-13 | Campylobacter coli RM2228 | DnaJ domain protein [Campylobacter coli RM2228] gb EAL57667.1 DnaJ domain protein [Campylobacter coli RM2228] | | | | |
| | | | | | | | | | |
| | | | | Legionella pneumophila subsp. pneumophila str. | reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27167.1 reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | 2.7.7.49 |
| 26649, | | | | | | | | | |
| 26650 | 52841315 | 56 | 7.00E-86 | Philadelphia 1 | | | | | |
| 26651, | | | | | | | | | |
| 26652 | 56964929 | 50 | 9.00E-11 | Bacillus clausii KSM-K16 | glycosyltransferase [Bacillus clausii KSM-K16] dbj BAD65699.1 glycosyltransferase [Bacillus clausii KSM-K16] | | | | |
| | | | | | | | | | |
| 26653, | | | | | | | | | |
| 26654 | 29345890 | 54 | 6.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.-.- |
| | | | | | | | | | |
| 26655, | | | | | | | | | |
| 26656 | 23114616 | 29 | 4.00E-09 | Desulfotobacterium hafnense DCB-2 | COG1196: Chromosome segregation ATPases [Desulfotobacterium hafnense DCB-2] | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|---|---|--|----|----------|----------|
| 26657, | 29347919 | 28 | 4.00E-13 | Bacteroides thetaiotaomicron VPI-5482 | putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO77616.1 putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 26658 | 48856481 | 56 | 4.00E-43 | Cytophaga hutchinsonii | COG1225: Peroxiredoxin [Cytophaga hutchinsonii] | | | | 1.11.1.- |
| 26659, | | | | | | Photobacterium profundum SS9 chromosome 2; segment 37 | | | |
| 26660 | 54302486 | 72 | 1.00E-98 | Photobacterium profundum SS9 | hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1 hypothetical maturase [Photobacterium profundum] excinuclease ABC, C subunit [Porphyromonas gingivalis W83] ref NP_906065.1 excinuclease ABC, C subunit [Porphyromonas gingivalis W83] | | 83 | 2.00E-16 | 2.7.7.49 |
| 26663, | 34397903 | 60 | 1.00E-60 | Porphyromonas gingivalis W83 | 1-deoxy-D-xylulose 5-phosphate synthase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO79204.1 1-deoxy-D-xylulose 5-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A0C2 DXS_BACTN 1-deoxy- D-xylulose-5-phosphate synthase (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS) | | | | 4.1.3.37 |
| 26664 | 29349507 | 49 | 1.00E-19 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BF4373 [Bacteroides fragilis YCH46] db BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 26665, | | | | | Desc:Human polypeptide SEQ ID NO 1661. Org:Homo sapiens | | | | |
| 26666 | 53715653 | 47 | 4.00E-21 | Bacteroides fragilis YCH46 | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | | | | |
| 26671, | ABP6961 | 4 | | | COG0637: Predicted phosphatase/phosphohexomutase [Enterococcus faecium] | | | | 5.4.2.6 |
| 26672 | 4 | 30 | 6.00E-15 | | COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | | |
| 26673, | 48853518 | 44 | 4.00E-59 | Cytophaga hutchinsonii | hypothetical protein Chut02003040 [Cytophaga hutchinsonii] | | | | |
| 26674 | 48825076 | 54 | 2.00E-37 | Enterococcus faecium | COG3279: Response regulator of the LytR/AigR family [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 26677, | 48853471 | 36 | 4.00E-07 | Cytophaga hutchinsonii | hypothetical protein BF4373 [Bacteroides fragilis YCH46] db BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 26678 | 48854367 | 46 | 2.00E-40 | Cytophaga hutchinsonii | sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AAM04689.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A] | | | | 2.7.3.- |
| 26683, | | | | | N-acetylneuraminase cytidyltransferase [Chromobacterium violaceum ATCC 12472] ref NP_903698.1 N-acetylneuraminase cytidyltransferase [Chromobacterium violaceum ATCC 12472] | | | | 2.7.7.43 |
| 26684 | 48854415 | 59 | 3.00E-80 | Cytophaga hutchinsonii | | | | | |
| 26685, | | | | | | | | | |
| 26686 | 53715653 | 51 | 5.00E-21 | Bacteroides fragilis YCH46 | | | | | |
| 26687, | 20090134 | 49 | 1.00E-21 | Methanosarcina acetivorans C2A | | | | | |
| 26688 | | | | Chromobacterium violaceum ATCC 12472 | | | | | |
| 26691, | | | | | | | | | |
| 26692 | 34105334 | 37 | 3.00E-13 | | | | | | |
| 26695, | | | | | | | | | |
| 26696 | | | | | | | | | |

| | | | | | | | | | |
|--------|----------|----|----------|--|-----------------------------------|---|--|--|---------------|
| 26697, | AAW9314 | 43 | 2.00E-10 | | | Desc:P. fluorescens xylanase protein Psexy. Org:Pseudomonas fluorescens | | | |
| 26698 | 1 | | | | | | | | |
| 26699, | | | | | Cytophaga | | | | |
| 26700 | 48854974 | 33 | 7.00E-10 | | hutchinsonii | hypothetical protein Chut02002032 [Cytophaga hutchinsonii] | | | |
| 267, | | | | | Photorhabdus | | | | |
| 268 | 37527378 | 31 | 2.00E-16 | | luminescens subsp. laumondii TTO1 | hypothetical protein plu3505 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15878.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] | | | 2.3.1.12 8 |
| 26701, | | | | | Cytophaga | | | | |
| 26702 | 48856922 | 43 | 7.00E-52 | | hutchinsonii | COG0841: Cation/multidrug efflux pump [Cytophaga hutchinsonii] | | | |
| 26703, | | | | | Cytophaga | | | | |
| 26704 | 48854245 | 31 | 4.00E-21 | | hutchinsonii | COG2227: 2-polyphenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinol methylase [Cytophaga hutchinsonii] | | | |
| 2671, | | | | | Gossypium | | | | |
| 2672 | 18077708 | 38 | 7.00E-25 | | hirsutum | reversibly glycosylated polypeptide [Gossypium hirsutum] | | | |
| 26713, | | | | | Thermotoga | | | | |
| 26714 | 15643285 | 53 | 2.00E-18 | | maritima MSB8 | hypothetical protein TM0519 [Thermotoga maritima MSB8] gb AAD35604.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir E72365 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | |
| 26715, | | | | | Bacteroides fragilis | | | | |
| 26716 | 53711344 | 41 | 4.00E-35 | | YCH46 | hypothetical protein BF0053 [Bacteroides fragilis YCH46] dbj BAD46802.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 26717, | | | | | Porphyromonas | | | | |
| 26718 | 34397767 | 49 | 2.00E-64 | | gingivalis W83 | glycogen synthase-related protein [Porphyromonas gingivalis W83] ref NP_905929.1 glycogen synthase-related protein [Porphyromonas gingivalis W83] | | | 2.4.1.21 |
| 26723, | | | | | Bacteroides | | | | |
| 26724 | 29349999 | 40 | 1.00E-32 | | thetataomicron VPI-5482 | putative nitrogen utilization substance protein [Bacteroides thetataomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetataomicron VPI-5482] | | | |
| 26725, | | | | | Bacteroides | | | | |
| 26726 | 29346358 | 52 | 6.00E-46 | | VPI-5482 | hypothetical protein BT0948 [Bacteroides thetataomicron VPI-5482] gb AAO76055.1 hypothetical protein [Bacteroides thetataomicron VPI-5482] | | | |
| 26727, | | | | | Clostridium | | | | |
| 26728 | 48859543 | 36 | 8.00E-34 | | thermocellum ATCC 27405 | COG0842: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | 2.7.3.- |
| 2673, | | | | | Enterococcus | | | | |
| 2674 | 48824414 | 47 | 2.00E-36 | | faecium | COG1134: ABC-type polysaccharide/polyol phosphate transport system, ATPase component [Enterococcus faecium] | | | 1.8.- |
| 26733, | | | | | Vibrio | | | | |
| 26734 | 28897278 | 54 | 1.00E-61 | | parahaemolyticus RIMD 2210633 | hypothetical protein VP0504 [Vibrio parahaemolyticus RIMD 2210633] sp Q87SC0 Y504_VIBPA Hypothetical UPF0246 protein VP0504 dbj BAC58767.1 conserved hypothetical protein [Vibrio parahaemolyticus] | | | |

| | | | | | | | | |
|-----------------|--------------|----|----------|---|--|--|--|----------|
| 26735, 26736 | 34396372 | 60 | 4.00E-80 | Porphyromonas gingivalis W83 | peptide chain release factor 3 [Porphyromonas gingivalis W83] ref NP_904540.1 peptide chain release factor 3 [Porphyromonas gingivalis W83] | | | 3.6.1.48 |
| 26739, 26740 | 23099975 | 30 | 4.00E-20 | Oceanobacillus theysensis HTE831 | two-component sensor histidine kinase [Oceanobacillus theysensis HTE831] dbj BAC14476.1 two-component sensor histidine kinase involved in degradative enzyme [Oceanobacillus theysensis HTE831] | | | 2.7.3.- |
| 26741, 26742 | 48855092 | 30 | 5.00E-11 | Cytophaga hutchinsonii | COG4594: Signal transduction histidine kinase [Cytophaga hutchinsonii] putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79072.1 putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI- 5482] | | | 2.7.3.- |
| 26743, 26744 | 29349375 | 40 | 8.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein VP2972 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61235.1 conserved hypothetical protein [Vibrio parahaemolyticus] | | | 2.7.3.- |
| 26745, 26746 | 28999746 | 42 | 2.00E-58 | Vibrio parahaemolyticus RIMD 2210633 | Desc:Beta-1,3-glucanase. Org:Bacillus sp | | | 3.2.1.- |
| 26747, 26748 | AAR1159 9 | 49 | 1.00E-29 | Shewanella oneidensis MR-1 | hypothetical protein SO0125 [Shewanella oneidensis MR-1] gb AAN53212.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | |
| 26751, 26752 | 45657308 | 30 | 1.00E-25 | Leptospira interrogans serovar Copenhagen str. Ficruz L1-130 | histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhagen str. Ficruz L1-130] gb AAS70031.1 histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhagen str. Ficruz L1-130] | | | 2.7.3.- |
| 26753, 26754 | 46446644 | 46 | 1.00E-47 | Parachlamydia sp. UWE25 | hypothetical protein pc1010 [Parachlamydia sp. UWE25] emb CAF23734.1 conserved hypothetical protein [Parachlamydia sp. UWE25] | | | |
| 26755, 26756 | 54309979 | 35 | 1.00E-19 | Photobacterium profundum SS9 | hypothetical protein PBPR2825 [Photobacterium profundum SS9] emb CAG21197.1 hypothetical protein [Photobacterium profundum] | | | |
| 26759, 26760 | 49235400 | 38 | 1.00E-22 | Moorella thermoacetica ATCC 39073 | COG0860: N-acetylmuramoyl-L-alanine amidase [Moorella thermoacetica ATCC 39073] | | | 3.5.1.28 |
| 26761, 26762 | 48783200 | 31 | 2.00E-16 | Burkholderia fungorum LB400 | COG0438: Glycosyltransferase [Burkholderia fungorum LB400] glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI- 5482] | | | 2.-.-.- |
| 26763, 26764 | 29345890 | 36 | 2.00E-43 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT1257 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76364.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 26765, 26766 | 29346667 | 62 | 2.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | | | | |

| | | | | | | | | |
|--------|----------|----|----------|--|--|--|--|---------------|
| 26767, | 55377565 | 28 | 7.00E-09 | Haloarcula marismortui ATCC 43049 | universal stress protein [Haloarcula marismortui ATCC 43049] | | | |
| 26768 | | | | Bacteroides fragilis YCH46 | glycosyltransferase [Bacteroides fragilis YCH46] | | | |
| 26769, | 53711775 | 45 | 3.00E-51 | | glycosyltransferase [Bacteroides fragilis YCH46] | | | |
| 26770 | | | | Dehalococcoides ethenogenes 195 | peptidase, M16 family [Dehalococcoides ethenogenes 195] gb AAW39284.1] | | | 3.4.99.- |
| 26771, | 57233779 | 27 | 1.00E-08 | Chloroflexus aurantiacus | COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus] | | | |
| 26772 | 53797086 | 34 | 4.00E-40 | Pseudomonas putida KT2440 | hypothetical protein PP1931 [Pseudomonas putida KT2440] | | | |
| 26777, | 26988659 | 27 | 3.00E-14 | Nostoc punctiforme PCC 73102 | hypothetical protein Npun02004704 [Nostoc punctiforme PCC 73102] | | | |
| 26778 | | | | Bacteroides thetaiotaomicron VPI-5482 | putative biotin--(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77345.1] putative biotin--(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | 6.3.4.15 |
| 26789, | 53687786 | 43 | 3.00E-14 | Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293 | COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293] | | | 2.1.1.- |
| 26790 | 23025146 | 31 | 7.00E-17 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd3175 [Bdellovibrio bacteriovorus HD100] emb CAE80931.1] pttB [Bdellovibrio bacteriovorus HD100] | | | 3.4.21.8 3 |
| 26799, | 42524558 | 44 | 4.00E-53 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] gb AAO78203.1] two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 26800 | | | | Bacteroides fragilis YCH46 | putative ABC transporter permease [Bacteroides fragilis YCH46] | | | |
| 26803, | 29348506 | 28 | 4.00E-12 | Cytophaga hutchinsonii | COG2319: FOG: WD40 repeat [Cytophaga hutchinsonii] | | | 2.7.1.37 |
| 26804 | | | | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |
| 26805, | 53712889 | 46 | 2.00E-09 | | | | | |
| 26806 | 48854768 | 30 | 9.00E-30 | | | | | |
| 2681, | 48854768 | 30 | 9.00E-30 | | | | | |
| 2682 | | | | | | | | |
| 26811, | 48854768 | 30 | 9.00E-30 | | | | | |
| 26812 | 48854548 | 34 | 2.00E-12 | | | | | |

| | | | | | | | | |
|-----------------|----------|----|----------|---|---|---|-------------|----------|
| 26813, 26814 | 53715360 | 48 | 2.00E-51 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50818.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] | | | 3.6.1.- |
| 26815, 26816 | 23126434 | 43 | 7.00E-15 | Nostoc punctiforme PCC 73102 | COG1112: Superfamily I DNA and RNA helicases and helicase subunits [Nostoc punctiforme PCC 73102] | | | 3.6.1.- |
| 26817, 26818 | | | | | | Vibrio vulnificus CMCP6 chromosome II section 2 of 6 of the complete sequence | 89 2.00E-13 | |
| 26819, 26820 | 56963185 | 28 | 4.00E-25 | Bacillus clausii KSM-K16 | hypothetical protein ABC1420 [Bacillus clausii KSM-K16] dbj BAD63955.1 hypothetical protein [Bacillus clausii KSM-K16] | | | |
| 26821, 26822 | 18309430 | 34 | 2.00E-15 | Clostridium perfringens str. 13 | probable transcriptional regulator [Clostridium perfringens str. 13] dbj BAB80154.1 probable transcriptional regulator [Clostridium perfringens str. 13] | | | 2.1.1.63 |
| 26823, 26824 | 48730285 | 54 | 7.00E-59 | Pseudomonas fluorescens Pfo-1 | COG1280: Putative threonine efflux protein [Pseudomonas fluorescens Pfo- 1] | | | |
| 26825, 26826 | 9654588 | 36 | 1.00E-21 | Vibrio cholerae O1 biovar eltor str. N16961 | hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229841.1 hypothetical protein VC0184 [Vibrio cholerae O1 biovar eltor str. N16961] pir C82355 hypothetical protein VC0184 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | |
| 26829, 26830 | 48869829 | 31 | 3.00E-08 | Pediococcus pentosaceus ATCC 25745 | COG0615: Cytidylyltransferase [Pediococcus pentosaceus ATCC 25745] L-sorbose dehydrogenase [Gloeobacter violaceus PCC 7421] dbj BAC90384.1 L-sorbose dehydrogenase [Gloeobacter violaceus PCC 7421] | | | 2.7.7.39 |
| 2683, 2684 | 37522012 | 30 | 1.00E-08 | Gloeobacter violaceus PCC 7421 | COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 26835, 26836 | 48854285 | 38 | 8.00E-41 | Cytophaga hutchinsonii | hypothetical protein RB4459 [Rhodopirellula baltica SH 1] emb CAD73798.1 conserved hypothetical protein [Pirellula sp.] | | | |
| 26837, 26838 | 32473118 | 30 | 3.00E-15 | Rhodopirellula baltica SH 1 | COG1999: Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems [Cytophaga hutchinsonii] | | | |
| 26841, 26842 | 48855464 | 37 | 1.00E-28 | Cytophaga hutchinsonii | hypothetical protein LMO2365_2347 [Listeria monocytogenes str. 4b F2365] gb AA05113.1 conserved domain protein [Listeria monocytogenes str. 4b F2365] | | | 2.7.7.49 |
| 26843, 26844 | 48908547 | 31 | 2.00E-16 | Listeria monocytogenes str. 4b F2365 | | | | |

| | | | | | | | | | | |
|-----------------|----------|----|-----------|---|---|---|----|-------|----------|---------|
| 26849, 26850 | 6457709 | 36 | 2.00E-13 | Deinococcus radiodurans | conserved hypothetical protein [Deinococcus radiodurans] pir F75565 conserved hypothetical protein - Deinococcus radiodurans (strain R1) ref NP_293774.1 hypothetical protein DR0048 [Deinococcus radiodurans R1] | | | | | |
| 26851, 26852 | 549039 | 42 | 5.00E-28 | | Type II restriction enzyme HpaII [Endonuclease HpaII] (R.HpaII) gb AAA20482.1 HpaII restriction endonuclease | | | | | |
| 26853, 26854 | 15995272 | 39 | 2.00E-24 | Clostridium acetobutylicum ATCC 824 | Predicted iron-sulfur flavoprotein [Clostridium acetobutylicum ATCC 824] gb AAK79961.1 Predicted iron-sulfur flavoprotein [Clostridium acetobutylicum ATCC 824] pir F97146 probable iron-sulfur flavoprotein [imported] - Clostridium acetobutylicum | | | | | |
| 26859, 26860 | 53713554 | 51 | 6.00E-37 | Bacteroides fragilis YCH46 | putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46] dbj BAD49012.1 putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46] | | | | | |
| 26861, 26862 | 29345937 | 46 | 1.00E-30 | Bacteroides thetaiotaomicron VPI-5482 | tryptophan synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO75634.1 tryptophan synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.2.1.20 | |
| 26863, 26864 | 19919301 | 48 | 2.00E-42 | Legionella pneumophila | putative ATP-dependent DNA helicase protein [Legionella pneumophila] | | | | | |
| 26867, 26868 | 53713283 | 37 | 2.00E-21 | Bacteroides fragilis YCH46 | hypothetical protein BF1993 [Bacteroides fragilis YCH46] dbj BAD48741.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | | |
| 26869, 26870 | 48854312 | 30 | 4.00E-23 | Cytophaga hutchinsonii | COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii] | Chromobacterium violaceum ATCC 12472 section 7 of 16 of the complete genome | | | | |
| 2687, 2688 | 47573321 | 90 | 1.00E-166 | Rubrivivax gelatinosus PM1 | COG2766: Putative Ser protein kinase [Rubrivivax gelatinosus PM1] | | 85 | ##### | | |
| 26873, 26874 | 47526988 | 25 | 8.00E-25 | Bacillus anthracis str. 'Ames Ancestor' | tpg glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. Sterne] | | | | 2.4.1.- | |
| 26875, 26876 | 48854156 | 37 | 6.00E-36 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | | | 2.7.3.- |

| | | | | | | | | |
|--------|----------|----|----------|--------------------------|---|--|--|----------|
| 26879, | 51245968 | 47 | 4.00E-28 | Desulfotalea | hypothetical membrane protein [Desulfotalea psychrophila LSV54] | | | |
| 26880 | | | | psychrophila LSV54 | emb[CAG36845.1] hypothetical membrane protein [Desulfotalea psychrophila LSV54] | | | |
| 26881, | 48856366 | 53 | 1.00E-69 | Cytophaga | COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii] | | | |
| 26882 | | | | hutchinsonii | | | | |
| 26883, | | | | Cytophaga | COG0084: Mg-dependent DNase [Cytophaga hutchinsonii] | | | 3.1.21.- |
| 26884 | 48855439 | 42 | 3.00E-52 | hutchinsonii | | | | |
| 26885, | | | | Cytophaga | hypothetical protein Chut02000024 [Cytophaga hutchinsonii] | | | |
| 26886 | 48856312 | 28 | 4.00E-10 | hutchinsonii | hypothetical protein PG0482 [Porphyromonas gingivalis W83] | | | |
| 26887, | | | | Porphyromonas | ref[NP_904777.1] hypothetical protein PG0482 [Porphyromonas gingivalis W83] | | | |
| 26888 | 34396610 | 39 | 1.00E-22 | gingivalis W83 | putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] | | | 4.1.99.4 |
| 26889, | | | | Acinetobacter sp. | emb[CAG67658.1] putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] | | | |
| 26890 | 50083970 | 49 | 5.00E-48 | ADP1 | COG0702: Predicted nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii] | | | |
| 2689, | 48856992 | 53 | 2.00E-56 | Cytophaga | COG0294: Dihydropteroate synthase and related enzymes [Cytophaga hutchinsonii] | | | 2.5.1.15 |
| 26895, | | | | Cytophaga | | | | |
| 26896 | 48855382 | 59 | 3.00E-35 | hutchinsonii | Uvs065 [uncultured bacterium] | | | |
| 26897, | | | | uncultured | | | | |
| 26898 | 37222114 | 49 | 6.00E-48 | bacterium | flavoprotein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76469.1 | | | 6.3.2.5 |
| 269, | | | | Bacteroides | flavoprotein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 270 | 29346772 | 47 | 5.00E-18 | thetaitaomicron VPI-5482 | COG1020: Non-ribosomal peptide synthetase modules and related proteins [Nostoc punctiforme PCC 73102] | | | 1.2.1.31 |
| 2691, | | | | Nostoc punctiforme | COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii] | | | 2.1.1.- |
| 2692 | 23129356 | 36 | 2.00E-30 | PCC 73102 | COG1033: Predicted exporters of the RND superfamily [Cytophaga hutchinsonii] | | | |
| 2693, | | | | Cytophaga | COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 2694 | 48854545 | 50 | 5.00E-59 | hutchinsonii | tyrosine-protein kinase [Bacteroides fragilis YCH46] dbj BAD49519.1 | | | 2.7.1.11 |
| 2695, | | | | Cytophaga | tyrosine-protein kinase [Bacteroides fragilis YCH46] | | | 2 |
| 2696 | 48854362 | 41 | 1.00E-61 | hutchinsonii | glucose-inhibited division protein B [Porphyromonas gingivalis W83] | | | |
| 2701, | | | | Cytophaga | ref[NP_905481.1] glucose-inhibited division protein B [Porphyromonas gingivalis W83] | | | |
| 2702 | 48854285 | 47 | 3.00E-55 | hutchinsonii | glucose-inhibited division protein B [Porphyromonas gingivalis W83] | | | |
| 2703, | | | | Bacteroides fragilis | ref[NP_905481.1] glucose-inhibited division protein B [Porphyromonas gingivalis W83] | | | |
| 2704 | 53714061 | 29 | 1.00E-26 | YCH46 | glucose-inhibited division protein B [Porphyromonas gingivalis W83] | | | |
| 2705, | | | | Porphyromonas | ref[NP_905481.1] glucose-inhibited division protein B [Porphyromonas gingivalis W83] | | | |
| 2706 | 34397317 | 46 | 8.00E-26 | gingivalis W83 | inhibited division protein B | | | |

| | | | | | | | | | |
|-------|----------|----|----------|---|---|--|--|--|----------|
| 2707, | 53693278 | 35 | 5.00E-08 | Pseudomonas syringae pv. syringae B728a | hypothetical protein Psyr03004855 [Pseudomonas syringae pv. syringae B728a] | | | | |
| 2708 | | | | | | | | | |
| 2709, | 54031433 | 24 | 4.00E-07 | Pseudomonas sp. JS666 | hypothetical protein PJS6w01001809 [Pseudomonas sp. JS666] | | | | |
| 2710 | | | | | probable topoisomerase IV, subunit B [Desulfotalea psychrophila LSV54] | | | | |
| 271, | | | | | emb[CAG37009.1] probable topoisomerase IV, subunit B [Desulfotalea psychrophila LSV54] | | | | 5.99.1.- |
| 272 | 51246132 | 56 | 8.00E-59 | Desulfotalea psychrophila LSV54 | | | | | |
| 2715, | | | | | conserved hypothetical protein [Plasmodium berghei] | | | | |
| 2716 | 56494344 | 26 | 2.00E-07 | Plasmodium berghei | | | | | |
| 2717, | | | | | TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO79003.1 TonB | | | | |
| 2718 | 29349306 | 36 | 8.00E-15 | Bacteroides thetaiotaomicron VPI-5482 | [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 2721, | | | | | phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78466.1 phosphoribosylglycinamide formyltransferase | | | | 2.1.2.2 |
| 2722 | 29348769 | 50 | 1.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| | | | | | hypothetical protein SF0994 [Shigella flexneri 2a str. 301] gb AAO42622.2 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] | | | | |
| 2731, | | | | | ref NP_836701.1 hypothetical protein S1062 [Shigella flexneri 2a str. 24571] | | | | |
| 2732 | 56479791 | 46 | 2.00E-31 | Shigella flexneri 2a str. 301 | gb AAP16507.1 hypothetical protein S1062 [Shigella flexneri 2a str. 24571] | | | | |
| | | | | | hypothetical protein b0992 [Escherichia coli K12] gb AAC74077.1 orf, hypothetical protein; putative ferredoxin-type protein [Escherichia coli K12] | | | | |
| 2733, | | | | | dbj BAA36134.1 Hypothetical protein in sfa 3' region . [Escherichia coli K12] | | | | |
| 2734 | 16128958 | 49 | 6.00E-54 | Escherichia coli K12 | pir F64840 probable ferredoxin-like protein yccM - Escherichia coli (strain K-12) sp P52636 YCCM_EC01 Putative electron transport protein yccM | | | | |
| 2735, | | | | | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator | | | | 2.7.3.- |
| 2736 | 27377973 | 48 | 8.00E-22 | Bradyrhizobium japonicum USDA 110 | [Bradyrhizobium japonicum USDA 110] | | | | |
| 2737, | | | | | cysteiny]-l-IRNA synthetase [uncultured crenarchaeote 74A4] | | | | 6.1.1.16 |
| 2738 | 15383990 | 58 | 2.00E-58 | uncultured crenarchaeote 74A4 | | | | | |
| 2739, | | | | | PREDICTED: hypothetical protein XP_540158 [Canis familiaris] | | | | 2.7.1.- |
| 2740 | 57098579 | 31 | 2.00E-08 | Canis familiaris | Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 65704. | | | | |
| 2741, | AAG5174 | | | | Org:Arabidopsis thaliana | | | | |
| 2742 | 5 | 38 | 1.00E-38 | | | | | | |
| 2743, | | | | | COG0706: Preprotein translocase subunit YidC [Cytophaga hutchinsonii] | | | | |
| 2744 | 48854398 | 37 | 4.00E-15 | Cytophaga hutchinsonii | | | | | |

| | | | | | | | | | |
|-------|----------|----|----------|---------------------------------------|---|--|--|--|----------|
| 2745, | 48854398 | 45 | 2.00E-14 | Cytophaga hutchinsonii | COG0706: Preprotein translocase subunit YidC [Cytophaga hutchinsonii] | | | | |
| 2746 | | | | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | | |
| 2749, | 48855448 | 30 | 7.00E-25 | Cytophaga hutchinsonii | | | | | |
| 2750 | | | | Anopheles gambiae | ENSANGP00000000470 [Anopheles gambiae] | | | | 2.3.1.- |
| 2751, | 31195995 | 54 | 1.00E-39 | Methanococcus maripaludis S2 | Sensory transduction histidine kinase [Methanococcus maripaludis S2] | | | | 2.7.3.- |
| 2752 | | | | Cytophaga hutchinsonii | SMC protein [Cytophaga hutchinsonii] ref ZP_00308092.1 COG1196: Chromosome segregation ATPases [Cytophaga hutchinsonii] | | | | |
| 2753, | 45358866 | 38 | 9.00E-33 | Rhodospirillum rubrum | COG1434: Uncharacterized conserved protein [Rhodospirillum rubrum] | | | | |
| 2754 | | | | Cytophaga hutchinsonii | COG2332: Cytochrome c-type biogenesis protein CcmE [Cytophaga hutchinsonii] | | | | |
| 2757, | 28375463 | 71 | 1.00E-87 | Nostoc sp. PCC 7120 | two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] | | | | |
| 2758 | | | | Shewanella oneidensis MR-1 | pir JAG1928 two-component hybrid sensor and regulator ali0878 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB72935.1 two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] | | | | 2.7.3.- |
| 2759, | 48766298 | 37 | 3.00E-21 | uncultured archaeon | gamma-glutamyltranspeptidase [Shewanella oneidensis MR-1] | | | | |
| 2760 | | | | Treponema denticola ATCC 35405 | hypothetical protein [uncultured archaeon] | | | | |
| 2761, | 48855401 | 30 | 2.00E-07 | Cytophaga hutchinsonii | hypothetical protein TDE1723 [Treponema denticola ATCC 35405] | | | | |
| 2762 | | | | Cytophaga hutchinsonii | gb AAS12238.1 hypothetical protein TDE1723 [Treponema denticola ATCC 35405] | | | | |
| 2763, | 17228473 | 41 | 9.00E-37 | Cytophaga hutchinsonii | hypothetical protein Chut02000314 [Cytophaga hutchinsonii] | | | | |
| 2764 | | | | Cytophaga hutchinsonii | hypothetical protein Chut02000253 [Cytophaga hutchinsonii] | | | | |
| 2769, | 24372330 | 45 | 1.00E-64 | Bacteroides thetaiotaomicron VPI-5482 | COG0854: Pyridoxal phosphate biosynthesis protein [Cytophaga hutchinsonii] | | | | |
| 2770 | | | | Bacteroides fragilis YCH46 | tryptophan synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 277, | 56295580 | 47 | 4.00E-26 | Cytophaga hutchinsonii | gb AAO75634.1 tryptophan synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.2.1.20 |
| 278 | | | | Treponema denticola ATCC 35405 | Na+/H+ antiporter [Bacteroides fragilis YCH46] | | | | |
| 2771, | 42527229 | 38 | 1.00E-36 | Cytophaga hutchinsonii | COG0188: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit [Cytophaga hutchinsonii] | | | | |
| 2772 | | | | Cytophaga hutchinsonii | | | | | |
| 2775, | 48856580 | 48 | 3.00E-32 | Cytophaga hutchinsonii | | | | | |
| 2776 | | | | Cytophaga hutchinsonii | | | | | |
| 2785, | 48856525 | 42 | 9.00E-16 | Cytophaga hutchinsonii | | | | | |
| 2786 | | | | Cytophaga hutchinsonii | | | | | |
| 2787, | 48853523 | 67 | 4.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | | | | | |
| 2788 | | | | Bacteroides fragilis YCH46 | | | | | |
| 2789, | 29345937 | 51 | 1.00E-39 | Cytophaga hutchinsonii | | | | | |
| 2790 | | | | Cytophaga hutchinsonii | | | | | |
| 279, | 53711736 | 34 | 7.00E-14 | Cytophaga hutchinsonii | | | | | |
| 280 | | | | Cytophaga hutchinsonii | | | | | |
| 2791, | 48853743 | 37 | 2.00E-16 | Cytophaga hutchinsonii | | | | | |
| 2792 | | | | Cytophaga hutchinsonii | | | | | |

| | | | | | | | | | |
|-------|----------|----|-----------|--|--|--|--|--|---------|
| 2795, | 48855969 | 59 | 1.00E-103 | Cytophaga hutchinsonii | COG0841: Cation/multidrug efflux pump [Cytophaga hutchinsonii] | | | | |
| 2796 | | | | Microbulbifer | COG0749: DNA polymerase I - 3'-5' exonuclease and polymerase domains | | | | 2.7.7.7 |
| 2803, | 48864493 | 36 | 2.00E-17 | degradans 2-40 | [Microbulbifer degradans 2-40] | | | | |
| 2804 | | | | | two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 2805, | 29345776 | 27 | 6.00E-13 | Bacteroides thetaiotaomicron VPI-5482 | regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 2806 | | | | | peptidyl-prolyl cis-trans isomerase SurA [Chlorobium tepidum TLS] | | | | |
| 2807, | 21675072 | 35 | 4.00E-24 | Chlorobium tepidum TLS | gblAAM73479.1] peptidyl-prolyl cis-trans isomerase SurA [Chlorobium tepidum TLS] | | | | 5.2.1.8 |
| 2808 | | | | | | | | | |
| 281, | 48855210 | 48 | 1.00E-35 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | | |
| 282 | | | | | ORF8 [Bacteriophage phi-105] p1f [T13548 hypothetical protein 8 - Bacillus phage phi-105 db][BAA36665.1] ORF8 [bacteriophage phi-105] | | | | |
| 2811, | 22855032 | 34 | 8.00E-37 | Bacteriophage phi-105 | | | | | |
| 2812 | | | | | | | | | |
| 2813, | | | | Rubrobacter xylanophilus DSM | COG4585: Signal transduction histidine kinase [Rubrobacter xylanophilus DSM 9941] | | | | 2.7.3.- |
| 2814 | 46106876 | 31 | 1.00E-13 | 9941 | | | | | |
| 2817, | | | | Bradyrhizobium japonicum USDA | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj[BAC48127.1] two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] | | | | 2.7.3.- |
| 2818 | 27377973 | 53 | 9.00E-29 | 110 | | | | | |
| 2819, | | | | Bradyrhizobium japonicum USDA | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj[BAC48127.1] two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] | | | | 2.7.3.- |
| 2820 | 27377973 | 50 | 1.00E-43 | 110 | | | | | |
| 2821, | | | | Cytophaga hutchinsonii | COG3968: Uncharacterized protein related to glutamine synthetase [Cytophaga hutchinsonii] | | | | 6.3.1.2 |
| 2822 | 48856327 | 58 | 8.00E-68 | | | | | | |
| 2823, | | | | Novosphingobium aromaticivorans DSM | hypothetical protein Sar02001624 [Novosphingobium aromaticivorans DSM 12444] | | | | |
| 2824 | 48849513 | 30 | 8.00E-18 | DSM 12444 | | | | | |
| 2825, | | | | Listeria monocytogenes str. 4b F2365 | hypothetical protein LMO2365_2347 [Listeria monocytogenes str. 4b F2365] | | | | |
| 2826 | 46908547 | 31 | 5.00E-11 | | gblAA105113.1] conserved domain protein [Listeria monocytogenes str. 4b F2365] | | | | |
| | | | | | glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gblAAL49448.1] unknown [Leptospira interrogans] gblAAK19913.1] unknown [Leptospira interrogans] gblAAS70700.1] glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | |
| 2829, | | | | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | | | | | |
| 2830 | 45657977 | 33 | 8.00E-13 | | | | | | |
| 2833, | | | | Cytophaga hutchinsonii | COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii] | | | | |
| 2834 | 48854312 | 57 | 1.00E-47 | | | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|---|----|----------|----------|
| 2837, 2838 | 30248905 | 34 | 3.00E-10 | Nitrosomonas europaea ATCC 19718 | PDZ domain (also known as DHR or GLGF) [Nitrosomonas europaea ATCC 19718] emb CAD84812.1 PDZ domain (also known as DHR or GLGF) [Nitrosomonas europaea ATCC 19718] | | | | 3.4.21.- |
| 2841, 2842 | 29346358 | 50 | 1.00E-34 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0948 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76055.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482] | | | | |
| 2843, 2844 | 56460817 | 39 | 5.00E-48 | Idiomarina loihensis L2TR | Predicted amidohydrolase [Idiomarina loihensis L2TR] gb AAV82549.1 Predicted amidohydrolase [Idiomarina loihensis L2TR] | | | | |
| 285, 286 | | | | | | Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence | ## | 5.00E-30 | |
| 2851, 2852 | 48862211 | 36 | 9.00E-41 | Microbulbifer degradans 2-40 | COG2899: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] | | | | |
| 2853, 2854 | 15678563 | 60 | 8.00E-51 | Methanothermobac ter thermautotrophicus str. Delta H | peptide methionine sulfoxide reductase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB8504.1.1 peptide methionine sulfoxide reductase [Methanothermobacter thermotrophicus str. Delta H] pir F69170 peptide methionine sulfoxide reductase - Methanobacterium thermautotrophicum (strain Delta H) sp O26635 MSRA_METH Peptide methionine sulfoxide reductase msrA (Protein-methionine-S-oxide reductase) (Peptide Met(O) reductase) | | | 1.8.4.6 | |
| 2855, 2856 | 49658888 | 50 | 1.00E-58 | Yersinia pseudotuberculosis | hypothetical protein [Yersinia pseudotuberculosis] | | | | |
| 2857, 2858 | 53715647 | 43 | 3.00E-27 | Bacteroides fragilis YCH46 | putative endo-1,4-beta-xylanase [Bacteroides fragilis YCH46] dbj BAD51105.1 putative endo-1,4-beta-xylanase [Bacteroides fragilis YCH46] | | | | |
| 2859, 2860 | 48854355 | 50 | 2.00E-71 | Cytophaga hutchinsonii | COG1200: RecG-like helicase [Cytophaga hutchinsonii] | | | | 3.6.1.- |
| 2861, 2862 | 15678404 | 55 | 2.00E-39 | Methanothermobac ter thermautotrophicus str. Delta H | hypothetical protein MTH376 [Methanothermobacter thermotrophicus str. Delta H] gb AAB84882.1 conserved protein [Methanothermobacter thermautotrophicus str. Delta H] pir F69148 hypothetical protein MTH376 - Methanobacterium thermotrophicum (strain Delta H)] | | | | 2.4.1.- |
| 2863, 2864 | 16329400 | 42 | 2.00E-25 | Synechocystis sp. PCC 6803 | hypothetical protein sir1790 [Synechocystis sp. PCC 6803] sp P72793 YH90_SYNY3 Hypothetical UPF0093 protein sir1790 dbj BAA16808.1 sir1790 [Synechocystis sp. PCC 6803] pir S74656 hypothetical protein sir1790 - Synechocystis sp. (strain PCC 6803) | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|---|----|----------|----------|
| 2867, 2868 | 32041369 | 37 | 3.00E-41 | Pseudomonas aeruginosa UCBPP- PA14 | COG1864: DNA/RNA endonuclease G, NUC1 [Pseudomonas aeruginosa UCBPP-PA14] | | | | |
| 287, 288 | | | | | | Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence | 98 | 8.00E-26 | |
| 2881, 2882 | 48855793 | 28 | 5.00E-12 | Cytophaga hutchinsonii | hypothetical protein Chut02001004 [Cytophaga hutchinsonii] | | | | |
| 2883, 2884 | 56678821 | 35 | 7.00E-08 | Silicibacter pomeroi DSS-3 | von Willebrand factor type A domain protein [Silicibacter pomeroi DSS-3] ref YP_167447.1 von Willebrand factor type A domain protein [Silicibacter pomeroi DSS-3] | | | | |
| 2885, 2886 | 27375314 | 28 | 2.00E-08 | Bradyrhizobium japonicum USDA 110 | hypothetical protein bli0203 [Bradyrhizobium japonicum USDA 110] dbj BAC45468.1 bli0203 [Bradyrhizobium japonicum USDA 110] conserved hypothetical protein 455 - Odontella sinensis chloroplast emb CAA91669.1 ORF455, homologous to Porphyra ORF565 [Odontella sinensis] ref NP_043637.1 ORF455 [Odontella sinensis] sp P49540 YC45_ODOSI HYPOTHETICAL 51.9 KD PROTEIN YCF45 (ORF455) | | | | |
| 289, 290 | 7484312 | 33 | 1.00E-16 | Odontella sinensis | | Cylindrotheca sp. chloroplast acyl carrier protein (ACP) gene, complete cds | 83 | 1.00E-12 | |
| 2891, 2892 | 20090585 | 82 | 5.00E-62 | Methanosarcina acetivorans C2A | hypothetical protein MA1733 [Methanosarcina acetivorans C2A] gb AA05140.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | Methanosarcina mazel strain Goe1, section 291 of 379 of the complete genome | 84 | 4.00E-81 | |
| 2895, 2896 | 45917111 | 47 | 9.00E-29 | Mesorhizobium sp. BNC1 | COG3618: Predicted metal-dependent hydrolase of the TIM-barrel fold [Mesorhizobium sp. BNC1] | | | 2.4.2.- | |
| 2897, 2898 | 53712889 | 33 | 2.00E-20 | Bacteroides fragilis YCH46 | putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46] | | | | |
| 2903, 2904 | 48855091 | 37 | 7.00E-36 | Cytophaga hutchinsonii | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii] | | | | 3.1.1.61 |
| 2905, 2906 | 16331101 | 33 | 7.00E-42 | Synechocystis sp. PCC 6803 | hemolysin [Synechocystis sp. PCC 6803] sp P74409 Y260_SYNY3 Hypothetical UPF0053 protein sl0260 dbj BAA18507.1 hemolysin [Synechocystis sp. PCC 6803] pir IS76248 hemolysin, 49K - Synechocystis sp. (strain PCC 6803) | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|--|---|----|---------------|
| 2907, 2908 | 16077350 | 43 | 8.00E-18 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU02810 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12075.1 ycdD [Bacillus subtilis subsp. subtilis str. 168] pir F69755 L-alanyl-D-glutamate peptidase homolog ycdD - Bacillus subtilis dbj BAA22242.1 YcdD [Bacillus subtilis] | | | | |
| 2913, 2914 | 48855609 | 79 | 7.00E-67 | Cytophaga hutchinsonii | COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii] | | Bacteroides fragilis YCH46 DNA, complete genome | 93 | 4.00E-07 |
| 2919, 2920 | 48860303 | 46 | 4.00E-43 | Clostridium thermocellum ATCC 27405 | COG0124: Histidyl-tRNA synthetase [Clostridium thermocellum ATCC 27405] | | | | 6.1.1.21 |
| 2923, 2924 | 48853834 | 69 | 2.00E-82 | Cytophaga hutchinsonii | COG0536: Predicted GTPase [Cytophaga hutchinsonii] | | | | |
| 2925, 2926 | 42548894 | 40 | 1.00E-26 | Gibberella zeae PH-1 | hypothetical protein FG03048.1 [Gibberella zeae PH-1] ref XP_383224.1 hypothetical protein FG03048.1 [Gibberella zeae PH-1] | | | | 5.1.3.2 |
| 2931, 2932 | 21227192 | 46 | 3.00E-57 | Methanosarcina mazel Go1 | putative DNA integration/recombination/inversion protein [Methanosarcina mazel Go1] gb AAM30786.1 putative DNA integration/recombination/inversion protein [Methanosarcina mazel Go1] | | | | |
| 2933, 2934 | 48854286 | 33 | 4.00E-38 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | | |
| 2935, 2936 | 54303474 | 31 | 3.00E-11 | Photobacterium profundum SS9 | hypothetical protein PBPRB1809 [Photobacterium profundum SS9] emb CAG23667.1 hypothetical protein [Photobacterium profundum] | | | | |
| 2937, 2938 | 18977621 | 32 | 7.00E-30 | Pyrococcus furfosus DSM 3638 | putative ABC transporter [Pyrococcus furiosus DSM 3638] gb AAL81373.1 putative ABC transporter (ATP-binding protein) [Pyrococcus furiosus DSM 3638] | | | | 1.8.- |
| 2939, 2940 | 45659189 | 48 | 7.00E-58 | Leptospira interrogans serovar Copenhageni str. F1000 | sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. F1000] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gb AAN51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gb AAS71912.1 sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. F1000] | | | | 2.7.7.4 |
| 2943, 2944 | 53757295 | 77 | 7.00E-61 | Methylococcus capsulatus str. Bath | conserved hypothetical protein TIGR00149 [Methylococcus capsulatus str. Bath] ref YP_114605.1 conserved hypothetical protein TIGR00149 | | Legionella pneumophila subsp. pneumophila str. Philadelphia 1, complete genome | 83 | 2.00E-12 |
| 2945, 2946 | 48853426 | 57 | 4.00E-51 | Cytophaga hutchinsonii | COG2140: Thermophilic glucose-6-phosphate isomerase and related metalloenzymes [Cytophaga hutchinsonii] | | | | 1.13.11. 6 |

| | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|----------|
| 2947, 2948 | 28211859 | 47 | 8.00E-37 | Clostridium tetani E88 | succinoglycan biosynthesis protein exoA [Clostridium tetani E88] gb AAO36740.1 succinoglycan biosynthesis protein exoA [Clostridium tetani E88] | | | 2.4.1.- |
| 2953, 2954 | 53713424 | 35 | 1.00E-37 | Bacteroides fragilis YCH46 | ATP-dependent helicase [Bacteroides fragilis YCH46] dbj BAD48882.1 ATP- dependent helicase [Bacteroides fragilis YCH46] | | | 3.1.11.5 |
| 2955, 2956 | 7270581 | 39 | 4.00E-07 | Arabidopsis thaliana | putative protein [Arabidopsis thaliana] emb CAA18134.1 putative protein [Arabidopsis thaliana] pir T04597 hypothetical protein F23E13.170 - Arabidopsis thaliana | | | |
| 2957, 2958 | 29350162 | 58 | 3.00E-97 | Bacteroides thetataoamicron VPI-5482 | putative cytosine-specific methyltransferase [Bacteroides thetataoamicron VPI-5482] gb AAO79859.1 putative cytosine-specific methyltransferase [Bacteroides thetataoamicron VPI-5482] | | | 2.1.1.73 |
| 2959, 2960 | 34397767 | 54 | 1.00E-81 | Porphyromonas gingivalis W83 | glycogen synthase-related protein [Porphyromonas gingivalis W83] ref NP_905929.1 glycogen synthase-related protein [Porphyromonas gingivalis W83] | | | 2.4.1.21 |
| 2965, 2966 | 29349967 | 61 | 3.00E-37 | Bacteroides thetataoamicron VPI-5482 | hypothetical protein BT4559 [Bacteroides thetataoamicron VPI-5482] gb AAO79664.1 conserved hypothetical protein [Bacteroides thetataoamicron VPI-5482] | | | |
| 2967, 2968 | 48853419 | 59 | 2.00E-37 | Cytophaga hutchinsonii | COG0251: Putative translation initiation inhibitor, yjgF family [Cytophaga hutchinsonii] | | | |
| 2969, 2970 | 48858374 | 51 | 7.00E-08 | Clostridium thermocellum ATCC 27405 | COG2908: Uncharacterized protein conserved in bacteria [Clostridium thermocellum ATCC 27405] | | | |
| 297, 298 | 48854724 | 46 | 3.00E-17 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 2971, 2972 | 48835731 | 57 | 4.00E-30 | Thermobifida fusca | COG0031: Cysteine synthase [Thermobifida fusca] | | | 4.2.1.22 |
| 2973, 2974 | 53764771 | 32 | 1.00E-32 | Anabaena variabilis ATCC 29413 | COG0031: Cysteine synthase [Anabaena variabilis ATCC 29413] | | | 4.2.1.22 |
| 2975, 2976 | 21227784 | 30 | 5.00E-25 | Methanosarcina mazel Go1 | DNA mismatch repair protein [Methanosarcina mazel Go1] gb AAM31378.1 DNA mismatch repair protein [Methanosarcina mazel Go1] | | | |
| 2977, 2978 | 56680238 | 33 | 3.00E-16 | Silicibacter pomeroiy DSS-3 | conserved hypothetical protein [Silicibacter pomeroiy DSS-3] ref YP_168877.1 hypothetical protein SPO3682 [Silicibacter pomeroiy DSS- 3] | | | |
| 2979, 2980 | 48856934 | 46 | 1.00E-69 | Cytophaga hutchinsonii | COG1058: Predicted nucleotide-utilizing enzyme related to molybdopterin- biosynthesis enzyme MoeA [Cytophaga hutchinsonii] | | | |
| 2981, 2982 | 41205694 | 41 | 4.00E-59 | Geobacillus stearothermophilus | putative rhamnosyltransferase [Geobacillus stearothermophilus] | | | 2.4.-.- |

| | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|---------------|
| 2983, 2984 | 56783477 | 63 | 4.00E-96 | Campylobacter [ejuni] | nucleotidyl-sugar pyranose mutase [Campylobacter [ejuni]] | | | 4.2.1.46 |
| 2985, 2986 | 48853539 | 32 | 7.00E-25 | Cytophaga hutchinsonii | COG3021: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 299, 300 | 48854664 | 44 | 6.00E-38 | Cytophaga hutchinsonii | COG2217: Cation transport ATPase [Cytophaga hutchinsonii] | | | 3.6.1.- |
| 2993, 2994 | 48854452 | 56 | 3.00E-57 | Cytophaga hutchinsonii | COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii] | | | |
| 2995, 2996 | 48854793 | 58 | 5.00E-75 | Cytophaga hutchinsonii | COG1109: Phosphomannomutase [Cytophaga hutchinsonii] | | | 5.4.2.8 |
| 2997, 2998 | 51244102 | 35 | 1.00E-10 | Desulfotalea psychrophila Lsv54 | related to O-succinylbenzoic acid-CoA ligase (MenE) [Desulfotalea psychrophila Lsv54] emb[CAG34979.1] related to O-succinylbenzoic acid- CoA ligase (MenE) [Desulfotalea psychrophila Lsv54] | | | 6.2.1.1 |
| 2999, 3000 | 29348878 | 35 | 1.00E-18 | Bacteroides thetataoimicron VPI-5482 | hypothetical protein BT3469 [Bacteroides thetataoimicron VPI-5482] gb AAO78575.1 conserved hypothetical protein [Bacteroides thetataoimicron VPI-5482] | | | |
| 3001, 3002 | 48856115 | 34 | 2.00E-29 | Cytophaga hutchinsonii | COG0793: Periplasmic protease [Cytophaga hutchinsonii] | | | |
| 3003, 3004 | 23112865 | 40 | 3.00E-29 | Desulfobacterium hafniense DCB-2 | COG4636: Uncharacterized protein conserved in cyanobacteria [Desulfobacterium hafniense DCB-2] | | | |
| 3009, 3010 | 17934157 | 45 | 1.00E-78 | Agrobacterium tumefaciens str. C58 | GTP-binding elongation factor [Agrobacterium tumefaciens str. C58] gb AAL41263.1 GTP-binding elongation factor [Agrobacterium tumefaciens str. C58] gb AAK86057.1 AGR_C_411p [Agrobacterium tumefaciens str. C58] sp Q8UIQ2 LEPA_AGR_T5 GTP-binding protein lepA ref NP_353272.1 hypothetical protein AGR_C_411 [Agrobacterium tumefaciens str. C58] pir A12605 GTP-binding elongation factor lepA [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir H97387 GTP-binding protein lepA [imported] - Agrobacterium tumefaciens (strain C58, Cereon) | | | |
| 301, 302 | 28077051 | 43 | 9.00E-28 | Mus musculus | neurolysin (metallopeptidase M3 family) [Mus musculus] gb AAH16224.1 Neurolysin (metallopeptidase M3 family) [Mus musculus] db BAC37533.1 unnamed protein product [Mus musculus] | | | 3.4.24.1 6 |
| 3011, 3012 | 13471565 | 43 | 1.00E-38 | Mesorhizobium loti MAFF303099 | hypothetical protein mlr1575 [Mesorhizobium loti MAFF303099] db BAB48917.1 mlr1575 [Mesorhizobium loti MAFF303099] | | | 2.1.1.- |
| 3015, 3016 | 48856245 | 54 | 2.00E-89 | Cytophaga hutchinsonii | COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii] | | | |
| 3017, 3018 | 23500570 | 43 | 1.00E-38 | Brucella suis 1330 | type I restriction-modification system, M subunit [Brucella suis 1330] gb AAN34015.1 type I restriction-modification system, M subunit [Brucella suis 1330] | | | 2.1.1.72 |

| | | | | | | | | | |
|---------------|----------|----|----------|---|--|--|----|----------|----------|
| 3019, 3020 | 48863731 | 30 | 1.00E-09 | Microbulbifer degradans 2-40 | COG0840: Methyl-accepting chemotaxis protein [Microbulbifer degradans 2-40] | | | | |
| 3021, 3022 | 37676553 | 45 | 4.00E-57 | Vibrio vulnificus YJ016 | methyl-accepting chemotaxis protein [Vibrio vulnificus YJ016] dbj BAC96919.1 methyl-accepting chemotaxis protein [Vibrio vulnificus YJ016] | | | | |
| 3025, 3026 | 15605828 | 28 | 8.00E-30 | Aquifex aeolicus VF5 | hypothetical protein ag_296 [Aquifex aeolicus VF5] gb AAC06608.1 hypothetical protein [Aquifex aeolicus VF5] pir A70327 conserved hypothetical protein ag_296 - Aquifex aeolicus | | | | |
| 3029, 3030 | 29346937 | 36 | 2.00E-42 | Bacteroides thetataoimicron VPI-5482 | hypothetical protein BT1527 [Bacteroides thetataoimicron VPI-5482] gb AAO76634.1 hypothetical protein [Bacteroides thetataoimicron VPI-5482] | | | | |
| 303, 304 | 53713020 | 41 | 3.00E-37 | Bacteroides fragilis YCH46 | slolate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAC56897.1 slolate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAD48478.1 slolate O-acetyltransferase [Bacteroides fragilis YCH46] | | | | 3.1.1.47 |
| 3031, 3032 | 48855460 | 32 | 2.00E-23 | Cytophaga hutchinsonii | hypothetical protein Chut02001797 [Cytophaga hutchinsonii] | | | | |
| 3035, 3036 | 48853913 | 41 | 1.00E-24 | Cytophaga hutchinsonii | COG0018: Arginyl-tRNA synthetase [Cytophaga hutchinsonii] | | | | 6.1.1.19 |
| 3039, 3040 | 48853471 | 32 | 7.00E-30 | Cytophaga hutchinsonii | COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | | |
| 3041, 3042 | 30021268 | 37 | 5.00E-28 | Bacillus cereus ATCC 14579 | Pyrimidine Reductase [Bacillus cereus ATCC 14579] gb AAP10100.1 Pyrimidine Reductase [Bacillus cereus ATCC 14579] | | | | |
| 3043, 3044 | 34397897 | 50 | 1.00E-21 | Porphyromonas gingivalis W83 | CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] ref NP_906059.1 CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] | | | | |
| 3045, 3046 | 34397897 | 40 | 5.00E-34 | Porphyromonas gingivalis W83 | CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] ref NP_906059.1 CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] | | | | |
| 3047, 3048 | 41409487 | 34 | 3.00E-14 | Mycobacterium avium subsp. paratuberculosis str. k10 | hypothetical protein MAP3389c [Mycobacterium avium subsp. paratuberculosis str. k10] gb AA050939.1 hypothetical protein MAP3389c [Mycobacterium avium subsp. paratuberculosis str. k10] | | | | 2.7.3.- |
| 305, 306 | 48854966 | 74 | 1.00E-51 | Cytophaga hutchinsonii | COG0013: Alanyl-tRNA synthetase [Cytophaga hutchinsonii] | Aspergillus nidulans FGSC A4, AN9419.2 predicted mRNA | 90 | 7.00E-08 | 6.1.1.7 |
| 3051, 3052 | 48771971 | 26 | 3.00E-14 | Ralstonia metallidurans CH34 | hypothetical protein Reut02000722 [Ralstonia metallidurans CH34] | | | | |

| | | | | | | | | | |
|-----------------------|----------|----|----------|---|---|--|--|--|----------------|
| 3053, 3054 | 29349375 | 35 | 4.00E-25 | Bacteroides thetaiotaomicron VPI-5482 | putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79072.1 putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI- 5482] | | | | 2.7.3.- |
| 3057, 3058 | 48864231 | 27 | 1.00E-18 | Microbulbifer degradans 2-40 | COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulbifer degradans 2-40] | | | | |
| 3069, 3070 | 15644598 | 29 | 2.00E-19 | Thermotoga maritima MSB8 | sugar ABC transporter, periplasmic sugar-binding protein, putative [Thermotoga maritima MSB8] gb AAD36917.1 sugar ABC transporter, periplasmic sugar-binding protein, putative [Thermotoga maritima MSB8] pir H72203 hypothetical protein TM1855 - Thermotoga maritima (strain MSB8) | | | | |
| 307, 3071, 3072 | 48856298 | 45 | 2.00E-39 | Cytophaga hutchinsonii | COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Cytophaga hutchinsonii] | | | | 2.7.6.5 |
| 3073, 3074 | 48855418 | 64 | 1.00E-87 | Cytophaga hutchinsonii | COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii] | | | | 1.14.99. 25 |
| 3075, 3076 | 48854274 | 40 | 6.00E-30 | Cytophaga hutchinsonii | COG3239: Fatty acid desaturase [Cytophaga hutchinsonii] | | | | 2.3.1.51 |
| 3077, 3078 | 54308824 | 47 | 3.00E-34 | Photobacterium profundum SS9 | Hypothetical acyltransferase family protein [Photobacterium profundum SS9] emb CAG20042.1 Hypothetical acyltransferase family protein [Photobacterium profundum] | | | | |
| 3079, 3080 | 48839924 | 57 | 6.00E-45 | Methanosarcina barkeri str. fusaro | COG5316: Uncharacterized conserved protein [Methanosarcina barkeri str. fusaro] | | | | |
| 3081, 3082 | 46907208 | 53 | 3.00E-13 | Listeria monocytogenes str. 4b F2365 | ribose 5-phosphate isomerase A [Listeria monocytogenes str. 4b F2365] gb AA103774.1 ribose 5-phosphate isomerase A [Listeria monocytogenes str. 4b F2365] | | | | 5.3.1.6 |
| 3083, 3084 | 30021199 | 33 | 2.00E-17 | Bacillus cereus ATCC 14579 | Phosphoenolpyruvate synthase [Bacillus cereus ATCC 14579] gb AAP10031.1 Phosphoenolpyruvate synthase [Bacillus cereus ATCC 14579] | | | | 2.7.9.2 |
| 3085, 3086 | 48853753 | 56 | 9.00E-65 | Cytophaga hutchinsonii | COG0225: Peptide methionine sulfoxide reductase [Cytophaga hutchinsonii] putative oxidoreductase [Streptomyces avermitilis MA-4680] ref NP_822862.1 putative oxidoreductase [Streptomyces avermitilis MA- 4680] | | | | 1.8.4.6 |
| 3087, 3088 | 29605330 | 28 | 2.00E-15 | Streptomyces avermitilis MA-4680 | hypothetical protein [Pseudoalteromonas haloplanktis] putative N6-adenine-specific DNA methylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78361.1 putative N6-adenine-specific DNA methylase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.1.1.52 |
| 309, 310 | 2879819 | 34 | 2.00E-30 | Pseudoalteromona s haloplanktis | hypothetical protein BT4447 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79552.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 3097, 3098 | 29348664 | 48 | 3.00E-12 | Bacteroides thetaiotaomicron VPI-5482 | | | | | |
| 3097, 3098 | 29349855 | 38 | 5.00E-30 | Bacteroides thetaiotaomicron VPI-5482 | | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|--|---------------|
| 3099, 3100 | 28211514 | 41 | 5.00E-14 | cytochrome c-553 | alcohol dehydrogenase [Cytochrome c-553], gamma chain-like protein [Clostridium tetani E88] gb AAO36395.1 alcohol dehydrogenase [cytochrome c-553], gamma chain-like protein [Clostridium tetani E88] | | | | |
| 3101, 3102 | 28211514 | 40 | 4.00E-14 | cytochrome c-553 | alcohol dehydrogenase [cytochrome c-553], gamma chain-like protein [Clostridium tetani E88] gb AAO36395.1 alcohol dehydrogenase [cytochrome c-553], gamma chain-like protein [Clostridium tetani E88] | | | | |
| 3103, 3104 | 48855539 | 54 | 6.00E-68 | Cytophaga hutchinsonii | COG0142: Geranylgeranyl pyrophosphate synthase [Cytophaga hutchinsonii] | | | | 2.5.1.1 |
| 3105, 3106 | 48854339 | 56 | 2.00E-79 | Cytophaga hutchinsonii | COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii] | | | | |
| 3109, 3110 | 48854025 | 47 | 2.00E-24 | Cytophaga hutchinsonii | hypothetical protein Chut02003116 [Cytophaga hutchinsonii] | | | | |
| 311, 312 | 15679640 | 27 | 2.00E-11 | Methanothermobacter thermautotrophicus str. Delta H | ABC transporter [Methanothermobacter thermautotrophicus str. Delta H] gb AAB86118.1 ABC transporter [Methanothermobacter thermautotrophicus str. Delta H] pir H69086 ABC transporter - Methanobacterium thermoautotrophicum (strain Delta H) | | | | |
| 3111, 3112 | 48891492 | 35 | 6.00E-33 | Trichodesmium erythraeum IMS101 | COG1110: Reverse gyrase [Trichodesmium erythraeum IMS101] | | | | |
| 3115, 3116 | 45531581 | 52 | 7.00E-19 | Exiguobacterium sp. 255-15 | COG0024: Methionine aminopeptidase [Exiguobacterium sp. 255-15] | | | | 3.4.11.1 8 |
| 3123, 3124 | 45358866 | 37 | 6.00E-33 | Methanococcus maripaludis S2 | Sensory transduction histidine kinase [Methanococcus maripaludis S2] emb CAF30859.1 Sensory transduction histidine kinase [Methanococcus maripaludis S2] | | | | 2.7.3.- |
| 3125, 3126 | 48855162 | 44 | 1.00E-12 | Cytophaga hutchinsonii | COG4095: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 3127, 3128 | 39995705 | 40 | 7.00E-22 | Geobacter sulfurreducens PCA | sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA] gb AAR33928.1 sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA] | | | | 2.7.3.- |
| 3135, 3136 | 37519844 | 29 | 8.00E-25 | Gloeobacter violaceus PCC 7421 | hypothetical protein glr0275 [Gloeobacter violaceus PCC 7421] dbj BAC88216.1 glr0275 [Gloeobacter violaceus PCC 7421] | | | | |
| 3137, 3138 | 29349121 | 40 | 1.00E-31 | Bacteroides thetaiotaomicron VPI-5482 | D-alanine-D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78818.1 D-alanine-D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine-D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase) | | | | 6.3.2.4 |
| 3139, 3140 | 29345890 | 51 | 9.00E-53 | Bacteroides thetaiotaomicron VPI-5482 | glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.8.6 |
| 3147, 3148 | 31195951 | 48 | 2.00E-23 | Anopheles gambiae | ENSANGP00000000471 [Anopheles gambiae] | | | | 1.1.1.95 |

| | | | | | | | | | |
|---------------|--------------|----|----------|---|--|--|--|--|---------------|
| 3153, 3154 | 45656356 | 47 | 1.00E-28 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC10458 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_713968.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AA50986.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AA569079.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | 3.1.- |
| 3155, 3156 | 53715428 | 58 | 8.00E-76 | Bacteroides fragilis YCH46 | histidine ammonia-lyase [Bacteroides fragilis YCH46] dbj BAD50886.1 histidine ammonia-lyase [Bacteroides fragilis YCH46] | | | | 4.3.1.3 |
| 3157, 3158 | AAM5260 8 | 50 | 7.00E-93 | | Desc:Aquifex pyrophilus DNA ligase. Org:Aquifex pyrophilus | | | | 6.5.1.2 |
| 3161, 3162 | 48854685 | 47 | 2.00E-36 | Cytophaga hutchinsonii | COG3832: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 3167, 3168 | 23297087 | 40 | 6.00E-07 | Arabidopsis thaliana | unknown protein [Arabidopsis thaliana] ref NP_563980.2 leucine-rich repeat family protein [Arabidopsis thaliana] | | | | |
| 3169, 3170 | 53711736 | 34 | 3.00E-12 | Bacteroides fragilis YCH46 | Na+/H+ antiporter [Bacteroides fragilis YCH46] dbj BAD47194.1 Na+/H+ antiporter [Bacteroides fragilis YCH46] | | | | |
| 317, 318 | 29346409 | 28 | 4.00E-11 | Bacteroides thetalaotomicron VPI-5482 | putative acetyltransferase [Bacteroides thetalaotomicron VPI-5482] gb AAO76106.1 putative acetyltransferase [Bacteroides thetalaotomicron VPI-5482] | | | | 2.3.1.12 8 |
| 3171, 3172 | 51246614 | 29 | 9.00E-22 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2762 [Desulfotalea psychrophila LSV54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila LSV54] | | | | 2.1.1.14 4 |
| 3173, 3174 | 51246614 | 29 | 1.00E-21 | Desulfotalea psychrophila LSV54 | hypothetical protein DP2762 [Desulfotalea psychrophila LSV54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila LSV54] | | | | 2.1.1.14 4 |
| 3175, 3176 | 48836108 | 56 | 7.00E-67 | Thermobifida fusca | COG2268: Uncharacterized protein conserved in bacteria [Thermobifida fusca] | | | | |
| 3179, 3180 | 56459231 | 29 | 2.00E-34 | Idiomarina lolhiensis L2TR | Membrane-associated protein [Idiomarina lolhiensis L2TR] gb AAV80963.1 Membrane-associated protein [Idiomarina lolhiensis L2TR] | | | | 2.4.1.15 1 |
| 3181, 3182 | 53712767 | 72 | 1.00E-31 | Bacteroides fragilis YCH46 | dioxygenase [Bacteroides fragilis YCH46] dbj BAD48225.1 dioxygenase [Bacteroides fragilis YCH46] | | | | 1.3.1.9 |
| 3185, 3186 | 48854993 | 39 | 6.00E-16 | Cytophaga hutchinsonii | COG2989: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 3187, 3188 | 21674674 | 34 | 2.00E-43 | Chlorobium tepidum TLS | hypothetical protein CT1862 [Chlorobium tepidum TLS] gb AAM73081.1 conserved hypothetical protein [Chlorobium tepidum TLS] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|--|---------------|
| 3191, 3192 | 29348773 | 42 | 1.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3364 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78470.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 3193, 3194 | 53715112 | 37 | 1.00E-59 | Bacteroides fragilis YCH46 | 4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4-alpha-glucanotransferase [Bacteroides fragilis YCH46] | | | | 2.4.1.25 |
| 3203, 3204 | 31790364 | 45 | 6.00E-47 | Acidobacteria bacterium Yersinia | putative glutamine cyclotransferase [uncultured Acidobacteria bacterium] putative DNA methyltransferase [Yersinia pseudotuberculosis IP 32953] | | | | |
| 3207, 3208 | 51596132 | 33 | 2.00E-31 | pseudotuberculosis IP 32953 | emb CAH21036.1 putative DNA methyltransferase [Yersinia pseudotuberculosis IP 32953] | | | | 2.1.1.11 3 |
| 3209, 3210 | 16272498 | 35 | 9.00E-21 | Haemophilus influenzae Rd KW20 | hypothetical protein HI0554 [Haemophilus influenzae Rd KW20] gb AAC22217.1 H. influenzae predicted coding region HI0554 [Haemophilus influenzae Rd KW20] pir E64009 hypothetical protein HI0554 - Haemophilus influenzae (strain Rd KW20) sp P44014 Y554_HAEIN Hypothetical protein HI0554 | | | | |
| 3211, 3212 | 48853959 | 46 | 8.00E-27 | Cytophaga hutchinsonii | COG0416: Fatty acid/phospholipid biosynthesis enzyme [Cytophaga hutchinsonii] | | | | |
| 3213, 3214 | 48855683 | 56 | 3.00E-36 | Cytophaga hutchinsonii | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | | |
| 3215, 3216 | AAW9850 | 35 | 4.00E-09 | | Desc:H. pylori GHPO 1224 protein. Org:Helicobacter pylori | | | | 2.1.1.72 |
| 3217, 3218 | AAW9850 | 35 | 4.00E-09 | | Desc:H. pylori GHPO 1224 protein. Org:Helicobacter pylori | | | | 2.1.1.72 |
| 3219, 3220 | ABP7901 | 62 | 2.00E-97 | | Desc:N. gonorrhoeae amino acid sequence SEQ ID 4556. Org:Neisseria gonorrhoeae | | | | 3.1.21.3 |
| 3221, 3222 | 48854777 | 47 | 2.00E-56 | Cytophaga hutchinsonii | COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii] | | | | |
| 3223, 3224 | 15606832 | 35 | 2.00E-33 | Aquifex aeolicus VF5 | leucyl-tRNA synthetase beta subunit [Aquifex aeolicus VF5] gb AAC07608.1 leucyl-tRNA synthetase beta subunit [Aquifex aeolicus VF5] pir D70452 leucine-tRNA ligase (EC 6.1.1.4) beta chain - Aquifex aeolicus sp O67646 SYLB_AQUAE Leucyl-tRNA synthetase beta subunit (Leucine- tRNA ligase beta subunit) (LeuRS) | | | | 6.1.1.4 |
| 3225, 3226 | 17229731 | 32 | 7.00E-37 | Nostoc sp. PCC 7120 | two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] pir AH2085 two-component hybrid sensor and regulator all2239 [Imported] - Nostoc sp. (strain PCC 7120) dbj BAB73938.1 two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] | | | | 2.7.3.- |
| 3227, 3228 | 48854665 | 45 | 7.00E-45 | Cytophaga hutchinsonii | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|--|----|----------|----------|
| 3237, 3238 | 9950513 | 51 | 5.00E-41 | Pseudomonas aeruginosa PAO1 | probable phosphate transporter [Pseudomonas aeruginosa PAO1] ref ZP_00137767.1 COG0306: Phosphate/sulphate permeases [Pseudomonas aeruginosa UCBPP-PA14] pir F83109 probable phosphate transporter PA4292 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_252982.1 probable phosphate transporter [Pseudomonas aeruginosa PAO1] | | | | |
| 3239, 3240 | 48856124 | 43 | 2.00E-20 | Cytophaga hutchinsonii | COG0770: UDP-N-acetylmuramyl pentapeptide synthase [Cytophaga hutchinsonii] | | | | 6.3.2.15 |
| 3241, 3242 | 16125881 | 32 | 6.00E-14 | Caulobacter crescentus CB15 | hypothetical protein CC1635 [Caulobacter crescentus CB15] gb AAK23613.1 conserved hypothetical protein [Caulobacter crescentus CB15] pir A87452 conserved hypothetical protein CC1635 [imported] - Caulobacter crescentus | | | | |
| 3243, 3244 | 48856104 | 29 | 1.00E-07 | Cytophaga hutchinsonii | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii] | | | | |
| 3245, 3246 | 48855273 | 40 | 3.00E-24 | Cytophaga hutchinsonii | COG4731: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 3249, 3250 | 29346131 | 47 | 4.00E-60 | Bacteroides thetaiotaomicron VPI-5482 | DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75828.1 DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 325, 326 | 56707295 | 33 | 2.00E-10 | Francisella tularensis subsp. tularensis Schu 4 | DNA helicase II [Francisella tularensis subsp. tularensis Schu 4] emb CAG44754.1 DNA helicase II [Francisella tularensis subsp. tularensis] | | | | 3.6.1.- |
| 3251, 3252 | 1185191 | 57 | 6.00E-63 | Odontella sinensis Bacillus thuringiensis serovar konkukian str. 97-27 | ORF 644 [Odontella sinensis] pir S78301 hypothetical protein 644 - Odontella sinensis chloroplast ref NP_043642.1 ORF 644 [Odontella sinensis] sp P49825 FTSH ODOS1 Cell division protein ftsH homolog | Odontella sinensis complete chloroplast genome | 89 | 1.00E-07 | 3.4.24.- |
| 3261, 3262 | 49479197 | 44 | 2.00E-18 | Cytophaga hutchinsonii | alcohol dehydrogenase, zinc containing [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT61399.1 alcohol dehydrogenase, zinc containing [Bacillus thuringiensis serovar konkukian str. 97-27] | | | | 1.1.1.1 |
| 3265, 3266 | 48855616 | 26 | 4.00E-22 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | | |
| 3269, 3270 | 48856849 | 34 | 5.00E-25 | Cytophaga hutchinsonii | COG0525: Valyl-tRNA synthetase [Cytophaga hutchinsonii] | | | | 6.1.1.9 |
| 327, 328 | 21243000 | 33 | 9.00E-09 | Xanthomonas axonopodis pv. citri str. 306 | helicase IV [Xanthomonas axonopodis pv. citri str. 306] gb AAM37118.1 helicase IV [Xanthomonas axonopodis pv. citri str. 306] | | | | 3.6.1.- |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|----------|--|--|--|
| 3279, 3280 | 52841151 | 66 | 2.00E-98 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | penicillin binding protein 3 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123305.1 Peptidoglycan synthetase FtsI precursor [Legionella pneumophila str. Paris] gb AAU27003.1 penicillin binding protein 3 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH12128.1 Peptidoglycan synthetase FtsI precursor [Legionella pneumophila str. Paris] | 2.3.2.- | | | |
| 3281, 3282 | 52550184 | 57 | 1.00E-95 | archaeon GZfos35D7 | leucine-rich-repeat protein [uncultured archaeon GZfos35D7] | 1.11.1.9 | | | |
| 329, 330 | 29348151 | 32 | 1.00E-13 | Bacteroides thetaiotaomicron VPI-5482 | integrase, site-specific recombinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77848.1 integrase, site-specific recombinase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 3291, 3292 | 15669150 | 57 | 4.00E-63 | Methanocaldococcus jannaschii DSM 2661 | transaldolase [Methanocaldococcus jannaschii DSM 2661] gb AAB98962.1 transaldolase [Methanocaldococcus jannaschii DSM 2661] sp Q58370 TAL_MET_JA Probable transaldolase pir H64419 transaldolase (EC 2.2.1.2) - Methanococcus jannaschii | 2.2.1.2 | | | |
| 3293, 3294 | 37222112 | 55 | 1.00E-63 | uncultured bacterium | Uvs063 [uncultured bacterium] | | | | |
| 3301, 3302 | 53713100 | 29 | 5.00E-22 | Bacteroides fragilis YCH46 | TonB-dependent outer membrane receptor [Bacteroides fragilis YCH46] db BAD48558.1 TonB-dependent outer membrane receptor [Bacteroides fragilis YCH46] | | | | |
| 3307, 3308 | 52840856 | 50 | 3.00E-31 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | glyoxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123011.1 hypothetical protein lpp0673 [Legionella pneumophila str. Paris] gb AAU26708.1 glyoxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH11821.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | |
| 3309, 3310 | 23501343 | 36 | 1.00E-49 | Brucella suis 1330 | ABC transporter, ATP-binding/permease protein [Brucella suis 1330] gb AAN29385.1 ABC transporter, ATP-binding/permease protein [Brucella suis 1330] | | | | |
| 331, 332 | 48856037 | 56 | 2.00E-30 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | | |
| 3313, 3314 | 56675038 | 41 | 9.00E-17 | uncultured bacterium | cellulase [uncultured bacterium] | | | | |
| 3315, 3316 | 21241377 | 45 | 5.00E-47 | Xanthomonas axonopodis pv. citri str. 306 | endonuclease [Xanthomonas axonopodis pv. citri str. 306] gb AAM35495.1 endonuclease [Xanthomonas axonopodis pv. citri str. 306] | 3.2.2.23 | | | |
| 3317, 3318 | 48860907 | 36 | 1.00E-28 | Microbulbifer degradans 2-40 | COG3279: Response regulator of the LysR/AigR family [Microbulbifer degradans 2-40] | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|---------|
| 3319, 3320 | 18313142 | 29 | 6.00E-26 | Pyrobaculum aerophilum str. IM2 | hypothetical protein PAE2159 [Pyrobaculum aerophilum str. IM2] gb AAL63991.1 conserved hypothetical protein [Pyrobaculum aerophilum str. IM2] | | | 1.5.5.- |
| 3321, 3322 | 29349974 | 42 | 2.00E-38 | Bacteroides thetataoimicron VPI-5482 | two-component system response regulator protein [Bacteroides thetataoimicron VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetataoimicron VPI-5482] | | | |
| 3323, 3324 | 48854732 | 29 | 3.00E-15 | Cytophaga hutchinsonii | COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 3327, 3328 | 45856536 | 51 | 1.00E-21 | Leptospira interrogans serovar Copenhagen str. Flocruz L1-130 | hypothetical protein LIC10638 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69259.1 conserved hypothetical protein [Leptospira Interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 3329, 3330 | 29345992 | 51 | 1.00E-20 | Bacteroides thetataoimicron VPI-5482 | hypothetical protein BT0582 [Bacteroides thetataoimicron VPI-5482] gb AAO75689.1 conserved hypothetical protein [Bacteroides thetataoimicron VPI-5482] | | | |
| 333, 334 | 37520160 | 50 | 6.00E-46 | Gloeobacter violaceus PCC 7421 | hypothetical protein glr0591 [Gloeobacter violaceus PCC 7421] dbj BAC88532.1 glr0591 [Gloeobacter violaceus PCC 7421] | | | |
| 3331, 3332 | 53715217 | 29 | 6.00E-18 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50675.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] | | | 3.6.1.- |
| 3335, 3336 | 23501247 | 39 | 6.00E-19 | Brucella suis 1330 | DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M) | | | |
| 3337, 3338 | 48856332 | 51 | 3.00E-22 | Cytophaga hutchinsonii | hypothetical protein Chut0200044 [Cytophaga hutchinsonii] | | | |
| 3339, 3340 | 29346104 | 56 | 4.00E-39 | Bacteroides thetataoimicron VPI-5482 | ABC transporter, ATP-binding protein [Bacteroides thetataoimicron VPI- 5482] gb AAO75801.1 ABC transporter, ATP-binding protein [Bacteroides thetataoimicron VPI-5482] | | | 1.8.- |
| 3341, 3342 | 28850513 | 67 | 3.00E-36 | Pseudomonas syringae pv. tomato str. DC3000 | helicase domain protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_789898.1 helicase domain protein [Pseudomonas syringae pv. tomato str. DC3000] | | | |
| 3345, 3346 | 48855191 | 51 | 9.00E-63 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |

| | | | | | | | | |
|-------|----------|----|----------|-----------------------------------|---|--|--|----------|
| 3349, | 48854964 | 28 | 5.00E-29 | Cytophaga hutchinsonii | COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | |
| 3350 | | | | Cytophaga hutchinsonii | | | | |
| 3351, | 48856102 | 47 | 3.00E-42 | Cytophaga hutchinsonii | COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 3352 | | | | Campylobacter coli RM2228 | type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] gbl[EAL56262.1] type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] | | | 2.1.1.72 |
| 3353, | 57169027 | 34 | 7.00E-24 | Campylobacter coli RM2228 | type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] gbl[EAL56262.1] type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] | | | 2.1.1.72 |
| 3354 | | | | Campylobacter coli RM2228 | | | | |
| 3355, | 57169027 | 39 | 6.00E-19 | Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 3356 | 48856489 | 49 | 1.00E-24 | Geobacter metallireducens GS | COG0417: DNA polymerase elongation subunit (family B) [Geobacter metallireducens GS-15] | | | 2.7.7.7 |
| 3357, | 48845074 | 28 | 5.00E-20 | 15 | | | | |
| 3358 | | | | Nostoc punctiforme PCC 73102 | COG0514: Superfamily II DNA helicase [Nostoc punctiforme PCC 73102] | | | 3.6.1.- |
| 3363, | 23125625 | 24 | 2.00E-16 | Cytophaga hutchinsonii | hypothetical protein Chut02000134 [Cytophaga hutchinsonii] | | | |
| 3364 | 48856416 | 39 | 4.00E-35 | Mesorhizobium sp. BNC1 | COG0057: Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Mesorhizobium sp. BNC1] | | | 1.2.1.12 |
| 3365, | 45684333 | 50 | 1.00E-19 | Micromonospora echinospora | putative NAD dependent dehydrogenase [Micromonospora echinospora] | | | 1.1.1.18 |
| 3366 | 23125625 | 24 | 2.00E-16 | Bradyrhizobium japonicum USDA 110 | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj[BAC48127.1] two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] | | | 2.7.3.- |
| 3367, | 45544475 | 35 | 2.00E-21 | Dehalococcoides ethenogenes 195 | sensory box sensor histidine kinase [Dehalococcoides ethenogenes 195] gblAAW40550.1] sensory box sensor histidine kinase [Dehalococcoides ethenogenes 195] | | | 2.7.3.- |
| 3368 | 27377973 | 43 | 8.00E-34 | Nostoc sp. PCC 7120 | two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] pir JAG1928 two-component hybrid sensor and regulator all0978 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB72935.1] two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] | | | 2.7.3.- |
| 3369, | 57235045 | 25 | 1.00E-19 | Cytophaga hutchinsonii | COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii] | | | |
| 3370 | 17228473 | 41 | 9.00E-37 | Cytophaga hutchinsonii | COG2137: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 3371, | 48854312 | 56 | 1.00E-45 | Cytophaga hutchinsonii | | | | |
| 3372 | 48854316 | 45 | 4.00E-32 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | |
|---------------------------------|----------------------|----------|----------------------|---|---|--|--|---------|
| 3389, 3390 3391, 3392 | 34396834 48855491 | 40 41 | 9.00E-33 1.00E-52 | Porphyrromonas gingivalis W83 Cytophaga hutchinsonii | D-alanine--D-alanine ligase [Porphyrromonas gingivalis W83] ref NP_905000.1 D-alanine--D-alanine ligase [Porphyrromonas gingivalis W83] sp Q7MWA2 DDL_PORGI D-alanine--D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase) hypothetical protein Chuf02001830 [Cytophaga hutchinsonii] | | | 6.3.2.4 |
| 3395, 3396 | 56459680 | 24 | 3.00E-10 | Idiomarina loihlensis L2TR | hypothetical protein IL0571 [Idiomarina loihlensis L2TR] gb AAV81412.1 Uncharacterized conserved protein [Idiomarina loihlensis L2TR] | | | |
| 3399, 3400 | 48891870 | 45 | 5.00E-51 | Trichodesmium erythraeum IMS101 | COG0566: rRNA methylases [Trichodesmium erythraeum IMS101] hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714691.1 conserved hypothetical protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51706.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS72145.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.1.1.- |
| 3401, 3402 | 45655699 | 30 | 3.00E-16 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC12133 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70704.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] Transcriptional activator HiyU [Vibrio vulnificus CMCP6] ref NP_933476.1 Transcriptional activator [Vibrio vulnificus YJ016] gb AAO09030.1 Transcriptional activator HiyU [Vibrio vulnificus CMCP6] dbj BAC93447.1 transcriptional activator [Vibrio vulnificus YJ016] | | | |
| 3405, 3406 | 45657981 | 34 | 7.00E-22 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | COG0644: Dehydrogenases (flavoproteins) [Cytophaga hutchinsonii] | | | |
| 3409, 3410, 3413, 3414 | 27363975 48854244 | 37 44 | 2.00E-10 2.00E-36 | Vibrio vulnificus CMCP6 Cytophaga hutchinsonii | DNA primase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79037.1 DNA primase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.7.- |
| 3417, 3418 | 29349340 | 60 | 2.00E-31 | Bacteroides thetaiotaomicron VPI-5482 | putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47418.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] | | | |
| 3423, 3424 | 53711960 | 28 | 1.00E-23 | Bacteroides fragilis YCH46 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 3425, 3426 | 48854564 | 52 | 2.00E-66 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | | | |
|-------|----------|----|--|--|---|--|--|----|----------|----------|
| 3427, | 53715112 | 48 | | | Bacteroides fragilis YCH46 | 4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4-alpha-glucanotransferase [Bacteroides fragilis YCH46] | Desc: Genomic sequence of Lactococcus lactis IL1403. | 90 | 2.00E-07 | 2.4.1.25 |
| 3428 | 48856129 | 43 | | | Cytophaga hutchinsonii | COG1011: Predicted hydrolase (HAD superfamily) [Cytophaga hutchinsonii] | | | | 3.8.1.2 |
| 343, | 48853894 | 35 | | | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | | |
| 3432 | | | | | Vibrio cholerae O1 biovar eltor str. N16961 | hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232850.1 hypothetical protein VCA0458 [Vibrio cholerae O1 biovar eltor str. N16961] pir A82458 hypothetical protein VCA0458 [Imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 3433, | 9657860 | 49 | | | Cytophaga hutchinsonii | COG0327: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 3434 | 48856395 | 57 | | | Staphylococcus aureus subsp. aureus COL | orotidine 5'-phosphate decarboxylase [Staphylococcus aureus subsp. aureus COL] ref YP_186079.1 orotidine 5'-phosphate decarboxylase [Staphylococcus aureus subsp. aureus COL] | | | | 4.1.1.23 |
| 3435, | 57285959 | 48 | | | Bacteroides thetaiotaomicron | ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gbl AA078949.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.6.1.- |
| 3436 | 29349252 | 61 | | | Cytophaga hutchinsonii | COG1250: 3-hydroxyacyl-CoA dehydrogenase [Cytophaga hutchinsonii] | Bacillus cereus ZK, complete genome | ## | 2.00E-07 | 1.1.1.35 |
| 3437, | 48854116 | 59 | | | Cytophaga hutchinsonii | COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii] | | | | |
| 3438 | 48853602 | 54 | | | Cytophaga hutchinsonii | COG1793: ATP-dependent DNA ligase [Cytophaga hutchinsonii] | | | | 6.5.1.1 |
| 3439, | 48853691 | 41 | | | Cytophaga hutchinsonii | hypothetical protein Chut02002321 [Cytophaga hutchinsonii] | | | | |
| 3440 | 48854655 | 33 | | | Cytophaga hutchinsonii | COG1280: Putative threonine efflux protein [Cytophaga hutchinsonii] | | | | |
| 3441, | 48854337 | 27 | | | Anabaena variabilis ATCC 29413 | COG3541: Predicted nucleotidyltransferase [Anabaena variabilis ATCC 29413] | | | | |
| 3442 | | | | | Crocospaera watsonii WH 8501 | COG5635: Predicted NTPase (NACHT family) [Crocospaera watsonii WH 8501] | | | | |
| 3443, | 45506934 | 28 | | | Gallus gallus | PREDICTED: similar to Palo protein, partial [Gallus gallus] | | | | |
| 3444, | 45526631 | 40 | | | | | | | | |
| 3445, | 50796980 | 61 | | | | | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|--|----------|
| 3469, 3470 | 48856411 | 53 | 1.00E-63 | Cytophaga hutchinsonii | COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | | 1.8.- |
| 3471, 3472 | 48855045 | 33 | 2.00E-24 | Cytophaga hutchinsonii | COG2027: D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 4) [Cytophaga hutchinsonii] | | | | 3.4.16.4 |
| 3473, 3474 | 23125186 | 36 | 4.00E-22 | Nostoc punctiforme PCC 73102 | hypothetical protein Npun02006402 [Nostoc punctiforme PCC 73102] | | | | |
| 3475, 3476 | 21673096 | 39 | 6.00E-45 | Chlorobium tepidum TLS | isopentenyl-diphosphate delta-isomerase, putative [Chlorobium tepidum TLS] gb AAM71503.1 isopentenyl-diphosphate delta-isomerase, putative [Chlorobium tepidum TLS] sp Q8KFR5 ID12_CHL TE isopentenyl-diphosphate delta-isomerase (IPP isomerase) (isopentenyl pyrophosphate isomerase) | | | | 5.3.3.2 |
| 3477, 3478 | 48855819 | 32 | 5.00E-33 | Cytophaga hutchinsonii | COG3361: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 3479, 3480 | 48856112 | 32 | 3.00E-26 | Cytophaga hutchinsonii | COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 3481, 3482 | 39936798 | 35 | 4.00E-10 | Rhodopseudomonas palustris CGA009 | putative phosphoacetate hydrolase [Rhodopseudomonas palustris CGA009] emb CAE29178.1 putative phosphoacetate hydrolase [Rhodopseudomonas palustris CGA009] | | | | |
| 3483, 3484 | 29347290 | 45 | 2.00E-66 | Bacteroides thetaiotaomicron VPI-5482 | tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76987.1 tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.1.13 |
| 3485, 3486 | 29425233 | 34 | 1.00E-07 | Mycobacteriophage Che9d | gp109 [Mycobacteriophage Che9d] ref NP_818074.1 gp109 [Mycobacteriophage Che9d] | | | | 0 |
| 3487, 3488 | 34764299 | 28 | 1.00E-06 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | Hypothetical Protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23266.1 Hypothetical Protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | | |
| 3489, 3490 | 48855209 | 62 | 1.00E-68 | Cytophaga hutchinsonii | COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Cytophaga hutchinsonii] | | | | |
| 349, 350 | 48855170 | 39 | 2.00E-35 | Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 3493, 3494 | 29346555 | 76 | 1.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76252.1 glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A8M2 GIDB_BACTN Methyltransferase gidB (Glucose inhibited division protein B) | | | | |

| | | | | | | | | |
|---|----------------------------------|----------------|----------------------------------|---|--|---|----------------|----------------------|
| 3495, 3496 3497, 3498 | 48855581 48856245 | 68 65 | 1.00E-92 1.00E-77 | Cytophaga hutchinsonii Cytophaga hutchinsonii | COG0112: Glycine/serine hydroxymethyltransferase [Cytophaga hutchinsonii] COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii] guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase [Coxiella burnetii RSA 493] gb AAO89860.1 guanosine-3,5-bis(diphosphate) 3- pyrophosphohydrolase [Coxiella burnetii RSA 493] | Photothabdus luminescens subsp. laumondii TTO1 complete genome; segment 12/17 | 89 5.00E-07 | 2.1.2.1 |
| 3499, 3500 | 29653654 | 54 | 2.00E-98 | Coxiella burnetii RSA 493 | carboxy-terminal protease [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_122899.1 hypothetical protein lp0561 [Legionella pneumophila str. Paris] ref YP_125903.1 hypothetical protein lp0537 [Legionella pneumophila str. Lens] gb AAU26596.1 carboxy-terminal protease [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH14767.1 hypothetical protein [Legionella pneumophila str. Lens] emb CAH11709.1 hypothetical protein [Legionella pneumophila str. Paris] COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Crocosphaera watsonii WH 8501] | | | 3.1.7.2 |
| 3501, 3502 3503, 3504 | 52840744 46119993 | 42 22 | 5.00E-29 3.00E-07 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 Crocosphaera watsonii WH 8501 | | | | 3.4.2.1- 2.3.1.51 |
| 3505, 3506 3507, 3508 | 39995764 48855704 | 54 28 | 4.00E-65 1.00E-21 | Geobacter sulfurreducens PCA Cytophaga hutchinsonii | CipB protein [Geobacter sulfurreducens PCA] gb AAR33988.1 CipB protein [Geobacter sulfurreducens PCA] sp Q74FF1 CLPB_GEOSL Chaperone clpB COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii] | Desc:N. meningitidis partial DNA sequence gnm_48 SEQ ID NO:48. Org:Neisseria meningitidis | 90 8.00E-09 | |
| 3509, 3510 | 52550522 | 45 | 1.00E-55 | uncultured archaeon GZfos9D8 | BpmI endonuclease-methyltransferase fusion protein type IIG [uncultured archaeon GZfos9D8] | | | 2.1.1.72 |
| 351, 352 3513, 3514 3515, 3516 | 23128081 48854656 48854655 | 50 54 29 | 5.00E-22 3.00E-48 1.00E-12 | Nostoc punctiforme PCC 73102 Cytophaga hutchinsonii Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] COG0348: Polyferredoxin [Cytophaga hutchinsonii] hypothetical protein Chut02002321 [Cytophaga hutchinsonii] | | | 2.7.3.- |

| | | | | | | | | | |
|-------|----------|----|-----------|---|--|---|----|----------|----------|
| 3521, | 53688664 | 33 | 4.00E-21 | Nostoc punctiforme PCC 73102 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 3522 | | | | | | | | | |
| 3523, | 48854120 | 58 | 8.00E-75 | Cytophaga hutchinsonii | COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] | | | | 6.2.1.3 |
| 3524 | | | | | | | | | |
| 3525, | 48853532 | 28 | 2.00E-17 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | | |
| 3526 | | | | | | | | | |
| 3529, | 48854362 | 39 | 6.00E-34 | Cytophaga hutchinsonii | COG1033: Predicted exporters of the RND superfamily [Cytophaga hutchinsonii] | | | | |
| 3530 | | | | | | | | | |
| 3531, | | | | Bacteroides thetaiotaomicron | putative type II restriction endonuclease [Bacteroides thetaiotaomicron VPI-5482] gb AAO79119.1 putative type II restriction endonuclease [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.1.21.4 |
| 3532 | 29349422 | 56 | 4.00E-45 | VPI-5482 | | | | | |
| | | | | | | | | | |
| 3533, | | | | | | | | | |
| 3534 | 13507849 | 28 | 2.00E-16 | Mycoplasma pneumoniae M129 | hypothetical protein MPN110 [Mycoplasma pneumoniae M129] gb AAB95692.1 conserved hypothetical protein [Mycoplasma pneumoniae M129] pir S73370 hypothetical protein C09_orf718 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75452 YB10_MYCPN Hypothetical protein MPN110 [C09_orf718] | | | | 3.1.21.4 |
| 3535, | | | | | | | | | |
| 3536 | 53713662 | 39 | 5.00E-14 | Bacteroides fragilis YCH46 | putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD49120.1 putative ABC transporter permease [Bacteroides fragilis YCH46] | | | | |
| | | | | | | | | | |
| 3537, | | | | | | | | | |
| 3538 | 28209998 | 36 | 6.00E-53 | Clostridium tetani E88 | DNA mismatch repair protein hexA [Clostridium tetani E88] gb AAO34879.1 DNA mismatch repair protein hexA [Clostridium tetani E88] | | | | |
| 3541, | | | | | | | | | |
| 3542 | 51893980 | 65 | 1.00E-100 | Symbiobacterium thermophilum IAM 14863 | tyrosine phenol-lyase [Symbiobacterium thermophilum IAM 14863] dbj BAD41827.1 tyrosine phenol-lyase [Symbiobacterium thermophilum IAM 14863] | C.freundii tpf gene for tyrosine phenol-lyase | 86 | 3.00E-18 | 4.1.99.2 |
| 3543, | | | | | | | | | |
| 3544 | 42523437 | 32 | 4.00E-22 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd1960 [Bdellovibrio bacteriovorus HD100] emb CAE79810.1 hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100] | | | | |
| 3545, | | | | | | | | | |
| 3546 | 29349485 | 44 | 2.00E-41 | Bacteroides thetaiotaomicron VPI-5482 | endo-1,4-beta-xylanase Z precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79182.1 endo-1,4-beta-xylanase Z precursor [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| | | | | | | | | | |
| 3547, | | | | | | | | | |
| 3548 | 21674468 | 71 | 3.00E-44 | Chlorobium tepidum TLS | leucyl-tRNA synthetase [Chlorobium tepidum TLS] gb AAM72875.1 leucyl-tRNA synthetase [Chlorobium tepidum TLS] sp Q8KBY2 SYL_CHL TE Leucyl-tRNA synthetase (Leucine-tRNA ligase) (LeuRS) | | | | 6.1.1.4 |
| | | | | | | | | | |
| 3549, | | | | | | | | | |
| 3550 | 19704204 | 27 | 4.00E-07 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Hydrolase (HAD superfamily) [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95065.1 Hydrolase (HAD superfamily) [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|---|----|-----------|
| 3551, 3552 | 29654168 | 27 | 2.00E-26 | Coxiella burnetii RSA 493 | asparagine synthetase B, glutamine-hydrolyzing [Coxiella burnetii RSA 493] gb AAO90374.1 asparagine synthetase B, glutamine-hydrolyzing [Coxiella burnetii RSA 493] | | | 6.3.5.4 |
| 3553, 3554 | 29349611 | 49 | 1.00E-22 | Bacteroides thetaiotaomicron VPI-5482 | tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79308.1 tRNA delta(2)- isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI- 5482] sp Q8A018 MIAA_BACTN tRNA delta(2)-isopentenylpyrophosphate transferase (IPP transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase) (IPTase) (PPT) | | | 2.5.1.8 |
| 3555, 3556 | 53714925 | 59 | 1.00E-48 | Bacteroides fragilis YCH46 | tRNA nucleotidyltransferase [Bacteroides fragilis YCH46] dbj BAD50383.1 tRNA nucleotidyltransferase [Bacteroides fragilis YCH46] | | | 2.7.7.19 |
| 3561, 3562 | 29348110 | 67 | 3.00E-87 | Bacteroides thetaiotaomicron VPI-5482 | DNA-directed RNA polymerase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO77807.1 DNA-directed RNA polymerase alpha chain [Bacteroides thetaiotaomicron VPI-5482] sp Q8A4A2 RPOA_BACTN DNA- directed RNA polymerase alpha chain (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit) | | | 2.7.7.6 |
| 3563, 3564 | 21233830 | 63 | 2.00E-41 | Proteus vulgaris | hypothetical protein Rts1_167 [Proteus vulgaris] dbj BAB93730.1 | | | |
| 3567, 3568 | 48855784 | 49 | 3.00E-62 | Cytophaga hutchinsonii | hypothetical protein [Proteus vulgaris] COG1741: Pirin-related protein [Cytophaga hutchinsonii] | | | |
| 357, 358 | 42557781 | 88 | 7.00E-95 | uncultured crenarchaeote | putative valyl tRNA synthetase [uncultured crenarchaeote] | Uncultured crenarchaeote genomic fragment 54d9 | 93 | 0 6.1.1.9 |
| 3571, 3572 | 48853634 | 42 | 2.00E-19 | Cytophaga hutchinsonii | COG0564: Pseudouridylyl synthases, 23S RNA-specific [Cytophaga hutchinsonii] conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | 4.2.1.70 |
| 3573, 3574 | 57169084 | 54 | 1.00E-22 | Campylobacter coli RM2228 | putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46] | | | |
| 3575, 3576 | 53712889 | 28 | 2.00E-20 | Bacteroides fragilis YCH46 | COG0608: Single-stranded DNA-specific exonuclease [Cytophaga hutchinsonii] | | | 3.1.-.- |
| 3579, 3580 | 48854369 | 36 | 3.00E-19 | Cytophaga hutchinsonii | ENSANGP00000013062 [Anopheles gambiae] | | | |
| 3581, 3582 | 31211505 | 32 | 3.00E-07 | Anopheles gambiae | COG0156: 7-keto-8-aminopelargonate synthetase and related enzymes [Cytophaga hutchinsonii] | | | 2.3.1.47 |
| 3583, 3584 | 48855098 | 68 | 1.00E-82 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|---------------------|
| 3585, 3586 | 53795203 | 45 | 2.00E-40 | Chloroflexus aurantiacus | COG1680: Beta-lactamase class C and other penicillin binding proteins [Chloroflexus aurantiacus] | | | 3.5.2.6 |
| 3589, 3590 | 23003059 | 34 | 1.00E-14 | Lactobacillus gasseri | COG0266: Formamidopyrimidine-DNA glycosylase [Lactobacillus gasser] | | | 3.2.2.23 |
| 359, 360 | 24214122 | 39 | 4.00E-28 | Leptospira interrogans serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gbl/AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] | | | |
| 3591, 3592 | 48855418 | 64 | 9.00E-99 | Cytophaga hutchinsonii | COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii] | | | |
| 3593, 3594 | 48845408 | 47 | 4.00E-21 | Geobacter metallireducens GS-15 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Geobacter metallireducens GS-15] conserved hypothetical protein [Neisseria meningitidis MC58] pir [G81000 conserved hypothetical protein NMB2153 [imported] - Neisseria meningitidis (strain MC58 serogroup B) ref NP_275138.1] hypothetical protein NMB2153 [Neisseria meningitidis MC58] | | | 3.4.13.9 |
| 3597, 3598 | 7227411 | 47 | 5.00E-47 | Neisseria meningitidis MC58 | SrA-binding protein [Bacteroides thetaiotaomicron VPI-5482] gbl/AAO75286.1 SrA-binding protein [Bacteroides thetaiotaomicron VPI-5482] sp [Q8ABD1 SSRP_BACTN SrA-binding protein sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gbl/AAN51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gbl/AAS71912.1] sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 2.7.7.4 |
| 3603, 3604 | 45659189 | 50 | 3.00E-74 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | COG2895: GTPases - Sulfate adenylyltransferase subunit 1 [Cytophaga hutchinsonii] | | | 2.7.7.4 |
| 3605, 3606 | 48856062 | 56 | 3.00E-82 | Cytophaga hutchinsonii | COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii] | | | |
| 3609, 3610 | 48853493 | 29 | 4.00E-11 | Cytophaga hutchinsonii | Glu-tRNA amidotransferase, subunit B (gatB-1) [Archaeoglobus fulgidus DSM 4304] gbl/AAB89807.1 Glu-tRNA amidotransferase, subunit B (gatB-1) [Archaeoglobus fulgidus DSM 4304] pir [G69429 Glu-tRNA amidotransferase, subunit B (gatB-1) homolog - Archaeoglobus fulgidus sp [O28832 GATE_ARCFU Glutamy-tRNA(Gln) amidotransferase subunit E (Glu-ADT subunit E)] | | | 6.3.5.- |
| 361, 362 | 11499035 | 32 | 9.00E-19 | Archaeoglobus fulgidus DSM 4304 | Methanosarcina mazel strain Goe1, section 214 of 379 of the complete genome | | | 82 1.00E-16 2.1.1.- |
| 3611, 3612 | 21228051 | 77 | 5.00E-70 | Methanosarcina mazel Go1 | | | | |

| | | | | | | | | | |
|------------|----------|----|----------|--|---|---|----|----------|-----------|
| 3613, 3614 | 21228051 | 70 | 4.00E-46 | Methanosarcina mazel Go1 | methyltransferase [Methanosarcina mazel Go1] gb AAM31645.1] | Methanosarcina mazel strain Goe1, section 214 of 379 of the complete genome | 82 | 8.00E-17 | 2.1.1.1.- |
| 3615, 3616 | 51892431 | 32 | 2.00E-25 | Symbiobacterium thermophilum IAM 14863 | hypothetical protein STH1293 [Symbiobacterium thermophilum IAM 14863] dbj BAD40278.1] conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863] | | | | |
| 3617, 3618 | 20808965 | 45 | 5.00E-29 | Thermoanaerobacter tengcongensis MB4 | Homoserine dehydrogenase [Thermoanaerobacter tengcongensis MB4] gb AAM25740.1] Homoserine dehydrogenase [Thermoanaerobacter tengcongensis MB4] | | | | 1.1.1.3 |
| 3619, 3620 | 15613411 | 41 | 2.00E-18 | Bacillus halodurans C-125 | hypothetical protein BH0848 [Bacillus halodurans C-125] dbj BAB04567.1] BH0848 [Bacillus halodurans C-125] pir H83755 hypothetical protein BH0848 [imported] - Bacillus halodurans (strain C-125) | | | | |
| 3621, 3622 | 48863150 | 39 | 3.00E-22 | Microbulbifer degradans 2-40 | COG4166: ABC-type oligopeptide transport system, periplasmic component [Microbulbifer degradans 2-40] | | | | |
| 3623, 3624 | 55246932 | 45 | 4.00E-35 | Anopheles gambiae str. PEST | ENSANGP00000029270 [Anopheles gambiae str. PEST] ref XP_561015.1] ENSANGP00000029270 [Anopheles gambiae str. PEST] | | | | 4.2.1.46 |
| 3625, 3626 | 27380888 | 48 | 5.00E-26 | Bradyrhizobium japonicum USDA 110 | hypothetical protein bfr5777 [Bradyrhizobium japonicum USDA 110] dbj BAC51042.1] bfr5777 [Bradyrhizobium japonicum USDA 110] | | | | |
| 3627, 3628 | 49235065 | 28 | 1.00E-12 | Morella thermoacetica ATCC 39073 | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Morella thermoacetica ATCC 39073] | | | | |
| 363, 364 | 54310134 | 43 | 3.00E-42 | Photobacterium profundum SS9 | putative chorismate mutase/prephenate dehydratase [Photobacterium profundum SS9] emb CAG21352.1] putative chorismate mutase/prephenate dehydratase [Photobacterium profundum] | | | | 4.2.1.51 |
| 3633, 3634 | 13473959 | 39 | 6.00E-09 | Mesorhizobium loti MAFF303099 | hypothetical protein mlr4723 [Mesorhizobium loti MAFF303099] dbj BAB51313.1] mlr4723 [Mesorhizobium loti MAFF303099] | | | | |
| 3635, 3636 | 48855120 | 51 | 4.00E-32 | Cytophaga hutchinsonii | COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii] | | | | 6.1.1.4 |
| 3637, 3638 | 30249879 | 40 | 2.00E-22 | Nitrosomonas europaea ATCC 19718 | Sulfate transporter [Nitrosomonas europaea ATCC 19718] emb CAD85838.1] Sulfate transporter [Nitrosomonas europaea ATCC 19718] | | | | |
| 3641, 3642 | 33862809 | 29 | 3.00E-19 | Prochlorococcus marinus str. MIT 9313 | putative oxidoreductase [Prochlorococcus marinus str. MIT 9313] emb CAE20711.1] putative oxidoreductase [Prochlorococcus marinus str. MIT 9313] | | | | 1.---- |

| | | | | | | | | | | |
|-------|----------|----|----------|--|---|---|--|--|--|---------|
| 3649, | | | | | Xanthomonas campestris pv. campestris str. ATCC 33913 | hypothetical protein XCC2739 [Xanthomonas campestris pv. campestris str. ATCC 33913] gblAAM42011.1] conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | | |
| 3650, | 21232170 | 33 | 2.00E-25 | | Xanthomonas campestris str. ATCC 33913 | hypothetical protein Chut02003580 [Cytophaga hutchinsonii] | | | | |
| 3651, | 48853721 | 35 | 1.00E-11 | | Cytophaga hutchinsonii | Desc:Protoporphyrinogen oxidase protein. Org:Glycine max | | | | 1.3.3.4 |
| 3652, | AAW7395 | 37 | 2.00E-28 | | | COG0642: Signal transduction histidine kinase [Anabaena variabilis ATCC 29413] | | | | 2.7.3.- |
| 3661, | 45507334 | 52 | 2.00E-24 | | Anabaena variabilis ATCC 29413 | hypothetical protein MTH296 [Methanothermobacter thermautotrophicus str. Delta H] gblAAB84802.1] unknown [Methanothermobacter thermautotrophicus str. Delta H] pirl[F69137 hypothetical protein MTH296 - Methanobacterium thermoautotrophicum (strain Delta H)] | | | | |
| 3663, | 15678324 | 38 | 8.00E-14 | | Methanothermobacter thermautotrophicus str. Delta H | hypothetical protein MTH296 [Methanothermobacter thermautotrophicus str. Delta H] gblAAB84802.1] unknown [Methanothermobacter thermautotrophicus str. Delta H] pirl[F69137 hypothetical protein MTH296 - Methanobacterium thermoautotrophicum (strain Delta H)] | | | | |
| 3665, | 15678324 | 38 | 4.00E-14 | | Methanothermobacter thermautotrophicus str. Delta H | COG3459: Cellulose phosphorylase [Dechloromonas aromatica RCB] | | | | |
| 3667, | 46140702 | 37 | 3.00E-23 | | Dechloromonas aromatica RCB | valyl-tRNA synthetase [Porphyromonas gingivalis W83] ref[NP_905340.1] valyl-tRNA synthetase [Porphyromonas gingivalis W83] | | | | |
| 3668 | | | | | | COG0118: Glutamine amidotransferase [Cytophaga hutchinsonii] | | | | |
| 3669, | 34397176 | 49 | 1.00E-61 | | Porphyromonas gingivalis W83 | Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3679. Org:Staphylococcus epidermidis | | | | |
| 3670 | | | | | | hypothetical protein AF0276 [Archaeoglobus fulgidus DSM 4304] gblAAB90956.1] conserved hypothetical protein [Archaeoglobus fulgidus DSM 4304] pirl[D69284 conserved hypothetical protein AF0276 - Archaeoglobus fulgidus sp[O29963]Y276_ARCFU Hypothetical UPF0284 protein AF0276 | | | | |
| 3671, | 48855136 | 58 | 8.00E-33 | | Cytophaga hutchinsonii | COG0307: Riboflavin synthase alpha chain [Cytophaga hutchinsonii] | | | | |
| 3672 | ABP3883 | 43 | 2.00E-15 | | | | | | | |
| 3673, | 11497892 | 46 | 6.00E-58 | | Archaeoglobus fulgidus DSM 4304 | | | | | |
| 3674 | | | | | | | | | | |
| 3675, | 48856513 | 48 | 2.00E-32 | | Cytophaga hutchinsonii | | | | | |
| 3676 | | | | | | | | | | 2.5.1.9 |

| | | | | | | | | | |
|---------------|--------------|----|----------|---|---|--|--|---------|---------------|
| 3683, 3684 | 15898659 | 56 | 2.00E-24 | Sulfolobus solfataricus P2 | hypothetical protein SSO1867 [Sulfolobus solfataricus P2] gb AAK42054.1] Conserved hypothetical protein [Sulfolobus solfataricus P2] pir G90349 conserved hypothetical protein [imported] - Sulfolobus solfataricus | | | | 2.1.1.10 7 |
| 3685, 3686 | 24374020 | 44 | 5.00E-40 | Shewanella oneidensis MR-1 | polysaccharide biosynthesis protein [Shewanella oneidensis MR-1] gb AAN55507.1 polysaccharide biosynthesis protein [Shewanella oneidensis MR-1] | | | | |
| 3687, 3688 | 29349856 | 31 | 2.00E-31 | Bacteroides thetataoamicron VPI-5482 | putative dehydrogenase [Bacteroides thetataoamicron VPI-5482] gb AAO79553.1 putative dehydrogenase [Bacteroides thetataoamicron VPI- 5482] | | | | |
| 369, 370 | 52841308 | 46 | 5.00E-40 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | hypothetical protein lpg1074 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27160.1 hypothetical protein lpg1074 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | |
| 3691, 3692 | 53713591 | 35 | 1.00E-39 | Bacteroides fragilis YCH46 | hypothetical protein BF2302 [Bacteroides fragilis YCH46] db BAD49049.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 3697, 3698 | 28170110 | 34 | 1.00E-10 | Vibrio vulnificus | unknown [Vibrio vulnificus] | | | | |
| 3699, 3700 | 48854153 | 70 | 3.00E-37 | Cytophaga hutchinsonii | hypothetical protein Chut02003248 [Cytophaga hutchinsonii] | | | | |
| 37, 38 | 42523010 | 26 | 3.00E-10 | Bdellovibrio bacteriovorus HD100 | putative heptosyltransferase [Bdellovibrio bacteriovorus HD100] emb CAE79382.1 putative heptosyltransferase [Bdellovibrio bacteriovorus HD100] | | | | |
| 3705, 3706 | 29349216 | 50 | 5.00E-57 | Bacteroides thetataoamicron VPI-5482 | hypothetical protein BT3808 [Bacteroides thetataoamicron VPI-5482] gb AAO78913.1 conserved hypothetical protein [Bacteroides thetataoamicron VPI-5482] | | | | |
| 3707, 3708 | 21673004 | 60 | 3.00E-71 | Chlorobium tepidum TLS | alpha oxoglutarate ferredoxin oxidoreductase, alpha subunit [Chlorobium tepidum TLS] gb AAM71411.1 alpha oxoglutarate ferredoxin oxidoreductase, alpha subunit [Chlorobium tepidum TLS] | | | 1.2.7.3 | |
| 3709, 3710 | 56476832 | 35 | 1.00E-27 | Azoarcus sp. EbN1 | hypothetical protein eba2472 [Azoarcus sp. EbN1] emb CAI07520.1 hypothetical protein [Azoarcus sp. EbN1] | | | | |
| 371, 372 | 16126664 | 43 | 5.00E-13 | Caulobacter crescentus CB15 | hypothetical protein CC2425 [Caulobacter crescentus CB15] gb AAK24396.1 conserved hypothetical protein [Caulobacter crescentus CB15] pir H87549 conserved hypothetical protein CC2425 [imported] - Caulobacter crescentus | | | | |
| 3711, 3712 | 48856332 | 45 | 1.00E-24 | Cytophaga hutchinsonii | hypothetical protein Chul02000044 [Cytophaga hutchinsonii] | | | | |
| 3713, 3714 | AAB3573 8 | 48 | 2.00E-35 | | Desc:Alpha-galactosidase amino acid sequence SEQ ID 4. Org:Clostridium josui | | | | 3.2.1.22 |

| | | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|--|----------|
| 3717, 3718 | 15896506 | 55 | 1.00E-41 | Clostridium acetobutylicum ATCC 824 | Methylated DNA-protein cysteine methyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK81195.1 Methylated DNA-protein cysteine methyltransferase [Clostridium acetobutylicum ATCC 824] pir H97300 methylated DNA-protein cysteine methyltransferase [imported] - Clostridium acetobutylicum | | | | 2.1.1.63 |
| 3719, 3720 | 29348575 | 35 | 2.00E-18 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3166 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78272.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 3721, 3722 | 56461500 | 39 | 1.00E-47 | Idiomarina loihlensis L2TR | Capsular polyglutamate biosynthesis secreted protein CapB, ATP- dependent mur ligase family [Idiomarina loihlensis L2TR] gb AAV83232.1 Capsular polyglutamate biosynthesis secreted protein CapB, ATP- dependent mur ligase family [Idiomarina loihlensis L2TR] | | | | 6.3.2.- |
| 3723, 3724 | 45657306 | 49 | 1.00E-55 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_712725.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AAN49743.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AAS70029.1 alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 3725, 3726 | 23124495 | 60 | 3.00E-82 | Nostoc punctiforme PCC 73102 | COG0667: Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) [Nostoc punctiforme PCC 73102] | | | | 1.-.-.- |
| 3727, 3728 | 48861126 | 42 | 1.00E-45 | Microbulbifer degradans 2-40 | COG2303: Choline dehydrogenase and related flavoproteins [Microbulbifer degradans 2-40] | | | | 1.-.-.- |
| 3729, 3730 | 48859646 | 40 | 2.00E-43 | Clostridium thermocellum ATCC 27405 | COG2189: Adenine specific DNA methylase Mod [Clostridium thermocellum ATCC 27405] | | | | 2.1.1.72 |
| 373, 374 | 32477896 | 39 | 2.00E-12 | Rhodopirella baltica SH 1 | hypothetical protein RB13143 [Rhodopirella baltica SH 1] emb CAD77988.1 hypothetical protein [Pirella sp.] | | | | |
| 3731, 3732 | 39997334 | 46 | 5.00E-47 | Geobacter sulfurreducens PCA | GTP pyrophosphokinase [Geobacter sulfurreducens PCA] gb AAR35612.1 GTP pyrophosphokinase [Geobacter sulfurreducens PCA] | | | | 2.7.6.5 |
| 3735, 3736 | 54295921 | 38 | 3.00E-11 | Legionella pneumophila str. Paris | hypothetical protein plpp0078 [Legionella pneumophila str. Paris] emb CAH17255.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | |

| | | | | | | | | | |
|---------------|----------|----|-----------|---|---|---|----|----------|----------|
| 3739, 3740 | 20807120 | 69 | 1.00E-101 | Thermoanaerobact er tengcongensis MB4 | ATP-dependent protease Clp, ATPase subunit [Thermoanaerobacter tengcongensis MB4] gb AAM23895.1 ATP-dependent protease Clp, ATPase subunit [Thermoanaerobacter tengcongensis MB4] sp Q8RC24 CLPX_THEIN ATP-dependent Clp protease ATP-binding subunit clpX | Azospirillum brasiliense trigger factor (tig), heat- shock protein ClpP (clpP), and heat- shock protein ClpX (clpX) genes, complete cds; and Lon protease (lon) gene, partial cds. | 85 | 3.00E-92 | 3,4,24,- |
| 3741, 3742 | 20806566 | 52 | 3.00E-64 | Thermoanaerobact er tengcongensis MB4 | Seryl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] gb AAM2334.1.1 Seryl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] sp Q8RDJ5 SYS_THEIN Seryl-tRNA synthetase (Seryl--tRNA ligase) (SerRS) | | | | 6.1.1.11 |
| 3743, 3744 | 48855590 | 70 | 1.00E-116 | Cytophaga hutchinsonii | COG1154: Deoxyxylulose-5-phosphate synthase [Cytophaga hutchinsonii] | | | | 4.1.3.37 |
| 3747, 3748 | 48856398 | 51 | 7.00E-42 | Cytophaga hutchinsonii | COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii] | | | | 4.1.3.- |
| 3749, 3750 | 32473810 | 47 | 4.00E-60 | Rhodopirellula baltica SH 1 | probable aminopeptidase [Rhodopirellula baltica SH 1] emb CAD74344.1 probable aminopeptidase [Pirellula sp.] | | | | |
| 375, 376 | 48891840 | 35 | 1.00E-16 | Trichodesmium erythraeum IMS101 | COG1232: Protoporphyrinogen oxidase [Trichodesmium erythraeum IMS101] | | | | 1.3.3.4 |
| 3751, 3752 | 49235971 | 54 | 6.00E-14 | Moorella thermoacetica ATCC 39073 | COG1555: DNA uptake protein and related DNA-binding proteins [Moorella thermoacetica ATCC 39073] | | | | |
| 3755, 3756 | 42557743 | 31 | 6.00E-12 | uncultured crenarchaeote | hypothetical protein [uncultured crenarchaeote] | | | | |
| 3757, 3758 | 53714487 | 56 | 1.00E-43 | Bacteroides fragilis YCH46 | SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD49945.1 SsrA- binding protein [Bacteroides fragilis YCH46] | | | | |
| 3759, 3760 | 48855337 | 64 | 3.00E-53 | Cytophaga hutchinsonii | COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii] | | | | |
| 3775, 3776 | 42548894 | 41 | 3.00E-27 | Gibberella zeae PH- 1 | hypothetical protein FG03048.1 [Gibberella zeae PH-1] ref XP_383224.1 hypothetical protein FG03048.1 [Gibberella zeae PH-1] | | | | 5.1.3.2 |
| 3777, 3778 | 53712889 | 36 | 2.00E-32 | Bacteroides fragilis YCH46 | putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46] | | | | |
| 3779, 3780 | 16802005 | 34 | 2.00E-21 | Listeria innocua Clp11262 | hypothetical protein lin2946 [Listeria innocua Clp11262] emb CAC98171.1 lin2946 [Listeria innocua] plr AC1800 hypothetical protein lin2946 [imported] Listeria innocua (strain Clp11262) | | | | |

| | | | | | | | |
|---|---|--|--|---|---|----------------|--|
| 3781, 3782, 3783, 3784, 3785, 3786, 3787, 3788, 379, 3793, 3794, 3797, 3798, 3803, 3804, 3805, 3806, 3807, 3808, 3809, 3810, 381, 382, 3813, 3814 | 53730651 31195995 23112518 48853493 2281663 48854463 53715112 20089111 42523157 53712342 15897361 57169064 39933400 | 25 54 40 32 57 58 30 69 23 60 35 32 33 | 1.00E-10 1.00E-39 1.00E-36 2.00E-14 1.00E-43 2.00E-34 5.00E-29 2.00E-53 2.00E-18 4.00E-86 2.00E-11 1.00E-10 4.00E-10 | Dechloromonas aromatica RCB Anopheles gambiae Desulfotobacterium hafniense DCB-2 Cytophaga hutchinsonii Flavobacterium johnsoniae Cytophaga hutchinsonii Bacteroides fragilis YCH46 Methanosarcina acetivorans C2A Bdellovibrio bacteriovorus HD100 Bacteroides fragilis YCH46 Sulfolobus solfataricus P2 Campylobacter coli RM2228 Rhodopseudomonas palustris CGA009 | COG0438: Glycosyltransferase [Dechloromonas aromatica RCB] ENSANGP00000000470 [Anopheles gambiae] COG1162: Predicted GTPases [Desulfotobacterium hafniense DCB-2] COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii] gliding motility protein [Flavobacterium johnsoniae] pilT44443 gliding motility protein [imported] - Flavobacterium johnsoniae COG0193: Peptidyl-tRNA hydrolase [Cytophaga hutchinsonii] 4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4- alpha-glucanotransferase [Bacteroides fragilis YCH46] Xaa-Pro dipeptidase (cobalt-dependent) [Methanosarcina acetivorans C2A] gb AA03666.1 Xaa-Pro dipeptidase (cobalt-dependent) [Methanosarcina acetivorans str. C2A] Sensory box histidine kinase [Bdellovibrio bacteriovorus HD100] emb CAE79530.1 Sensory box histidine kinase [Bdellovibrio bacteriovorus HD100] valyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD47800.1 valyl- tRNA synthetase [Bacteroides fragilis YCH46] HAM1 protein [Sulfolobus solfataricus P2] gb AAK40756.1 HAM1 protein [Sulfolobus solfataricus P2] pir E90187 HAM1 protein [imported] - Sulfolobus solfataricus conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228] Protein of unknown function UPF0102 [Rhodopseudomonas palustris CGA009] emb CAE25767.1 Protein of unknown function UPF0102 [Rhodopseudomonas palustris CGA009] | 90 92 92 | 5.00E-09 6.00E-10 6.1.1.9 2.7.3.- 6.1.1.9 3.6.1.15 3.1.- |
|---|---|--|--|---|---|----------------|--|

| | | | | | | | | | |
|-------|----------|----|----------|--|---|--|--|--|----------|
| 3815, | 15644379 | 38 | 1.00E-09 | Thermotoga maritima MSB8 | hypothetical protein TM1631 [Thermotoga maritima MSB8] gbl AAD36698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 | | | | |
| 3816 | 48856757 | 31 | 3.00E-18 | Cytophaga hutchinsonii | COG3735: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 3823, | 53715867 | 50 | 1.00E-46 | Bacteroides fragilis YCH46 | putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46] dbj BAD51325.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46] | | | | 2.7.7.56 |
| 3826 | 51891981 | 35 | 2.00E-39 | Symbiobacterium thermophilum IAM 14863 | two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863] dbj BAD39828.1 two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863] | | | | 2.7.3.- |
| 3827, | 51891981 | 36 | 1.00E-38 | Symbiobacterium thermophilum IAM 14863 | two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863] dbj BAD39828.1 two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863] | | | | 2.7.3.- |
| 3831, | 32472461 | 32 | 6.00E-19 | Rhodopirellula baltica SH 1 | conserved hypothetical protein-putative sodium:solute symporter [Rhodopirellula baltica SH 1] emb CAD73139.1 conserved hypothetical protein-putative sodium:solute symporter [Pirellula sp.] | | | | |
| 3833, | 56494802 | 36 | 1.00E-19 | Plasmodium berghel | thymidylate kinase, putative [Plasmodium berghel] | | | | 2.7.4.9 |
| 3835, | 42523044 | 34 | 5.00E-43 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd1537 [Bdellovibrio bacteriovorus HD100] emb CAE79417.1 hypothetical protein predicted by Glimmer/Critica | | | | |
| 3837, | 45358689 | 37 | 9.00E-31 | Methanococcus maripaludis S2 | putative proliferating-cell nucleolar antigen [Methanococcus maripaludis S2] emb CAF30682.1 putative proliferating-cell nucleolar antigen [Methanococcus maripaludis S2] | | | | 2.1.1.- |
| 3839, | 48855704 | 26 | 3.00E-28 | Cytophaga hutchinsonii | COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii] | | | | |
| 3843, | 48853471 | 38 | 9.00E-09 | Cytophaga hutchinsonii | COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | | |
| 3845, | 48853824 | 47 | 3.00E-68 | Cytophaga hutchinsonii | COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii] | | | | |
| 3849, | 33593091 | 26 | 7.00E-09 | Bordetella pertussis Tohama I | putative lipoprotein [Bordetella pertussis Tohama I] emb CAE42350.1 putative lipoprotein [Bordetella pertussis Tohama I] | | | | |
| 385, | 48862505 | 40 | 1.00E-35 | Microbulifer degradans 2-40 | COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Microbulifer degradans 2-40] | | | | 2.7.3.- |
| 3851, | 48853176 | 34 | 2.00E-39 | Ferroplasma acidarmanus | COG0624: Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacetylases [Ferroplasma acidarmanus] | | | | 3.5.1.16 |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|---|----|----------|
| 3853, 3854 | 52550513 | 36 | 2.00E-08 | uncultured archaeon GZfos9D8 | conserved hypothetical protein [uncultured archaeon GZfos9D8] | | | |
| 3859, 3860 | 29345424 | 24 | 1.00E-11 | Bacteroides thetaiotaomicron VPI-5482 | rteA, two-component system histidine kinase, with response regulator receiver domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO75121.1 rteA, two-component system histidine kinase, with response regulator receiver domain [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.3.- |
| 3861, 3862 | 53715302 | 53 | 2.00E-32 | Bacteroides fragilis YCH46 | adenylosuccinate lyase [Bacteroides fragilis YCH46] dbj BAD50760.1 adenylosuccinate lyase [Bacteroides fragilis YCH46] | | | 4.3.2.2 |
| 3863, 3864 | 29349999 | 21 | 2.00E-10 | Bacteroides thetaiotaomicron VPI-5482 | putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 3865, 3866 | | | | | | Bacteroides fragilis YCH46 DNA, complete genome | 90 | 6.00E-08 |
| 3867, 3868 | 18314195 | 24 | 2.00E-08 | Pyrobaculum aerophilum str. IM2 | nitrate reductase subunit, conjectural [Pyrobaculum aerophilum str. IM2] gb AAL65044.1 nitrate reductase subunit, conjectural [Pyrobaculum aerophilum str. IM2] | | | |
| 387, 388 | 48854286 | 42 | 2.00E-30 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 3871, 3872 | 42548911 | 30 | 6.00E-27 | Gibberella zeae PH- 1 | hypothetical protein FG03065.1 [Gibberella zeae PH-1] ref XP_383241.1 hypothetical protein FG03065.1 [Gibberella zeae PH-1] | | | |
| 3873, 3874 | 29347149 | 56 | 2.00E-83 | Bacteroides thetaiotaomicron VPI-5482 | exonuclease ABC subunit A [Bacteroides thetaiotaomicron VPI-5482] gb AAO76846.1 exonuclease ABC subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | 1.8.- |
| 3875, 3876 | 48855211 | 43 | 3.00E-55 | Cytophaga hutchinsonii | COG4953: Membrane carboxypeptidase/penicillin-binding protein PbpC [Cytophaga hutchinsonii] | | | 2.4.2.- |
| 3877, 3878 | 53714076 | 28 | 2.00E-16 | Bacteroides fragilis YCH46 | putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD49534.1 putative glycosyltransferase [Bacteroides fragilis YCH46] | | | 2.4.1.- |
| 3879, 3880 | 28211867 | 40 | 6.00E-12 | Clostridium tetani E88 | glycosyl transferase [Clostridium tetani E88] gb AAO36748.1 glycosyl transferase [Clostridium tetani E88] | | | 2.4.1.- |
| 3881, 3882 | 48854367 | 38 | 8.00E-44 | Cytophaga hutchinsonii | hypothetical protein Chut02003040 [Cytophaga hutchinsonii] | | | |
| 3887, 3888 | 37521381 | 32 | 1.00E-09 | Gloeobacter violaceus PCC 7421 | hypothetical protein gl1812 [Gloeobacter violaceus PCC 7421] dbj BAC89753.1 gl1812 [Gloeobacter violaceus PCC 7421] | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|---|----|----------|----------|
| 389, 390 | 48856849 | 35 | 2.00E-30 | Cytophaga hutchinsonii | COG0525: Valyl-tRNA synthetase [Cytophaga hutchinsonii] AGR_C_2408p [Agrobacterium tumefaciens str. C58] pir[C97518 hypothetical protein AGR_C_2408 [Imported] - Agrobacterium tumefaciens (strain C58, Cereon) ref NP_354315.1 hypothetical protein AGR_C_2408 [Agrobacterium tumefaciens str. C58] | Desc:Listeria monocytogenes 4b contig DNA sequence #315. Org:Listeria monocytogenes 4b | 95 | 6.00E-07 | 6.1.1.19 |
| 3895, 3896 | 15156362 | 40 | 6.00E-16 | Agrobacterium tumefaciens str. C58 | | | | | |
| 3899, 3900 | 53795436 | 34 | 8.00E-40 | Chloroflexus aurantiacus | COG1232: Protoporphyrinogen oxidase [Chloroflexus aurantiacus] tRNA and rRNA cytosine-C5-methylase [Bacteroides fragilis YCH46] dbj BAD50469.1 tRNA and rRNA cytosine-C5-methylase [Bacteroides fragilis YCH46] | | | | |
| 39, 40 | 53715011 | 34 | 9.00E-32 | Bacteroides fragilis YCH46 | | | | | |
| 3905, 3906 | 29348744 | 36 | 7.00E-36 | Bacteroides thetalaotomicron VPI-5482 | hypothetical protein BT3335 [Bacteroides thetalaotomicron VPI-5482] gb AAO78441.1 hypothetical protein [Bacteroides thetalaotomicron VPI- 5482] | | | | |
| 3907, 3908 | 34557103 | 38 | 6.00E-59 | Wolliella succinogenes DSM 1740 | hypothetical protein WS0692 [Wolliella succinogenes DSM 1740] emb CAE09818.1 conserved hypothetical protein [Wolliella succinogenes] COG0071: Molecular chaperone (small heat shock protein) [Cytophaga hutchinsonii] | | | | |
| 3909, 3910 | 48855680 | 58 | 2.00E-35 | Cytophaga hutchinsonii | | | | | |
| 3913, 3914 | 53756150 | 34 | 2.00E-29 | Methylococcus capsulatus str. Bath | conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_112939.1 hypothetical protein MCA0408 [Methylococcus capsulatus str. Bath] | | | | |
| 3915, 3916 | 45659045 | 54 | 3.00E-30 | Leptospira interrogans serovar Copenhagen str. Flocruz L1-130 | Inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714220.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar Lai str. 56601] gb AAN51238.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar lai str. 56601] sp Q8EZ21 IPYR_LEPIN Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (Pase) gb AAS71768.1 Inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ATP-dependent protease Clp, ATPase subunit [Thermoanaerobacter tengcongensis MB4] gb AAM23895.1 ATP-dependent protease Clp, ATPase subunit [Thermoanaerobacter tengcongensis MB4] sp Q8RC24 CLPX_THETN ATP-dependent Clp protease ATP-binding subunit clpX | Gloeobacter violaceus PCC 7421 DNA, complete genome | 84 | 7.00E-19 | 3.4.24.- |
| 3917, 3918 | 20807120 | 67 | 2.00E-94 | Thermoanaerobact er tengcongensis MB4 | | | | | |

| | | | | | | | | |
|---------------|--------------|----|-----------|---|---|--|--|----------|
| 3923, 3924 | 48870695 | 41 | 7.00E-19 | Pediococcus pentosaceus ATCC 25745 | COG1234: Metal-dependent hydrolases of the beta-lactamase superfamily III [Pediococcus pentosaceus ATCC 25745] | | | |
| 3925, 3926 | 28211584 | 38 | 4.00E-19 | Clostridium tetani E88 | histidyl-tRNA synthetase [Clostridium tetani E88] gb AAO36465.1 histidyl- tRNA synthetase [Clostridium tetani E88] sp Q892X7 SYH_CLOTE Histidyl- tRNA synthetase (Histidine-tRNA ligase) (HisRS) | | | 6.1.1.21 |
| 3927, 3928 | 51573655 | 40 | 9.00E-10 | Borrelia garinii PBI | isoleucyl-tRNA synthetase [Borrelia garinii PBI] ref YP_073272.1 isoleucyl- tRNA synthetase [Borrelia garinii PBI] | | | 6.1.1.5 |
| 3929, 3930 | 13475838 | 36 | 8.00E-27 | Mesorhizobium loti MAFF303099 | hypothetical protein ml7009 [Mesorhizobium loti MAFF303099] dbj BAB53194.1 ml7009 [Mesorhizobium loti MAFF303099] | | | |
| 393, 394 | 34397028 | 62 | 7.00E-59 | Porphyromonas gingivalis W83 | prolyl-tRNA synthetase [Porphyromonas gingivalis W83] ref NP_905193.1 prolyl-tRNA synthetase [Porphyromonas gingivalis W83] | | | 6.1.1.15 |
| 3931, 3932 | 45657291 | 46 | 1.00E-33 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | acyl-CoA thioesterase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70014.1 acyl-CoA thioesterase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 3.1.2.- |
| 3933, 3934 | AAB3573 8 | 47 | 8.00E-35 | | Desc:Alpha-galactosidase amino acid sequence SEQ ID 4. Org:Clostridium josui | | | 3.2.1.22 |
| 3937, 3938 | 23112865 | 41 | 1.00E-35 | Desulfotobacterium hafnense DCB-2 | COG4636: Uncharacterized protein conserved in cyanobacteria [Desulfotobacterium hafnense DCB-2] | | | |
| 3939, 3940 | 48856298 | 62 | 1.00E-118 | Cytophaga hutchinsonii | COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Cytophaga hutchinsonii] | | | 2.7.6.5 |
| 3941, 3942 | 56542586 | 31 | 8.00E-08 | Zymomonas mobilis subsp. mobilis ZM4 | conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_161851.1 hypothetical protein ZMO0116 [Zymomonas mobilis subsp. mobilis ZM4] | | | |
| 3947, 3948 | 7489371 | 33 | 6.00E-16 | Hordeum vulgare subsp. vulgare | endonuclease (EC 3.1.30.-) precursor - barley dbj BAA28942.1 endonuclease [Hordeum vulgare subsp. vulgare] | | | |
| 3949, 3950 | 48855592 | 25 | 1.00E-17 | Cytophaga hutchinsonii | COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Cytophaga hutchinsonii] | | | |
| 3953, 3954 | 48845393 | 49 | 2.00E-74 | Geobacter metallireducens GS 15 | COG0504: CTP synthase (UTP-ammonia lyase) [Geobacter metallireducens GS-15] | | | 6.3.4.2 |
| 3957, 3958 | 48853733 | 30 | 2.00E-08 | Cytophaga hutchinsonii | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | |
| 3959, 3960 | 28170110 | 34 | 1.00E-10 | Vibrio vulnificus | unknown [Vibrio vulnificus] | | | |

| | | | | | | | | | |
|-------|----------|----|-----------|--|--|--|--|--|----------|
| 3961, | 48855076 | 67 | 1.00E-110 | Cytophaga hutchinsonii | COG1251: NAD(P)H-nitrite reductase [Cytophaga hutchinsonii] | | | | 1.6.6.4 |
| 3962 | | | | | COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 3963, | 48855703 | 36 | 3.00E-32 | Cytophaga hutchinsonii | excinuclease ABC subunit C [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 3964 | | | | Bacteroides thetaiotaomicron VPI-5482 | gb AAO78372.1 excinuclease ABC subunit C [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 3965, | 29348675 | 43 | 2.00E-73 | Oceanobacillus thetaiotaomicron VPI-5482 | deoxypurine kinase subunit [Oceanobacillus thetaiotaomicron VPI-5482] | | | | |
| 3966 | | | | | dbj BAC11971.1 deoxypurine kinase subunit [Oceanobacillus thetaiotaomicron VPI-5482] | | | | 2.7.1.11 |
| 3967, | 23097470 | 43 | 2.00E-40 | Oceanobacillus thetaiotaomicron VPI-5482 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | | 2.7.3.- |
| 3968 | | | | Geobacter metallireducens GS-15 | FOG TPR repeat [uncultured archaeon GZfos17F1] | | | | |
| 3969, | 48846077 | 29 | 6.00E-13 | uncultured archaeon | COG0861: Membrane protein TerC, possibly involved in tellurium resistance [Geobacter metallireducens GS-15] | | | | |
| 3970 | | | | | two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 3971, | 52548588 | 27 | 3.00E-32 | Geobacter metallireducens GS-15 | two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 3972 | | | | Bacteroides thetaiotaomicron VPI-5482 | histidine kinase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |
| 3973, | 29347576 | 44 | 2.00E-65 | Haloarcula marismortui ATCC 33049 | putative sulfatase [Haloarcula marismortui ATCC 33049] | | | | |
| 3974 | | | | | putative sulfatase [Haloarcula marismortui ATCC 33049] | | | | 3.1.6.- |
| 3975, | 55377316 | 27 | 3.00E-17 | Chlorobium tepidum TLS | hypothetical protein CT1862 [Chlorobium tepidum TLS] | | | | |
| 3976 | | | | Cytophaga hutchinsonii | conserved hypothetical protein [Chlorobium tepidum TLS] | | | | |
| 3977, | 21674674 | 36 | 5.00E-43 | Geobacillus kaustophilus HTA426 | COG0469: Pyruvate kinase [Cytophaga hutchinsonii] | | | | 2.7.1.40 |
| 3978 | | | | | ABC transporter (ATP-binding protein) [Geobacillus kaustophilus HTA426] | | | | |
| 3979, | 48855011 | 52 | 8.00E-54 | Geobacillus kaustophilus HTA426 | dbj BAD74525.1 ABC transporter (ATP-binding protein) [Geobacillus kaustophilus HTA426] | | | | |
| 3980 | | | | Cytophaga hutchinsonii | COG0726: Predicted xylanase/chitin deacetylase [Cytophaga hutchinsonii] | | | | 3.5.1.- |
| 3981, | 56418775 | 40 | 3.00E-32 | Cytophaga hutchinsonii | COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Cytophaga hutchinsonii] | | | | |
| 3982 | | | | | hypothetical protein MS1906 [Mannheimia succiniciproducens MBEL55E] | | | | |
| 3983, | 48856688 | 39 | 1.00E-14 | Cytophaga hutchinsonii | gb AAU38513.1 unknown [Mannheimia succiniciproducens MBEL55E] | | | | 3.8.1.2 |
| 3984 | | | | | | | | | |
| 3985, | 48855209 | 49 | 5.00E-54 | Cytophaga hutchinsonii | | | | | |
| 3986 | | | | Mannheimia succiniciproducens MBEL55E | | | | | |
| 3987, | 52425961 | 40 | 1.00E-18 | MBEL55E | | | | | |
| 3988 | | | | | | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|--|---------------|
| 3999, 4000 | 13475625 | 52 | 5.00E-44 | Mesorhizobium loti MAFF303099 | long chain acyl-CoA synthetase [Mesorhizobium loti MAFF303099]: dbj BAB52978.1 long chain acyl-CoA synthetase [Mesorhizobium loti MAFF303099] | | | | 6.2.1.3 |
| 4001, 4002 | 46445809 | 38 | 1.00E-16 | Parachlamydia sp. UWE25 | hypothetical protein pc0175 [Parachlamydia sp. UWE25] emb CAF22899.1 hypothetical protein [Parachlamydia sp. UWE25] | | | | |
| 4003, 4004 | 48855817 | 41 | 1.00E-14 | Cytophaga hutchinsonii | COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | | |
| 4013, 4014 | 48833968 | 47 | 3.00E-56 | Magnetococcus sp. MC-1 | COG0673: Predicted dehydrogenases and related proteins [Magnetococcus sp. MC-1] | | | | 1.1.1.18 |
| 4015, 4016 | 24371751 | 53 | 1.00E-53 | Shewanella oneidensis MR-1 | hypothetical SAM-dependent methyltransferase [Shewanella oneidensis MR- 1] gb AAN53238.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | | 2.1.1.64 |
| 4017, 4018 | 48856843 | 56 | 5.00E-81 | Cytophaga hutchinsonii | COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Cytophaga hutchinsonii] | | | | 6.2.1.1 |
| 4021, 4022 | 56421844 | 38 | 2.00E-17 | Geobacillus kaustophilus HTA426 | serine acetyltransferase [Geobacillus kaustophilus HTA426] dbj BAD77594.1 serine acetyltransferase [Geobacillus kaustophilus HTA426] | | | | 2.3.1.30 |
| 4023, 4024 | 45657668 | 42 | 5.00E-22 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | dihydroliipoamide dehydrogenase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70391.1 dihydroliipoamide dehydrogenase [Leptospira interrogans serovar Copenhageni str. Flocruz L1- 130] | | | | 1.8.1.4 |
| 4025, 4026 | 32471201 | 38 | 2.00E-44 | Rhodopirella baltica SH 1 | probable hexosyltransferase [Rhodopirella baltica SH 1] emb CAD71871.1 probable hexosyltransferase [Pirella sp.] | | | | |
| 4027, 4028 | 23130298 | 37 | 2.00E-25 | Nostoc punctiforme PCC 73102 | COG2319: FOG: WD40 repeat [Nostoc punctiforme PCC 73102] | | | | 2.7.1.37 |
| 4029, 4030 | 48855761 | 40 | 7.00E-31 | Cytophaga hutchinsonii | COG0248: Exopolyphosphatase [Cytophaga hutchinsonii] | | | | 3.6.1.11 |
| 403, 404 | 53685426 | 33 | 8.00E-08 | Desulfotobacterium hafnense DCB-2 | COG1587: Uroporphyrinogen-III synthase [Desulfotobacterium hafnense DCB-2] | | | | 2.1.1.10 7 |
| 4031, 4032 | 48855761 | 41 | 6.00E-36 | Cytophaga hutchinsonii | COG0248: Exopolyphosphatase [Cytophaga hutchinsonii] | | | | 3.6.1.11 |
| 4039, 4040 | 7225870 | 58 | 9.00E-55 | Neisseria meningitidis MC58 | inorganic pyrophosphatase [Neisseria meningitidis MC58] ref NP_273684.1 inorganic pyrophosphatase [Neisseria meningitidis MC58] pir F81175 inorganic pyrophosphatase NMB0641 [imported] - Neisseria meningitidis (strain MC58 serogroup B) sp Q9K0G4 IPYR_NEIMB Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase) | | | | 3.6.1.1 |

| | | | | | | | | | |
|---------------|----------|----|-----------|---|--|---|----|----------|----------|
| 4041, 4042 | 21674725 | 65 | 2.00E-92 | Chlorobium tepidum TLS | DNA methylase, putative [Chlorobium tepidum TLS] gb AAM73132.1 DNA methylase, putative [Chlorobium tepidum TLS] | | | | |
| 4043, 4044 | 15669283 | 38 | 6.00E-40 | Methanocaldococ- us jannaschii DSM 2661 | hypothetical protein MJ1095 [Methanocaldococcus jannaschii DSM 2661] gb AAB99098.1 conserved hypothetical protein [Methanocaldococcus jannaschii DSM 2661] pir F64436 hypothetical protein MJ1095 - Methanococcus jannaschii sp Q58495 YA95_METJA Hypothetical protein MJ1095 | | | | |
| 4045, 4046 | 48854971 | 43 | 2.00E-32 | Cytophaga hutchinsonii | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | | |
| 4047, 4048 | 53764442 | 46 | 7.00E-74 | Anabaena variabilis ATCC 29413 | COG3280: Maltotigiosyl trehalose synthase [Anabaena variabilis ATCC 29413] | | | | 2.4.1.- |
| 4051, 4052 | 15894850 | 67 | 1.00E-102 | Clostridium acetobutylicum ATCC 824 | Fructose-1,6-bisphosphatase (YYDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] gb AAK79539.1 Fructose-1,6-bisphosphatase (YYDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] pir H97093 fructose-bisphosphatase (EC 3.1.3.11) [similarity] - Clostridium acetobutylicum | Desc:Staphylococc us epidermidis ORF nucleic acid sequence SEQ ID NO:1485. Org:Staphylococcus epidermidis | 85 | 6.00E-13 | 3.1.3.11 |
| 4053, 4054 | 15894850 | 67 | 1.00E-122 | Clostridium acetobutylicum ATCC 824 | Fructose-1,6-bisphosphatase (YYDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] gb AAK79539.1 Fructose-1,6-bisphosphatase (YYDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] pir H97093 fructose-bisphosphatase (EC 3.1.3.11) [similarity] - Clostridium acetobutylicum | Desc:Staphylococc us epidermidis ORF nucleic acid sequence SEQ ID NO:1485. Org:Staphylococcus epidermidis | 88 | 5.00E-11 | 3.1.3.11 |
| 4055, 4056 | 48854003 | 23 | 2.00E-10 | Cytophaga hutchinsonii | hypothetical protein Chut02003091 [Cytophaga hutchinsonii] | | | | |
| 4057, 4058 | 48856470 | 37 | 2.00E-19 | Cytophaga hutchinsonii | COG2932: Predicted transcriptional regulator [Cytophaga hutchinsonii] heat shock protein (dnaJ) [Mycoplasma genitalium G-37] gb AAC71235.1 heat shock protein (dnaJ) [Mycoplasma genitalium G-37] pir A64202 heat shock protein dnaJ - Mycoplasma genitalium sp P47265 DNAJ_MYCGE Chaperone protein dnaJ | | | | |
| 4063, 4064 | 12044869 | 35 | 5.00E-30 | Mycoplasma genitalium G-37 | COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii] | | | | |
| 4065, 4066 | 48854182 | 33 | 2.00E-40 | Cytophaga hutchinsonii | COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii] | | | | 3.2.1.52 |
| 4067, 4068 | 31194343 | 50 | 6.00E-48 | Anopheles gambiae | ENSANGP00000000181 [Anopheles gambiae] | | | | |

| | | | | | | | | | |
|---------------|----------|----|-----------|---|---|---|----|----------|----------|
| 4069, 4070 | 29349624 | 54 | 5.00E-45 | Bacteroides thetaiotaomicron VPI-5482 | ubiquinone/menaquinone biosynthesis methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79321.1 ubiquinone/menaquinone biosynthesis methyltransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A005 UBIE_BACTN Menaquinone biosynthesis methyltransferase ubIE | | | | 2.1.1.- |
| 407, 408 | 17549722 | 31 | 4.00E-17 | Ralstonia solanacearum GM11000 | PROBABLE MAJOR ANAEROBICALLY INDUCED OUTER MEMBRANE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GM11000] emb CAD18654.1 PROBABLE MAJOR ANAEROBICALLY INDUCED OUTER MEMBRANE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] | | | | 1.7.99.3 |
| 4073, 4074 | 53712342 | 63 | 1.00E-109 | Bacteroides fragilis YCH46 | valyl-tRNA synthetase [Bacteroides fragilis YCH46] db BAD47800.1 valyl- tRNA synthetase [Bacteroides fragilis YCH46] | | | | |
| 4075, 4076 | 21226558 | 33 | 2.00E-16 | Methanosarcina mazel Go1 | hydrolase [Methanosarcina mazel Go1] gb AAM30152.1 hydrolase [Methanosarcina mazel Go1] sp Q8PZN6 PGP_METMA Phosphoglycolate phosphatase (PGP) | Porphyromonas gingivalis W83 section 5 of 8 of the complete genome | 92 | 7.00E-10 | 6.1.1.9 |
| 4077, 4078 | 15679388 | 34 | 2.00E-42 | Methanothermobac ter thermautotrophicus str. Delta H | nifS protein [Methanothermobacter thermotrophicus str. Delta H] gb AAB85866.1 nifS protein [Methanothermobacter thermotrophicus str. Delta H] pir G69051 nifS protein - Methanobacterium thermoautotrophicum (strain Delta H) sp O27442 CSD_METTH Probable cysteine desulfurase | | | | 4.4.1.- |
| 4079, 4080 | ABP3961 | 23 | 2.00E-09 | | Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4464. Org:Staphylococcus epidermidis | | | | |
| 4081, 4082 | 135244 | 44 | 2.00E-53 | | Type II restriction enzyme PstI (Endonuclease PstI) (R.PstI) pir NDOFS type II site-specific deoxyribonuclease (EC 3.1.21.4) PstI - Providencia stuartii gb AAA25673.1 PstI restriction endonuclease (PstI) | | | | |
| 4087, 4088 | 53757742 | 35 | 8.00E-21 | Methylococcus capsulatus str. Bath | TonB-dependent receptor, putative [Methylococcus capsulatus str. Bath] ref YP_114390.1 TonB-dependent receptor, putative [Methylococcus capsulatus str. Bath] | | | | |
| 409, 410 | 53712708 | 44 | 6.00E-24 | Bacteroides fragilis YCH46 | hypothetical protein BF1415 [Bacteroides fragilis YCH46] db BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---------------------------------------|--|--|----------|--|----------|
| 4091, 4092 | 23501247 | 38 | 1.00E-21 | Brucella suis 1330 | DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M) | | | | |
| 4093, 4094 | 23501247 | 39 | 6.00E-19 | Brucella suis 1330 | DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M) | | | | |
| 4097, 4098 | 48860541 | 25 | 3.00E-11 | Clostridium thermocellum ATCC 27405 | COG0417: DNA polymerase elongation subunit (family B) [Clostridium thermocellum ATCC 27405] | | | | |
| 41, 42 | 48855377 | 69 | 9.00E-52 | Cytophaga hutchinsonii | COG0413: Ketopantoate hydroxymethyltransferase [Cytophaga hutchinsonii] | | | | 2.1.2.11 |
| 4103, 4104 | 56965163 | 36 | 6.00E-23 | Bacillus clausii KSM-K16 | hypothetical protein ABC3401 [Bacillus clausii KSM-K16] dbj BAD65934.1 conserved hypothetical protein [Bacillus clausii KSM-K16] | | | | |
| 4107, 4108 | 52548310 | 56 | 3.00E-54 | uncultured archaeon GZfos11A10 | conserved hypothetical protein [uncultured archaeon GZfos11A10] | Methanosarcina acetivorans str. C2A, section 412 of 534 of the complete genome | 88 ##### | | |
| 4109, 4110 | 34397897 | 36 | 6.00E-23 | Porphyromonas gingivalis W83 | CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] ref NP_906059.1 CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] | | | | |
| 411, 412 | 29349046 | 37 | 4.00E-33 | Bacteroides thetaiotaomicron VPI-5482 | Na ⁺ /H ⁺ antiporter [Bacteroides thetaiotaomicron VPI-5482] gb AAO78743.1 Na ⁺ /H ⁺ antiporter [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 4111, 4112 | 34397897 | 42 | 2.00E-43 | Porphyromonas gingivalis W83 | CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] ref NP_906059.1 CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] | | | | |
| 4119, 4120 | 42761500 | 44 | 4.00E-28 | Dictyostelium discoideum | hypothetical protein [Dictyostelium discoideum] | | | | 2.3.1.- |
| 4121, 4122 | 48858151 | 29 | 3.00E-23 | Clostridium thermocellum ATCC 27405 | COG0769: UDP-N-acetylmuramyl tripeptide synthase [Clostridium thermocellum ATCC 27405] | | | | 6.3.2.13 |

| | | | | | | | | | |
|---------------|--------------|----|----------|--|--|---|----|----------|---------|
| 4123, 4124 | 48831856 | 38 | 7.00E-45 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | | 2.7.3.- |
| 4125, 4126 | 48859986 | 31 | 2.00E-23 | Clostridium thermocellum ATCC 27405 | hypothetical protein Cht02000708 [Clostridium thermocellum ATCC 27405] | | | | |
| 4127, 4128 | 48862089 | 48 | 1.00E-84 | Microbulifer degradans 2-40 | hypothetical protein Mdeg02002723 [Microbulifer degradans 2-40] | | | | |
| 4129, 4130 | 48853816 | 36 | 3.00E-29 | Cytophaga hutchinsonii | COG2928: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 413, 414 | 34396551 | 45 | 7.00E-44 | Porphyrromonas gingivialis W83 | ATP-dependent DNA helicase RecQ [Porphyrromonas gingivialis W83] ref NP_904718.1 ATP-dependent DNA helicase RecQ [Porphyrromonas gingivialis W83] | | | | 3.6.1.- |
| 4133, 4134 | AAU0488 0 | 68 | 4.00E-90 | | Desc: Micromonospora evernimycin biosynthetic enzyme evbX. Org: Micromonospora carbonacea var africana | Leifsonia xyli subsp. xyli str. CTC807, complete genome | 86 | 2.00E-08 | 1.2.1.3 |
| 4135, 4136 | 16329496 | 53 | 2.00E-53 | Synechocystis sp. PCC 6803 | hypothetical protein sir1610 [Synechocystis sp. PCC 6803] dbj BAA16904.1 sir1610 [Synechocystis sp. PCC 6803] pir S74753 hypothetical protein sir1610 - Synechocystis sp. (strain PCC 6803) | | | | 2.1.1.- |
| 4137, 4138 | 56421809 | 34 | 2.00E-11 | Geobacillus kaustophilus HTA426 | sugar ABC transporter (sugar-binding protein) [Geobacillus kaustophilus HTA426] dbj BAD77559.1 sugar ABC transporter (sugar-binding protein) [Geobacillus kaustophilus HTA426] | | | | |
| 4139, 4140 | 46580428 | 38 | 3.00E-16 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | hypothetical protein DVU2021 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96496.1 hypothetical protein DVU2021 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | |
| 4141, 4142 | 46580428 | 38 | 4.00E-16 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | hypothetical protein DVU2021 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96496.1 hypothetical protein DVU2021 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | | |
| 4145, 4146 | 53715217 | 29 | 1.00E-28 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50675.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] | | | | |
| 4149, 4150 | 23619313 | 23 | 8.00E-07 | Plasmodium falciparum 3D7 | hypothetical protein [Plasmodium falciparum 3D7] emb CAD52512.1 hypothetical protein [Plasmodium falciparum 3D7] | | | | |
| 415, 416 | 32476012 | 45 | 5.00E-55 | Rhodopirella baltica SH 1 | hypothetical protein RB3659 [Rhodopirella baltica SH 1] emb CAD76391.1 conserved hypothetical protein [Pirella sp.] | | | | |
| 4153, 4154 | 46105872 | 37 | 5.00E-29 | Rubrobacter xylanophilus DSM 9941 | COG0761: Penicillin tolerance protein [Rubrobacter xylanophilus DSM 9941] | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|----------|
| 4157, 4158 | 48855845 | 61 | 1.00E-38 | Cytophaga hutchinsonii | COG0477: Permeases of the major facilitator superfamily [Cytophaga hutchinsonii] | | | |
| 4165, 4166 | 23098317 | 30 | 1.00E-10 | Oceanobacillus ihayensis HTE831 | L-lysine dehydrogenase [Oceanobacillus ihayensis HTE831] dbj BAC12818.1 L-lysine dehydrogenase [Oceanobacillus ihayensis HTE831] | | | |
| 4167, 4168 | 48854163 | 32 | 2.00E-10 | Cytophaga hutchinsonii | COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii] | | | |
| 4169, 4170 | 23126274 | 28 | 7.00E-16 | Nostoc punctiforme PCC 73102 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] | | | 2.7.3.- |
| 4171, 4172 | 49236839 | 55 | 1.00E-67 | Moorella thermoacetica ATCC 39073 | COG1219: ATP-dependent protease Clp, ATPase subunit [Moorella thermoacetica ATCC 39073] | | | |
| 4173, 4174 | 48854863 | 53 | 3.00E-85 | Cytophaga hutchinsonii | COG0358: DNA primase (bacterial type) [Cytophaga hutchinsonii] | | | 2.7.7.- |
| 4175, 4176 | 21244775 | 41 | 1.00E-63 | Xanthomonas axonopodis pv. citri str. 306 | beta-xylosidase [Xanthomonas axonopodis pv. citri str. 306] gb AAM38893.1 beta-xylosidase [Xanthomonas axonopodis pv. citri str. 306] | | | 3.2.1.37 |
| 4183, 4184 | | | | | | | | |
| 4187, 4188 | 48831484 | 40 | 9.00E-69 | Magnetococcus sp. MC-1 | COG0550: Topoisomerase IA [Magnetococcus sp. MC-1] | | | 5.99.1.2 |
| 4189, 4190 | 56418811 | 51 | 7.00E-66 | NAD+ | DNA ligase (polydeoxyribonucleotide synthase[NAD+]) [Geobacillus kaustophilus HTA426] dbj BAD74561.1 DNA ligase (polydeoxyribonucleotide synthase[NAD+]) [Geobacillus kaustophilus HTA426] | | | |
| 419, 420 | 48855612 | 40 | 9.00E-25 | Cytophaga hutchinsonii | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] | | | 6.5.1.2 |
| 4195, 4196 | 23126888 | 61 | 2.00E-42 | Nostoc punctiforme PCC 73102 | COG0784: FOG: CheY-like receiver [Nostoc punctiforme PCC 73102] | | | 2.7.3.- |
| 4197, 4198 | 48854003 | 32 | 5.00E-22 | Cytophaga hutchinsonii | hypothetical protein Chut02003091 [Cytophaga hutchinsonii] | | | |
| 4201, 4202 | 48853843 | 65 | 8.00E-62 | Cytophaga hutchinsonii | COG0451: Nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii] | | | 5.1.3.- |

| | | | | | | | | | |
|-------|----------|----|-----------|---|--|--|--|--|---------|
| 4203, | 29348773 | 42 | 1.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3364 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78470.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 4204 | | | | | | | | | |
| 4205, | 48855009 | 45 | 4.00E-35 | Cytophaga hutchinsonii | COG1801: Uncharacterized conserved protein [Cytophaga hutchinsonii] transcriptional regulator, Crp family [Porphyromonas gingivalis W83] ref NP_905705.1 transcriptional regulator, Crp family [Porphyromonas gingivalis W83] | | | | |
| 421, | | | | | | | | | |
| 422 | 34397542 | 40 | 1.00E-31 | Porphyromonas gingivalis W83 | hypothetical protein TDE2139 [Treponema denticola ATCC 35405] gb AAS12659.1 hypothetical protein TDE2139 [Treponema denticola ATCC 35405] | | | | |
| 4211, | | | | | | | | | |
| 4212 | 42527642 | 28 | 4.00E-10 | Treponema denticola ATCC 35405 | Adenosylhomocysteinase [Gluconobacter oxydans 621H] hypothetical protein Mdeg02002723 [Microbulbifer degradans 2-40] probable cytochrome C-type biogenesis protein [Clostridium perfringens str. 13] dbj BAB80447.1 probable cytochrome C-type biogenesis protein [Clostridium perfringens str. 13] | | | | |
| 4213, | | | | | | | | | |
| 4214 | 58001953 | 79 | 1.00E-129 | Gluconobacter oxydans 621H | glyoxylase family protein [Bacillus anthracis str. Sterne] gb AAT55291.1 glyoxylase family protein [Bacillus anthracis str. Sterne] | | | | |
| 4219, | | | | | | | | | |
| 4220 | 48862089 | 46 | 6.00E-79 | Microbulbifer degradans 2-40 | hypothetical protein GKP41 [Geobacillus kaustophilus HTA426] dbj BAD74284.1 hypothetical protein [Geobacillus kaustophilus HTA426] COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] | | | | 6.2.1.3 |
| 4221, | | | | | | | | | |
| 4222 | 18309723 | 36 | 3.00E-18 | Clostridium perfringens str. 13 | hypothetical protein Chut02002781 [Cytophaga hutchinsonii] hypothetical protein BT3364 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78470.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 4223, | | | | | | | | | |
| 4224 | 49185988 | 35 | 2.00E-10 | Bacillus anthracis str. Sterne | Desc: Putative P. abyssal dihydroorotase #1. Org: Pyrococcus abyssal | | | | 3.5.4.2 |
| 4225, | | | | | | | | | |
| 4226 | 56410478 | 45 | 3.00E-27 | Geobacillus kaustophilus HTA426 | COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii] unknown [Rattus norvegicus] ref NP_942073.1 chromosome 11 open reading frame 8 [Rattus norvegicus] | | | | |
| 4227, | | | | | | | | | |
| 4228 | 48854120 | 51 | 2.00E-70 | Cytophaga hutchinsonii | | | | | |
| 4229, | | | | | | | | | |
| 4230 | 48854579 | 38 | 2.00E-12 | Cytophaga hutchinsonii | | | | | |
| 4231, | | | | | | | | | |
| 4232 | 29348773 | 42 | 1.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | | | | | |
| 4233, | AAB9607 | | | | | | | | |
| 4234 | 3 | 49 | 5.00E-19 | | | | | | |
| 4245, | | | | | | | | | |
| 4246 | 48856245 | 25 | 2.00E-07 | Cytophaga hutchinsonii | | | | | |
| 4249, | | | | | | | | | |
| 4250 | 25989494 | 36 | 9.00E-11 | Rattus norvegicus | | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|-------------------------------------|--|--|--|----------|
| 425, 426 | 13508372 | 45 | 3.00E-21 | Mycoplasma pneumoniae M129 | hypothetical protein MPN633 [Mycoplasma pneumoniae M129] conserved hypothetical protein, see: MPN635 [Mycoplasma pneumoniae M129] pir S73535 hypothetical protein C12_orf247 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75164 YG33_MYCPN Hypothetical protein MPN633 (C12_orf247) | | | |
| 4251, 4252 | 42557703 | 63 | 3.00E-77 | uncultured crenarchaeote | hypothetical protein [uncultured crenarchaeote] | | | |
| 4253, 4254 | 48856081 | 50 | 4.00E-76 | Cytophaga hutchinsonii | COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii] | | | 2.7.7.- |
| 4255, 4256 | 48856514 | 38 | 4.00E-31 | Cytophaga hutchinsonii | COG2148: Sugar transferases involved in lipopolysaccharide synthesis [Cytophaga hutchinsonii] | | | 2.-.-.- |
| 4261, 4262 | 17940055 | 33 | 3.00E-16 | Leptospira interrogans | unknown [Leptospira interrogans] | | | 2.4.-.- |
| 4263, 4264 | 18310494 | 31 | 9.00E-24 | Clostridium perfringens str. 13 | two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] dbj BAB81218.1 two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] | | | |
| 4265, 4266 | 48856475 | 45 | 3.00E-34 | Cytophaga hutchinsonii | COG2602: Beta-lactamase class D [Cytophaga hutchinsonii] | | | 3.5.2.6 |
| 4267, 4268 | 16554506 | 31 | 3.00E-15 | Halobacterium salinarum NRC-1 | Predicted kinase [Halobacterium salinarum NRC-1] | | | 2.7.1.12 |
| 4269, 4270 | 57234724 | 40 | 1.00E-14 | Dehalococcoides ethenogenes 195 | hypothetical protein DE10514 [Dehalococcoides ethenogenes 195] gb AAW40229.1 conserved hypothetical protein [Dehalococcoides ethenogenes 195] | | | 2.7.1.12 |
| 427, 428 | 48855641 | 38 | 8.00E-23 | Cytophaga hutchinsonii | COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] | | | |
| 4271, 4272 | 53712767 | 78 | 2.00E-59 | Bacteroides fragilis YCH46 | dioxygenase [Bacteroides fragilis YCH46] dbj BAD48225.1 dioxygenase [Bacteroides fragilis YCH46] | | | 1.3.1.9 |
| 4281, 4282 | 48853419 | 59 | 2.00E-37 | Cytophaga hutchinsonii | COG0251: Putative translation initiation inhibitor, yigF family [Cytophaga hutchinsonii] | | | |
| 4283, 4284 | 48858374 | 33 | 3.00E-08 | Clostridium thermocellum ATCC 27405 | COG2908: Uncharacterized protein conserved in bacteria [Clostridium thermocellum ATCC 27405] | | | |
| 4287, 4288 | 23126588 | 29 | 4.00E-26 | Nostoc punctiforme PCC 73102 | COG0438: Glycosyltransferase [Nostoc punctiforme PCC 73102] | | | |
| 4289, 4290 | 48783455 | 41 | 8.00E-24 | Burkholderia fungorum LB400 | COG5483: Uncharacterized conserved protein [Burkholderia fungorum LB400] | | | |
| 429, 430 | 53713709 | 39 | 1.00E-25 | Bacteroides fragilis YCH46 | conserved hypothetical protein BatB [Bacteroides fragilis YCH46] gb AAD30859.1 BatB [Bacteroides fragilis] dbj BAD49167.1 conserved hypothetical protein BatB [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | |
|--------|----------|----|----------|---|---|--|--|----------|
| 4293, | 48854274 | 40 | 6.00E-47 | Cytophaga hutchinsonii | COG3239: Fatty acid desaturase [Cytophaga hutchinsonii] | | | 1.14.99. |
| 4294 | | | | Geobacter metallireducens GS-15 | | | | 25 |
| 4297, | | | | | | | | |
| 4298 | 48847270 | 46 | 3.00E-33 | Vibrio vulnificus | COG0796: Glutamate racemase [Geobacter metallireducens GS-15] | | | 5.1.1.3 |
| 4299, | | | | | Glycosyltransferase [Vibrio vulnificus CMCP6] | | | |
| 4300 | 27364227 | 34 | 4.00E-16 | CMCP6 | Glycosyltransferase [Vibrio vulnificus CMCP6] | | | 2.4.1.- |
| | | | | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT3641 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 43, 44 | 29349049 | 30 | 3.00E-18 | VPI-5482 | conserved hypothetical protein, possible glycosyl transferase [Bacillus thuringiensis serovar konkukian str. 97-27] | | | |
| 4301, | | | | Bacillus thuringiensis serovar konkukian str. 97-27 | hypothetical protein, possible glycosyl transferase [Bacillus thuringiensis serovar konkukian str. 97-27] | | | |
| 4302 | 49478938 | 25 | 2.00E-07 | str. 97-27 | | | | |
| | | | | | | | | |
| 4303, | | | | Aquifex aeolicus VF5 | dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] | | | |
| 4304 | 15606924 | 45 | 1.00E-66 | VF5 | gb AAC07699.1 dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] pir G70463 dolichol-phosphate mannosyltransferase - Aquifex aeolicus | | | 2.4.1.83 |
| | | | | | | | | |
| 4305, | | | | Aquifex aeolicus VF5 | dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] | | | |
| 4306 | 15606924 | 40 | 7.00E-27 | VF5 | gb AAC07699.1 dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] pir G70463 dolichol-phosphate mannosyltransferase - Aquifex aeolicus | | | 2.4.1.83 |
| 4307, | | | | Cytophaga hutchinsonii | COG3278: Response regulator of the LysR/AIGR family [Cytophaga hutchinsonii] | | | |
| 4308 | 48854415 | 33 | 1.00E-10 | hutchinsonii | | | | |
| 4309, | | | | Clostridium perfringens str. 13 | hypothetical protein CPE1285 [Clostridium perfringens str. 13] | | | |
| 4310 | 18310267 | 26 | 2.00E-16 | perfringens str. 13 | dbj BAB80991.1 hypothetical protein [Clostridium perfringens str. 13] | | | |
| | | | | Bacteroides fragilis YCH46 | ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] | | | |
| 4311, | | | | | dbj BAD47773.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] | | | |
| 4312 | 53712315 | 35 | 8.00E-15 | YCH46 | | | | |
| | | | | Aspergillus nidulans FGSC A4 | hypothetical protein AN6925.2 [Aspergillus nidulans FGSC A4] | | | |
| 4313, | | | | | ref XP_411062.1 hypothetical protein AN6925.2 [Aspergillus nidulans FGSC A4] | | | |
| 4314 | 40738490 | 39 | 6.00E-12 | nidulans FGSC A4 | | | | |
| | | | | Geobacter metallireducens GS-15 | COG0500: SAM-dependent methyltransferases [Geobacter metallireducens GS-15] | | | |
| 4315, | | | | | | | | |
| 4316 | 48844445 | 24 | 6.00E-11 | 15 | | | | |
| 4323, | | | | Cytophaga hutchinsonii | COG1092: Predicted SAM-dependent methyltransferases [Cytophaga hutchinsonii] | | | 2.1.1.- |
| 4324 | 48856165 | 53 | 2.00E-70 | hutchinsonii | | | | |
| 4325, | | | | Cytophaga hutchinsonii | hypothetical protein Chut02001987 [Cytophaga hutchinsonii] | | | |
| 4326 | 48854930 | 51 | 1.00E-60 | hutchinsonii | | | | |
| 4327, | | | | | | | | |
| 4328 | 2244692 | 35 | 1.00E-31 | Vibrio cholerae | ORF71x8 [Vibrio cholerae] | | | 6.3.5.4 |

| | | | | | | | | | |
|---------------|----------|----|-----------|---|---|--|----|----------|----------|
| 433, 434 | 48832592 | 46 | 8.00E-32 | Magnetococcus sp. MC-1 | COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Magnetococcus sp. MC-1] | | | | |
| 4333, 4334 | 29349972 | 64 | 2.00E-95 | Bacteroides thetaiotaomicron VPI-5482 | putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | Bacteroides thetaiotaomicron VPI-5482, section 20 of 21 of the complete genome | 85 | 2.00E-07 | 2.4.1.83 |
| 4337, 4338 | 5578853 | 30 | 4.00E-07 | Streptomyces coelicolor A3(2) | putative secreted protease [Streptomyces coelicolor A3(2)] pir T35287 probable secreted proteinase - Streptomyces coelicolor ref NP_626424.1 putative secreted protease [Streptomyces coelicolor A3(2)] | | | | 3.4.21.- |
| 4339, 4340 | 53714925 | 59 | 3.00E-49 | Bacteroides fragilis YCH46 | tRNA nucleotidyltransferase [Bacteroides fragilis YCH46] dbj BAD50383.1 tRNA nucleotidyltransferase [Bacteroides fragilis YCH46] | | | | 2.7.7.19 |
| 4341, 4342 | 53712197 | 33 | 1.00E-13 | Bacteroides fragilis YCH46 | hypothetical protein BF0904 [Bacteroides fragilis YCH46] dbj BAD47655.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 4343, 4344 | 34396924 | 27 | 1.00E-16 | Porphyromonas gingivalis W83 | Integrase [Porphyromonas gingivalis W83] ref NP_905090.1 Integrase | | | | |
| 4347, 4348 | 48854856 | 53 | 4.00E-91 | Cytophaga hutchinsonii | COG0519: GMP synthase, PP-ATPase domain/subunit [Cytophaga hutchinsonii] | | | | 6.3.5.2 |
| 4349, 4350 | 57158267 | 27 | 4.00E-15 | Thermococcus kodakaraensis | predicted DNA methylase [Thermococcus kodakaraensis] ref YP_182421.1 predicted DNA methylase [Thermococcus kodakaraensis] | | | | |
| 435, 436 | 48853532 | 45 | 4.00E-39 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | | |
| 4351, 4352 | 20091500 | 89 | 1.00E-142 | Methanosarcina acetivorans C2A | transposase [Methanosarcina acetivorans C2A] gb AAM06055.1 transposase [Methanosarcina acetivorans str. C2A] | Methanosarcina acetivorans str. C2A, section 309 of 534 of the complete genome | 89 | 0 | |
| 4355, 4356 | 46317628 | 28 | 2.00E-12 | Burkholderia cepacia R18194 | COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Burkholderia cepacia R18194] | | | | |
| 4357, 4358 | 53713993 | 27 | 4.00E-20 | Bacteroides fragilis YCH46 | transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD49451.1 transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 4359, 4360 | 29346614 | 27 | 2.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | conserved hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76311.1 conserved hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|----|----------|----------|
| 4363, 4364 | 59964719 | 72 | 1.00E-55 | Bacillus clausii KSM-K16 | thymidylate synthase [Bacillus clausii KSM-K16] dbj BAD5489.1 thymidylate synthase [Bacillus clausii KSM-K16] | Coxiella burnetii strain RSA 493, section 5 of 7 of the complete genome | 81 | 1.00E-06 | 2.1.1.45 |
| 4373, 4374 | 53763896 | 31 | 3.00E-25 | Anabaena variabilis ATCC 29413 | COG0860: N-acetylmuramoyl-L-alanine amidase [Anabaena variabilis ATCC 29413] | | | | 3.5.1.28 |
| 4375, 4376 | 48845074 | 28 | 7.00E-24 | Geobacter metallireducens GS-15 | COG0417: DNA polymerase elongation subunit (family B) [Geobacter metallireducens GS-15] | | | | 2.7.7.7 |
| 4377, 4378 | 29349976 | 27 | 4.00E-21 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT4568 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79673.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 4381, 4382 | 21227241 | 30 | 4.00E-11 | Methanosarcina mazei Go1 | Dolichyl-phosphate mannose synthase related protein [Methanosarcina mazei Go1] gb AAM30835.1 Dolichyl-phosphate mannose synthase related protein [Methanosarcina mazei Go1] | | | | 2.--- |
| 4383, 4384 | 48839273 | 62 | 1.00E-54 | Methanosarcina barkeri str. fusaro | COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro] | Methanosarcina acetivorans str. C2A, section 242 of 534 of the complete genome | 95 | 1.00E-54 | 3.1.21.3 |
| 4385, 4386 | 48838982 | 67 | 2.00E-67 | Methanosarcina barkeri str. fusaro | COG2043: Uncharacterized protein conserved in archaea [Methanosarcina barkeri str. fusaro] | | | | |
| 4389, 4390 | 17549722 | 31 | 4.00E-17 | Ralstonia solanacearum GMI1000 | PROBABLE MAJOR ANAEROBICALLY INDUCED OUTER MEMBRANE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GMI1000] emb CAD18654.1 PROBABLE MAJOR ANAEROBICALLY INDUCED OUTER MEMBRANE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] | | | | 1.7.99.3 |
| 439, 440 | 48856925 | 32 | 7.00E-23 | Cytophaga hutchinsonii | COG1309: Transcriptional regulator [Cytophaga hutchinsonii] | | | | |
| 4391, 4392 | 48855725 | 24 | 3.00E-11 | Cytophaga hutchinsonii | hypothetical protein Chut02000929 [Cytophaga hutchinsonii] | | | | |
| 4393, 4394 | 48855974 | 30 | 3.00E-19 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | | |
| 4395, 4396 | 46134478 | 35 | 3.00E-37 | Anabaena variabilis ATCC 29413 | COG0642: Signal transduction histidine kinase [Anabaena variabilis ATCC 29413] | | | | 2.7.3.- |
| 4397, 4398 | 6691605 | 70 | 1.00E-89 | Flavobacterium psychrophilum | gyrase B [Flavobacterium psychrophilum] | | | | 5.99.1.- |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|----------|
| 4399, 4400 | 53715112 | 32 | 2.00E-40 | Bacteroides fragilis YCH46 | 4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4-alpha-glucanotransferase [Bacteroides fragilis YCH46] | | | 2.4.1.25 |
| 4401, | 48853434 | 68 | 1.00E-50 | Cytophaga hutchinsonii | COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] | | | 2.7.7.24 |
| 4402 | 48853434 | 68 | 1.00E-50 | Cytophaga hutchinsonii | putative helicase [Staphylococcus phage K] gb AAO47520.1 ORF71 | | | |
| 4403, | 48696459 | 27 | 4.00E-12 | Staphylococcus phage K | [Staphylococcus phage K] | | | |
| 4404, | 48853532 | 26 | 3.00E-18 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 4405, | 48853532 | 26 | 3.00E-18 | Cytophaga hutchinsonii | COG2226: Methylase Involved in ubiquinone/menaquinone biosynthesis | | | |
| 4406 | 48854545 | 52 | 2.00E-59 | Cytophaga hutchinsonii | [Cytophaga hutchinsonii] | | | 2.1.1.- |
| 4407, | 48854545 | 52 | 2.00E-59 | Cytophaga hutchinsonii | hypothetical protein BT0164 [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 4408 | 48854545 | 52 | 2.00E-59 | Cytophaga hutchinsonii | gb AAO75271.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 441, | 29345574 | 38 | 1.00E-31 | Bacteroides thetaitaomicron VPI-5482 | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 442 | 48855616 | 28 | 2.00E-24 | Cytophaga hutchinsonii | hypothetical protein CPE2540 [Clostridium perfringens str. 13] | | | |
| 4413, | 48855616 | 28 | 2.00E-24 | Cytophaga hutchinsonii | dbj BAB82246.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | 3.1.2.6 |
| 4415, | 18311522 | 31 | 1.00E-10 | Clostridium perfringens str. 13 | COG1357: Uncharacterized low-complexity proteins [Cytophaga hutchinsonii] | | | |
| 4416 | 18311522 | 31 | 1.00E-10 | Clostridium perfringens str. 13 | putative two-component system sensor histidine kinase, putative heat shock protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79860.1 putative two-component system sensor histidine kinase, putative heat shock protein [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.3.- |
| 4419, | 48854397 | 48 | 6.00E-32 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 4420 | 48854397 | 48 | 6.00E-32 | Cytophaga hutchinsonii | ABC-type sugar/spermidine/putrescine/iron/thiamine transport systems, ATPase component [Thermoanaerobacter tengcongensis MB4] | | | |
| 4427, | 29350163 | 23 | 6.00E-13 | Bacteroides thetaitaomicron VPI-5482 | gb AAM25158.1 ABC-type sugar/spermidine/putrescine/iron/thiamine transport systems, ATPase component [Thermoanaerobacter tengcongensis MB4] | | | |
| 4428 | 29350163 | 23 | 6.00E-13 | Bacteroides thetaitaomicron VPI-5482 | COG0325: Predicted enzyme with a TIM-barrel fold [Cytophaga hutchinsonii] | | | |
| 4431, | 48854286 | 34 | 2.00E-23 | Cytophaga hutchinsonii | transaldolase [Methanocaldococcus jannaschii DSM 2661] gb AAB98982.1 transaldolase [Methanocaldococcus jannaschii DSM 2661] | | | |
| 4432 | 48854286 | 34 | 2.00E-23 | Cytophaga hutchinsonii | sp Q58370 TAL_METJA Probable transaldolase pir H64419 transaldolase (EC 2.2.1.2) - Methanococcus jannaschii | | | 2.2.1.2 |
| 4447, | 20803383 | 75 | 5.00E-99 | Thermoanaerobact er tengcongensis MB4 | | | | |
| 4448 | 20803383 | 75 | 5.00E-99 | Thermoanaerobact er tengcongensis MB4 | | | | |
| 4451, | 48854499 | 53 | 7.00E-48 | Cytophaga hutchinsonii | | | | |
| 4452 | 48854499 | 53 | 7.00E-48 | Cytophaga hutchinsonii | | | | |
| 4453, | 15669150 | 57 | 4.00E-63 | Methanocaldococc us jannaschii DSM 2661 | | | | |
| 4454 | 15669150 | 57 | 4.00E-63 | Methanocaldococc us jannaschii DSM 2661 | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|--|----------|
| 4457, 4458 | 29346936 | 66 | 8.00E-84 | Bacteroides thetaiotaomicron VPI-5482 | myo-inositol-1-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76633.1 myo-inositol-1-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482] | | | | 5.5.1.4 |
| 4459, 4460 | 29346936 | 65 | 9.00E-86 | Bacteroides thetaiotaomicron VPI-5482 | myo-inositol-1-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76633.1 myo-inositol-1-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482] | | | | 5.5.1.4 |
| 4463, 4464 | 48853540 | 35 | 6.00E-14 | Cytophaga hutchinsonii | COG0779: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 4465, 4466 | 48853541 | 43 | 8.00E-23 | Cytophaga hutchinsonii | COG0195: Transcription elongation factor [Cytophaga hutchinsonii] | | | | |
| 4467, 4468 | 50252056 | 33 | 3.00E-11 | Oryza sativa (japonica cultivar- group) | putative 4-coumarate coenzyme A ligase [Oryza sativa (japonica cultivar- group)] | | | | 6.2.1.12 |
| 4469, 4470 | 18920646 | 28 | 2.00E-15 | Microcystis aeruginosa | McyA [Microcystis aeruginosa] | | | | 6.2.1.1 |
| 447, 448 | 53711736 | 34 | 6.00E-13 | Bacteroides fragilis YCH46 | Na ⁺ /H ⁺ antiporter [Bacteroides fragilis YCH46] antiporter [Bacteroides fragilis YCH46] | | | | |
| 4471, 4472 | 15669064 | 42 | 4.00E-42 | Methanocaldococ- cus jannaschii DSM 2661 | ferric enterobactin transport ATP-binding protein [Methanocaldococcus jannaschii DSM 2661] gb AAB98878.1 ferric enterobactin transport ATP- binding protein [Methanocaldococcus jannaschii DSM 2661] spiQ58283 Y873_METJA Hypothetical ABC transporter ATP-binding protein MJ0873 | | | | 3.6.3.33 |
| 4473, 4474 | 15613299 | 41 | 5.00E-31 | Bacillus halodurans C-125 | hypothetical protein BH0736 [Bacillus halodurans C-125] db BAB04455.1 BH0736 [Bacillus halodurans C-125] pir H83741 hypothetical protein BH0736 [imported] - Bacillus halodurans (strain C-125) | | | | |
| 4475, 4476 | 48855819 | 32 | 6.00E-33 | Cytophaga hutchinsonii | COG3361: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 4477, 4478 | 39995136 | 27 | 2.00E-17 | Geobacter sulfurreducens PCA | tolB protein [Geobacter sulfurreducens PCA] gb AAR33360.1 tolB protein [Geobacter sulfurreducens PCA] | | | | |
| 4479, 4480 | 34396304 | 36 | 3.00E-07 | Porphyromonas gingivalis W83 | mannosyltransferase [Porphyromonas gingivalis W83] ref NP_904472.1 mannosyltransferase [Porphyromonas gingivalis W83] | | | | 2.4.1.- |
| 4481, 4482 | 21226752 | 39 | 1.00E-23 | Methanosarcina mazel Go1 | mannosyltransferase [Methanosarcina mazel Go1] gb AAM30346.1 mannosyltransferase [Methanosarcina mazel Goe1] | | | | 2.4.1.- |
| 4485, 4486 | 53714487 | 56 | 3.00E-44 | Bacteroides fragilis YCH46 | SsrA-binding protein [Bacteroides fragilis YCH46] db BAD49945.1 SsrA- binding protein [Bacteroides fragilis YCH46] | | | | |
| 4487, 4488 | 49236141 | 51 | 4.00E-48 | Moorella thermoacetica ATCC 39073 | COG0231: Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A) [Moorella thermoacetica ATCC 39073] | | | | |

| | | | | | | | | | |
|---------------|----------|----|-----------|------|---|--|--|----|----------|
| 4489, 4490 | 17231259 | 45 | 1.00E-18 | 7120 | Nostoc sp. PCC | two-component sensor histidine kinase [Nostoc sp. PCC 7120] pir AH2276 two-component sensor histidine kinase all3767 [Imported] - Nostoc sp. (strain PCC 7120) dbj BAB75466.1 two-component sensor histidine kinase [Nostoc sp. PCC 7120] | | | 2.7.3.- |
| 449, 450 | 20094204 | 43 | 3.00E-37 | | Methanopyrus kandleri AV19 | Undecaprenyl pyrophosphate synthase [Methanopyrus kandleri AV19] gb AA01981.1 Undecaprenyl pyrophosphate synthase [Methanopyrus kandleri AV19] sp Q8TXA7 UPPS_METKA Undecaprenyl pyrophosphate synthetase (UPP synthetase) (Di-trans,poly-cis-decaprenylcistransferase) (Undecaprenyl diphosphate synthase) (UDS) | | | 2.5.1.31 |
| 4491, 4492 | 48856903 | 39 | 3.00E-56 | | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | |
| 4493, 4494 | 48844178 | 34 | 4.00E-35 | 15 | Geobacter metallireducens GS | COG0260: Leucyl aminopeptidase [Geobacter metallireducens GS-15] | | | 2.3.1.43 |
| 4497, 4498 | 48854264 | 69 | 1.00E-120 | | Cytophaga hutchinsonii | COG0069: Glutamate synthase domain 2 [Cytophaga hutchinsonii] | Desc:Listeria monocytogenes EGD-e genome sequence. Org:Listeria monocytogenes | 87 | 4.00E-15 |
| 4499, 4500 | 48854264 | 62 | 1.00E-106 | | Cytophaga hutchinsonii | COG0069: Glutamate synthase domain 2 [Cytophaga hutchinsonii] | | | 1.4.1.13 |
| 4509, 4510 | 48854452 | 66 | 1.00E-109 | | Cytophaga hutchinsonii | COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii] | | | 2.4.2.14 |
| 451, 452 | 48832080 | 29 | 6.00E-21 | | Magnetococcus sp. MC-1 | COG1352: Methylase of chemotaxis methyl-accepting proteins [Magnetococcus sp. MC-1] | | | 2.1.1.80 |
| 4511, 4512 | 14520856 | 43 | 9.00E-26 | | Pyrrococcus abyssi GE5 | transcriptional regulatory protein, AsnC family [Pyrrococcus abyssi GE5] emb CAB49562.1 Transcriptional regulatory protein, Lrp-AsnC family [Pyrrococcus abyssi] sp Q9V0Y9 REG6_PYRAB Putative HTH-type transcriptional regulator PYRAB06490 pir A75106 transcription regulatory protein, asnC family PAB1938 - Pyrrococcus abyssi (strain Orsay) | | | |
| 4513, 4514 | 29346036 | 46 | 1.00E-71 | | Bacteroides thetaiotaomicron VPI-5482 | phenylalanyl-tRNA synthetase beta chain [Bacteroides thetaiotaomicron VPI- 5482] gb AA075733.1 phenylalanyl-tRNA synthetase beta chain [Bacteroides thetaiotaomicron VPI-5482] sp Q8AA39 SYFB_BACTN Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS) | | | 6.1.1.20 |
| 4515, 4516 | 53714672 | 35 | 1.00E-26 | | Bacteroides fragilis YCH46 | RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD50130.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|----------|
| 4517, 4518 | 48856262 | 56 | 1.00E-27 | Cytophaga hutchinsonii | COG1134: ABC-type polysaccharide/polyol phosphate transport system, ATPase component [Cytophaga hutchinsonii] | | | 1.8.- |
| 4523, 4524 | 48838433 | 39 | 2.00E-47 | Methanosarcina barkeri str. fusaro | COG1002: Type II restriction enzyme, methylase subunits [Methanosarcina barkeri str. fusaro] | | | 2.1.1.72 |
| 4527, 4528 | 6968646 | 42 | 3.00E-38 | Campylobacter jejuni subsp. jejuni NCTC 11168 | putative glycolate oxidase subunit D [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282360.1 putative glycolate oxidase subunit D [Campylobacter jejuni subsp. jejuni NCTC 11168] pir G81327 probable glycolate oxidase chain D Cj1213c [imported] - Campylobacter jejuni (strain NCTC 11168) | | | 1.1.3.15 |
| 4529, 4530 | 29349593 | 60 | 2.00E-20 | Bacteroides thetaiotaomicron VPI-5482 | xylosidase/arabinosidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79290.1 xylosidase/arabinosidase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 4531, 4532 | 48893181 | 29 | 4.00E-28 | Trichodesmium erythraeum IMS101 | COG1089: GDP-D-mannose dehydratase [Trichodesmium erythraeum IMS101] | | | 4.2.1.47 |
| 4533, 4534 | 23125015 | 50 | 4.00E-29 | Nostoc punctiforme PCC 73102 | COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | | | 2.7.3.- |
| 4535, 4536 | 48854194 | 46 | 1.00E-53 | Cytophaga hutchinsonii | COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii] | | | |
| 4537, 4538 | 48854195 | 32 | 2.00E-13 | Cytophaga hutchinsonii | COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii] | | | |
| 4539, 4540 | 23129857 | 50 | 1.00E-10 | Nostoc punctiforme PCC 73102 | COG3920: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | | | 2.7.3.- |
| 4541, 4542 | 57234806 | 27 | 1.00E-15 | Dehalococcoides ethenogenes 195 uncultured archaeon | conserved hypothetical protein TIGR00147 [Dehalococcoides ethenogenes 195] gb AAW40311.1 conserved hypothetical protein TIGR00147 [Dehalococcoides ethenogenes 195] | | | |
| 4543, 4544 | 52548759 | 50 | 2.00E-69 | GZfos18F2 | putative glycosyl transferase [uncultured archaeon GZfos18F2] cadmium resistance protein [Methanocaldococcus jannaschii DSM 2661] gb AAB99335.1 cadmium resistance protein [Methanocaldococcus jannaschii DSM 2661] sp Q58721 YD25_METJA Putative HTH-type transcriptional regulator MJ1325 pir D64465 hypothetical protein MJ1325 - Methanococcus jannaschii | | | 2.- |
| 4547, 4548 | 15669515 | 37 | 4.00E-09 | Methanocaldococcus jannaschii DSM 2661 | putative GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD50830.1 putative GTP-binding protein [Bacteroides fragilis YCH46] | | | |
| 455, 456 | 53715372 | 48 | 1.00E-32 | Bacteroides fragilis YCH46 | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|----------|
| 4551, 4552 | 42524924 | 63 | 1.00E-57 | Bdellovibrio bacteriovorus HD100 | hydroxymethylglutaryl-CoA lyase [Bdellovibrio bacteriovorus HD100] embjCAE80958.1 hydroxymethylglutaryl-CoA lyase [Bdellovibrio bacteriovorus HD100] | | | 4.1.3.4 |
| 4559, 4560 | 48848789 | 68 | 1.00E-29 | Novosphingobium aromaticivorans DSM 12444 | COG0553: Preprotein translocase subunit SecA (ATPase, RNA helicase) [Novosphingobium aromaticivorans DSM 12444] hypothetical protein air2112 [Nostoc sp. PCC 7120] dbj BAB73811.1 air2112 [Nostoc sp. PCC 7120] pir JAB2070 hypothetical protein air2112 [Imported] - Nostoc sp. (strain PCC 7120) gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [Imported] - Flavobacterium johnsoniae | | | |
| 4561, 4562 | 17229604 | 40 | 2.00E-19 | Nostoc sp. PCC 7120 | COG0496: Predicted acid phosphatase [Cytophaga hutchinsonii] | | | 3.1.3.2 |
| 4563, 4564 | 2281663 | 63 | 3.00E-68 | Flavobacterium johnsoniae | COG0193: Peptidyl-RNA hydrolase [Cytophaga hutchinsonii] putative dipeptidyl-peptidase III [Bacteroides thetaiotaomicron VPI-5482] gb AAO76953.1 putative dipeptidyl-peptidase III [Bacteroides thetaiotaomicron VPI-5482] | | | 3.1.1.29 |
| 4569, 4570 | 48854858 | 55 | 5.00E-29 | Cytophaga hutchinsonii | putative peptidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78570.1 putative peptidase [Bacteroides thetaiotaomicron VPI-5482] COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii] | | | |
| 4571, 4572 | 48854463 | 51 | 2.00E-48 | Cytophaga hutchinsonii | hypothetical protein Chut02003855 [Cytophaga hutchinsonii] COG2137: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 4573, 4574 | 29347256 | 56 | 1.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein nfa2750 [Nocardia farcinica IFM 10152] dbj BAD55117.1 hypothetical protein [Nocardia farcinica IFM 10152] COG0622: Predicted phosphoesterase [Cytophaga hutchinsonii] | | | |
| 4577, 4578 | 29348873 | 26 | 2.00E-13 | Bacteroides thetaiotaomicron VPI-5482 | COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] COG4564: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 4579, 4580 | 48853613 | 38 | 2.00E-24 | Cytophaga hutchinsonii | glycosyl transferase [Pyrococcus furiosus DSM 3638] gb AAL81485.1 glycosyl transferase [Pyrococcus furiosus DSM 3638] | | | 2.4.1.- |
| 4581, 4582 | 48853429 | 46 | 9.00E-16 | Cytophaga hutchinsonii | VV A18 helicase [Mimivirus] gb AAV50665.1 VV A18 helicase [Mimivirus] | | | 3.6.3.14 |
| 4583, 4584 | 48854316 | 37 | 9.00E-22 | Cytophaga hutchinsonii | | | | |
| 4585, 4586 | 54022239 | 25 | 8.00E-07 | Nocardia farcinica IFM 10152 | | | | |
| 4587, 4588 | 48854510 | 57 | 7.00E-46 | Cytophaga hutchinsonii | | | | |
| 4595, 4596 | 48892769 | 23 | 5.00E-07 | Trichodesmium erythraeum IMS101 | | | | |
| 4597, 4598 | 48853443 | 26 | 3.00E-11 | Cytophaga hutchinsonii | | | | |
| 4599, 4600 | 18977733 | 31 | 1.00E-08 | Pyrococcus furiosus DSM 3638 | | | | |
| 4603, 4604 | 55819271 | 37 | 3.00E-16 | Mimivirus | | | | |

| | | | | | | | | |
|---------------|--------------|----|-----------|---|---|--|--|---------------|
| 4605, 4606 | 31195963 | 49 | 1.00E-59 | Anopheles gambiae | ENSANGP00000000454 [Anopheles gambiae] SSU ribosomal protein S13AB (rps13AB) [Sulfolobus solfataricus P2] gb AAK40436.1 SSU ribosomal protein S13AB (rps13AB) [Sulfolobus solfataricus P2] emb CAA69528.1 ribosomal protein S18 [Sulfolobus solfataricus] pir S75414 probable ribosomal protein S18 - Sulfolobus solfataricus sp P95986 RS13_SULSO 30S ribosomal protein S13P | | | 4.2.1.22 |
| 4609, 4610 | 15897041 | 50 | 3.00E-35 | Sulfolobus solfataricus P2 | Desc:N. gonorrhoeae amino acid sequence SEQ ID 4556. Org:Neisseria gonorrhoeae | | | 3.1.21.3 |
| 4611, 4612 | ABP7901 3 | 57 | 2.00E-51 | | UDP-N-acetylenolpyruvoylglucosamine reductase [EC:1.1.1.158] [Rickettsia conorii str. Malish 7] gb AAL02870.1 UDP-N-acetylenolpyruvoylglucosamine reductase [EC:1.1.1.158] [Rickettsia conorii str. Malish 7] pir D97741 hypothetical protein murB [imported] - Rickettsia conorii (strain Malish 7) COG0286: Type I restriction-modification system methyltransferase subunit [Haemophilus somnus 2336] | | | 1.1.1.15 8 |
| 4613, 4614 | 15892255 | 32 | 1.00E-16 | EC:1.1.1.158 | [Haemophilus somnus 2336] type I restriction-modification system S subunit [Geobacillus kaustophilus HTA426] dbj BAD74629.1 type I restriction-modification system S subunit [Geobacillus kaustophilus HTA426] | | | 3.1.21.3 |
| 4615, 4616 | 46156664 | 32 | 2.00E-20 | Haemophilus sommus 2336 | GTP pyrophosphokinase [Geobacter sulfurreducens PCA] gb AAR35612.1 GTP pyrophosphokinase [Geobacter sulfurreducens PCA] hypothetical protein Chut02003580 [Cytophaga hutchinsonii] | | | 2.7.6.5 |
| 4617, 4618 | 56418879 | 35 | 3.00E-22 | Geobacter sulfurreducens PCA | putative exopolysaccharide production protein [Bradyrhizobium japonicum USDA 110] dbj BAC51575.1 bl6310 [Bradyrhizobium japonicum USDA 110] COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] COG1463: ABC-type transport system involved in resistance to organic solvents, periplasmic component [Cytophaga hutchinsonii] | | | 2.--- |
| 4619, 4620 | 39997334 | 63 | 1.00E-102 | Cytophaga hutchinsonii | hypothetical protein LA1652 [Leptospira interrogans serovar Lai str. 56601] gb AAN48851.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] | | | |
| 4623, 4624 | 48853721 | 33 | 2.00E-13 | Bradyrhizobium japonicum USDA 110 | hypothetical protein UM04845.1 [Ustilago maydis 521] ref XP_402460.1 hypothetical protein UM04845.1 [Ustilago maydis 521] | | | 2.3.1.51 |
| 4629, 4630 | 27381421 | 49 | 3.00E-42 | Cytophaga hutchinsonii | | | | |
| 463, 464 | 48855210 | 44 | 4.00E-30 | Cytophaga hutchinsonii | | | | |
| 4631, 4632 | 48853578 | 31 | 5.00E-14 | Cytophaga hutchinsonii | | | | |
| 4633, 4634 | 24214352 | 45 | 2.00E-36 | Leptospira interrogans serovar Lai str. 56601 | | | | |
| 4635, 4636 | 46100876 | 30 | 2.00E-13 | Ustilago maydis | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|----|------------------|
| 4637, 4638 | 15628781 | 29 | 4.00E-13 | Mycoplasma pulmonis UAB CTIP | FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE) [Mycoplasma pulmonis UAB CTIP] emb[CAC13483.1] FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE) [Mycoplasma pulmonis] sp[Q98QQ1]FPG_MYCPU Formamidopyrimidine-DNA glycosylase (FAPY-DNA glycosylase) (DNA- apurinic or apyrimidinic site) lyase mutM (AP lyase mutM) pir[IF90550 hypothetical protein MYPU_3100 [Imported] - Mycoplasma pulmonis (strain UAB CTIP) | | | 3.2.2.23 |
| 4639, 4640 | 29348887 | 37 | 7.00E-33 | Bacteroides thetaiotaomicron VPI-5482 | Integrase [Bacteroides thetaiotaomicron VPI-5482] gb[AAO78584.1] Integrase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 4643, 4644 | 48856526 | 75 | 3.00E-98 | Cytophaga hutchinsonii | COG1899: Deoxyhypusine synthase [Cytophaga hutchinsonii] | | | 2.5.1.46 |
| 4645, 4646 | 48854545 | 56 | 7.00E-46 | Cytophaga hutchinsonii | COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii] | | | 2.1.1.- |
| 4647, 4648 | 53765097 | 29 | 9.00E-22 | Anabaena variabilis ATCC 29413 | COG0438: Glycosyltransferase [Anabaena variabilis ATCC 29413] | | | |
| 465, 466 | 48848776 | 82 | 2.00E-58 | Novosphingobium aromaticivorans DSM 12444 | COG0499: S-adenosylhomocysteine hydrolase [Novosphingobium aromaticivorans DSM 12444] | Mesorhizobium loti MAFF303099 DNA, complete genome | 81 | 8.00E-45 3.3.1.1 |
| 4651, 4652 | 48856685 | 30 | 6.00E-12 | Cytophaga hutchinsonii | COG0764: 3-hydroxymeristoyl(3-hydroxydecanoyl)-(acyl carrier protein) dehydratases [Cytophaga hutchinsonii] | | | |
| 4655, 4656 | 45657684 | 26 | 2.00E-11 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC11819 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb[AAS70407.1] conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 4657, 4658 | 21227195 | 38 | 8.00E-18 | Methanosarcina mazei Go1 | hypothetical sensory transduction histidine kinase [Methanosarcina mazei Go1] gb[AAM30789.1] hypothetical sensory transduction histidine kinase [Methanosarcina mazei Go1] | | | 2.7.3.- |
| 4659, 4660 | 17230661 | 38 | 2.00E-19 | Nostoc sp. PCC 7120 | hypothetical protein all3169 [Nostoc sp. PCC 7120] pir[AB2202 hypothetical protein all3169 [Imported] - Nostoc sp. (strain PCC 7120) dbj[BAB74868.1] all3169 [Nostoc sp. PCC 7120] | | | 2.7.1.37 |
| 4665, 4666 | 48853603 | 51 | 2.00E-69 | Cytophaga hutchinsonii | COG0809: S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (guanine synthetase) [Cytophaga hutchinsonii] | | | 5.--- |
| 4667, 4668 | 48839466 | 93 | 1.00E-66 | Methanosarcina barkeri str. fusaro | COG1335: Amidases related to nicotinamide [Methanosarcina barkeri str. fusaro] | | | 3.5.1.19 |

| | | | | | | | | |
|--------------------------------|----------|----|----------|---|---|--|----|----------|
| 4669, 4670 | 52548310 | 52 | 6.00E-55 | uncultured archaeon GZfos11A10 | conserved hypothetical protein [uncultured archaeon GZfos11A10] | Methanosarcina acetivorans str. C2A, section 412 of 534 of the complete genome | 88 | 0 |
| 467, 468 | 28553411 | 45 | 6.00E-13 | Pseudomonas syringae pv. tomato str. DC3000 | conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_792784.1 hypothetical protein PSPTO2987 [Pseudomonas syringae pv. tomato str. DC3000] | | | |
| 4673, 4674 4675, 4676 | 34397317 | 51 | 2.00E-45 | Porphyrromonas gingivalis W83 | glucose-inhibited division protein B [Porphyrromonas gingivalis W83] ref NP_905481.1 glucose-inhibited division protein B [Porphyrromonas gingivalis W83] sp Q7MV10 GIDB_PORGI Methyltransferase gidB (Glucose inhibited division protein B) | | | |
| 4681, 4682 4683, 4684 | 4885392 | 27 | 9.00E-08 | Cytophaga hutchinsonii | endonuclease [EC 3.1.30.-] precursor - barley dbj BAA28942.1 endonuclease [Hordeum vulgare subsp. vulgare] COG0823: Periplasmic component of the Tol biopolymer transport system [Cytophaga hutchinsonii] | | | |
| | 48854977 | 57 | 4.00E-89 | Cytophaga hutchinsonii | COG0885: 5,10-methylenetetrahydrofolate reductase [Cytophaga hutchinsonii] | | | 1.7.99.5 |
| 4685, 4686 4687, 4688 | 15615605 | 37 | 3.00E-30 | Bacillus halodurans C-125 | glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus halodurans C- 125] dbj BAB06762.1 glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus halodurans C-125] sp Q9K8G3 GSA_BACHD Glutamate-1- semialdehyde 2,1-aminotransferase (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT) pir C84030 glutamate-1-semialdehyde 2,1- aminotransferase hemL [imported] - Bacillus halodurans (strain C-125) unnamed protein product [Kluyveromyces fragilis] emb CAG99481.1 unnamed protein product [Kluyveromyces fragilis] NRRL Y-1140] | | | 5.4.3.8 |
| 4691, 4692 4693, 4694 | 50308779 | 37 | 3.00E-36 | Kluyveromyces fragilis | COG0151: Phosphoribosylamine-glycine ligase [Cytophaga hutchinsonii] | | | 1.--- |
| | 48855741 | 55 | 8.00E-81 | Cytophaga hutchinsonii | COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii] | | | 6.3.4.13 |
| 4697, 4698 4699, 4700 | 37523515 | 77 | 8.00E-77 | Gloeobacter violaceus PCC 7421 | rifampin ADP-ribosyl transferase [Gloeobacter violaceus PCC 7421] dbj BAC91887.1 rifampin ADP-ribosyl transferase [Gloeobacter violaceus PCC 7421] COG1290: Cytochrome b subunit of the bc complex [Mesorhizobium sp. BNC1] | Gloeobacter violaceus PCC 7421 DNA, complete genome | 82 | 6.00E-81 |
| 4701, 4702 | 45680978 | 27 | 3.00E-20 | Mesorhizobium sp. BNC1 | putative cell-cycle protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76700.1 putative cell-cycle protein [Bacteroides thetaiotaomicron VPI-5482] | | | 1.2.99.5 |
| | 29347003 | 37 | 5.00E-43 | Bacteroides thetaitaomicron VPI-5482 | | | | |

| | | | | | | | | | |
|---------------|----------|----|-----------|---|--|---|----|----------|----------|
| 4703, 4704 | 20089503 | 35 | 1.00E-44 | Methanosarcina acetivorans C2A | 3-hydroxyisobutyrate dehydrogenase [Methanosarcina acetivorans str. C2A] | | | | 1.1.1.31 |
| 4705, 4706 | 48854136 | 22 | 2.00E-16 | Cytophaga hutchinsonii | COG1566: Multidrug resistance efflux pump [Cytophaga hutchinsonii] | | | | |
| 4707, 4708 | 37523705 | 23 | 4.00E-07 | Gloeobacter violaceus PCC 7421 | hypothetical protein glt4136 [Gloeobacter violaceus PCC 7421] dbj BAC92077.1 glt4136 [Gloeobacter violaceus PCC 7421] | | | | |
| 4709, 4710 | 23125049 | 56 | 3.00E-32 | Nostoc punctiforme PCC 73102 | COG1225: Peroxiredoxin [Nostoc punctiforme PCC 73102] putative ABC transporter permease [Bacteroides fragilis YCH46] | | | | 1.6.4.- |
| 471, 472 | 53713334 | 24 | 2.00E-12 | Bacteroides fragilis YCH46 | dbj BAD48792.1 putative ABC transporter permease [Bacteroides fragilis YCH46] | | | | |
| 4711, 4712 | 48854837 | 31 | 8.00E-20 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | | |
| 4715, 4716 | 48854837 | 38 | 6.00E-31 | Cytophaga hutchinsonii | COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii] | | | | |
| 4717, 4718 | 53713847 | 69 | 1.00E-104 | Bacteroides fragilis YCH46 | GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD49305.1 GTP- binding protein [Bacteroides fragilis YCH46] | Bacillus halodurans C-125 DNA, complete genome, section 5/14 | 86 | 7.00E-19 | |
| 4719, 4720 | 40643170 | 55 | 5.00E-94 | Leptospira biflexa temperate bacteriophage LE1 | unnamed protein product [Leptospira biflexa temperate bacteriophage LE1] | | | | |
| 4721, 4722 | 48856951 | 36 | 3.00E-13 | Cytophaga hutchinsonii | COG0019: Diaminopimelate decarboxylase [Cytophaga hutchinsonii] tRNA pseudouridine synthase A [Clostridium tetani E88] gb AAO37030.1 tRNA pseudouridine synthase A [Clostridium tetani E88] sp Q890R5 TRA2_CLOTE tRNA pseudouridine synthase A 2 (Pseudouridylylase synthase 12) (Pseudouridylylase synthase 12) (Uracil hydrolyase 2) | | | 4.1.1.20 | |
| 4725, 4726 | 28212149 | 48 | 2.00E-35 | Clostridium tetani E88 | phosphoribosylglycinamide synthetase ATP-grasp (A) domain protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU26174.1 phosphoribosylglycinamide synthetase ATP-grasp (A) domain protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | 4.2.1.70 | |
| 4729, 4730 | 52840322 | 47 | 2.00E-58 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | | | | | |

| | | | | | | | | |
|---------------|----------|----|-----------|--|---|--|-------------|----------|
| 4731, 4732 | 29347017 | 62 | 4.00E-97 | Bacteroides thetaiotaomicron VPI-5482 | methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76714.1 methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase [Bacteroides thetaiotaomicron VPI-5482] | | | 1.5.1.5 |
| 4733, 4734 | 48893492 | 36 | 1.00E-42 | Trichodesmium erythraeum IMS101 | COG0587: DNA polymerase III, alpha subunit [Trichodesmium erythraeum IMS101] | | | 2.7.7.7 |
| 4735, 4736 | 48840221 | 35 | 4.00E-30 | Methanosarcina barkeri str. fusaro | COG0463: Glycosyltransferases involved in cell wall biogenesis [Methanosarcina barkeri str. fusaro] | | | |
| 4737, 4738 | 42780089 | 46 | 8.00E-21 | Bacillus cereus ATCC 10987 | hypothetical protein BCE1013 [Bacillus cereus ATCC 10987] gb AAS39944.1 conserved hypothetical protein [Bacillus cereus ATCC 10987] | | | |
| 4739, 4740 | 48856971 | 65 | 2.00E-94 | Cytophaga hutchinsonii | COG0138: AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in AfcI) [Cytophaga hutchinsonii] | | | 2.1.2.3 |
| 4741, 4742 | 48854286 | 35 | 5.00E-19 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 4743, 4744 | 48853692 | 53 | 6.00E-47 | Cytophaga hutchinsonii | COG1273: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | 6.5.1.2 |
| 4745, 4746 | 48847026 | 34 | 1.00E-52 | Geobacter metallireducens GS 15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | Oryza sativa (japonica cultivar- group), mRNA | ## 8.00E-07 | 2.7.3.- |
| 4749, 4750 | 27904689 | 35 | 6.00E-09 | Buchnera aphidicola str. Bp (Baizongia pistaciae) | GMP reductase [Buchnera aphidicola str. Bp (Baizongia pistaciae)] gb AAO26920.1 GMP reductase [Buchnera aphidicola str. Bp (Baizongia pistaciae)] sp P59443 GUAC_BUCBP GMP reductase (Guanosine 5'- monophosphate oxidoreductase) (Guanosine monophosphate reductase) | | | 1.6.6.8 |
| 4751, 4752 | 48863265 | 34 | 5.00E-09 | Microbulifer degradans 2-40 | COG0402: Cytosine deaminase and related metal-dependent hydrolases [Microbulifer degradans 2-40] | | | |
| 4753, 4754 | 48854732 | 35 | 8.00E-36 | Cytophaga hutchinsonii | COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | |
| 4755, 4756 | 48853949 | 67 | 1.00E-141 | Cytophaga hutchinsonii | COG0187: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit [Cytophaga hutchinsonii] | | | 5.99.1.- |
| 4757, 4758 | 16329398 | 34 | 1.00E-17 | Synechocystis sp. PCC 6803 | hybrid sensory kinase [Synechocystis sp. PCC 6803] dbj BAA16806.1 hybrid sensory kinase [Synechocystis sp. PCC 6803] pir S74654 sensory transduction histidine kinase sll1672 - Synechocystis sp. (strain PCC 6803) | Aspergillus fumigatus histidine kinase gene, partial sequence | 90 6.00E-07 | 2.7.3.- |
| 4759, 4760 | 16329398 | 34 | 6.00E-18 | Synechocystis sp. PCC 6803 | hybrid sensory kinase [Synechocystis sp. PCC 6803] dbj BAA16806.1 hybrid sensory kinase [Synechocystis sp. PCC 6803] pir S74654 sensory transduction histidine kinase sll1672 - Synechocystis sp. (strain PCC 6803) | Aspergillus fumigatus histidine kinase gene, partial sequence | 90 4.00E-07 | 2.7.3.- |

| | | | | | | | | | |
|-------|----------|----|----------|-------------------------------------|---|--|--|--|----------|
| 4761, | 23125020 | 25 | 1.00E-09 | Nostoc punctiforme PCC 73102 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 4762 | | | | Cytophaga hutchinsonii | COG1024: Enoyl-CoA hydratase/carnitine racemase [Cytophaga hutchinsonii] | | | | 4.2.1.17 |
| 4763, | 48853568 | 40 | 1.00E-45 | Geobacter metallireducens GS | | | | | |
| 4764 | | | | metallireducens GS | | | | | |
| 4767, | 48845451 | 30 | 1.00E-33 | Nanoarchaeum equitans Kin4-M | COG0366: Glycosidases [Geobacter metallireducens GS-15] | | | | |
| 4768 | | | | equitans Kin4-M | hypothetical protein NEQ511 [Nanoarchaeum equitans Kin4-M] | | | | |
| 477, | 41615293 | 35 | 8.00E-13 | Bacteroides fragilis YCH46 | gb AAP39352.1 NEQ511 [Nanoarchaeum equitans Kin4-M] | | | | 3.5.1.16 |
| 4771, | | | | Bacteroides fragilis YCH46 | sialate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAC56897.1 | | | | |
| 4772 | 53713020 | 41 | 2.00E-37 | Pyrococcus furiosus DSM 3638 | sialate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAD48478.1 | | | | 3.1.1.47 |
| | | | | Pyrococcus furiosus DSM 3638 | sialate O-acetyltransferase [Bacteroides fragilis YCH46] | | | | |
| 4773, | 18977752 | 37 | 2.00E-27 | Cytophaga hutchinsonii | arginyl-tRNA synthetase [Pyrococcus furiosus DSM 3638] | | | | |
| 4774 | | | | Cytophaga hutchinsonii | arginyl-tRNA synthetase [Pyrococcus furiosus DSM 3638] | | | | |
| 4775, | 48855955 | 34 | 3.00E-32 | Neisseria meningitidis Z2491 | sp Q8U149 SYR_PYRFU Arginyl-tRNA synthetase (Arginine--tRNA ligase) (ArgRS) | | | | 6.1.1.19 |
| 4776 | | | | Neisseria meningitidis Z2491 | (ArgRS) | | | | |
| 4779, | 15794814 | 62 | 2.00E-60 | Geobacter metallireducens GS | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] | | | | 1.11.1.5 |
| 4780 | | | | Geobacter metallireducens GS | DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] | | | | |
| 4781, | 48844153 | 42 | 1.00E-13 | Cytophaga hutchinsonii | emb CAB85151.1 DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] | | | | |
| 4782 | | | | Cytophaga hutchinsonii | meningitidis Z2491] pir A81821 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) NMA1931 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) | | | | 3.2.2.20 |
| 4783, | 48853683 | 57 | 2.00E-25 | Geobacter metallireducens GS | hypothetical protein Gmet02003361 [Geobacter metallireducens GS-15] | | | | |
| 4784 | | | | Geobacter metallireducens GS | COG0721: Asp-tRNAAsn/Glu-tRNA Gln amidotransferase C subunit | | | | |
| 4787, | AAG4650 | 0 | 51 | 3.00E-15 | [Cytophaga hutchinsonii] | | | | 6.3.5.- |
| 4788 | | | | Clostridium thermocellum ATCC 27405 | Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 58507. | | | | |
| 479, | 48860398 | 28 | 9.00E-11 | Geobacter metallireducens GS | Org:Arabidopsis thaliana | | | | |
| 480 | | | | Geobacter metallireducens GS | COG1408: Predicted phosphohydrolases [Clostridium thermocellum ATCC 27405] | | | | |
| 4791, | 48846050 | 34 | 1.00E-16 | Cytophaga hutchinsonii | hypothetical protein Gmet02001503 [Geobacter metallireducens GS-15] | | | | |
| 4792 | | | | Cytophaga hutchinsonii | COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Cytophaga hutchinsonii] | | | | |
| 4793, | 48853682 | 33 | 2.00E-07 | | | | | | |
| 4794 | | | | | | | | | |

| | | | | | | | | |
|-------|----------|----|-----------|--|---|---|----|----------|
| 4795, | 48854564 | 53 | 5.00E-67 | Cytophaga hutchinsonii | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 4796 | 48854564 | 53 | 5.00E-67 | Cytophaga hutchinsonii | COG1131: ABC-type multidrug transport system, ATPase component [Cytophaga hutchinsonii] | | | 3.6.3.33 |
| 4797, | 48854757 | 43 | 5.00E-35 | Cytophaga hutchinsonii | ferredoxin [Bordetella parapertussis 12822] ref NP_879432.1 ferredoxin [Bordetella pertussis Tohama I] ref NP_886828.1 ferredoxin [Bordetella bronchiseptica RB50] emb CAE30777.1 ferredoxin [Bordetella bronchiseptica RB50] emb CAE40017.1 ferredoxin [Bordetella parapertussis] emb CAE44914.1 ferredoxin [Bordetella pertussis Tohama I] | | | 1.-.-.- |
| 4799, | 33594991 | 36 | 7.00E-13 | Bordetella parapertussis 12822 | ferredoxin [Bordetella parapertussis 12822] ref NP_879432.1 ferredoxin [Bordetella pertussis Tohama I] ref NP_886828.1 ferredoxin [Bordetella bronchiseptica RB50] emb CAE30777.1 ferredoxin [Bordetella bronchiseptica RB50] emb CAE40017.1 ferredoxin [Bordetella parapertussis] emb CAE44914.1 ferredoxin [Bordetella pertussis Tohama I] | Chlamydia muridarum section 27 of 85 of the complete genome | 93 | 1.00E-06 |
| 4800 | 33594991 | 36 | 7.00E-13 | Bordetella parapertussis 12822 | ferredoxin [Bordetella parapertussis 12822] ref NP_879432.1 ferredoxin [Bordetella pertussis Tohama I] ref NP_886828.1 ferredoxin [Bordetella bronchiseptica RB50] emb CAE30777.1 ferredoxin [Bordetella bronchiseptica RB50] emb CAE40017.1 ferredoxin [Bordetella parapertussis] emb CAE44914.1 ferredoxin [Bordetella pertussis Tohama I] | | | 1.-.-.- |
| 4803, | 48855541 | 79 | 2.00E-62 | Cytophaga hutchinsonii | COG1875: Predicted ATPase related to phosphate starvation-inducible protein PhoH [Cytophaga hutchinsonii] | | | 3.4.11.9 |
| 4804 | 48855541 | 79 | 2.00E-62 | Cytophaga hutchinsonii | COG1875: Predicted ATPase related to phosphate starvation-inducible protein PhoH [Cytophaga hutchinsonii] | | | 2.7.6.5 |
| 4809, | 48853628 | 48 | 1.00E-41 | Cytophaga hutchinsonii | COG0006: Xaa-Pro aminopeptidase [Cytophaga hutchinsonii] | | | 3.4.11.9 |
| 4810 | 48853628 | 48 | 1.00E-41 | Cytophaga hutchinsonii | COG0006: Xaa-Pro aminopeptidase [Cytophaga hutchinsonii] | | | 2.7.6.5 |
| 481, | 48856298 | 68 | 3.00E-43 | Cytophaga hutchinsonii | COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Cytophaga hutchinsonii] | | | 2.7.6.5 |
| 482 | 48856298 | 68 | 3.00E-43 | Cytophaga hutchinsonii | COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Cytophaga hutchinsonii] | | | 2.7.6.5 |
| 4811, | 45657163 | 57 | 3.00E-30 | Leptospira interrogans serovar Copenhagen str. | hypothetical protein LIC11281 [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] ref NP_712912.1 hypothetical protein LA2731 [Leptospira interrogans serovar Lai str. 56601] gb AA49930.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AA569886.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] | | | |
| 4812 | 45657163 | 57 | 3.00E-30 | Leptospira interrogans serovar Copenhagen str. | hypothetical protein LIC11281 [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] ref NP_712912.1 hypothetical protein LA2731 [Leptospira interrogans serovar Lai str. 56601] gb AA49930.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AA569886.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] | | | |
| 4813, | 28210089 | 25 | 5.00E-09 | Clostridium tetani E88 | aminopeptidase Y [Clostridium tetani E88] gb AAO34970.1 aminopeptidase Y [Clostridium tetani E88] | | | |
| 4814 | 28210089 | 25 | 5.00E-09 | Clostridium tetani E88 | aminopeptidase Y [Clostridium tetani E88] gb AAO34970.1 aminopeptidase Y [Clostridium tetani E88] | | | |
| 4815, | 27377973 | 49 | 2.00E-59 | Bradyrhizobium japonicum USDA 110 | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] | | | 2.7.3.- |
| 4816 | 27377973 | 49 | 2.00E-59 | Bradyrhizobium japonicum USDA 110 | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] | | | 2.7.3.- |
| 4817, | 27377973 | 46 | 3.00E-52 | Bradyrhizobium japonicum USDA 110 | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] | | | 2.7.3.- |
| 4818 | 27377973 | 46 | 3.00E-52 | Bradyrhizobium japonicum USDA 110 | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] | | | 2.7.3.- |
| 4819, | 56963101 | 25 | 2.00E-11 | Bacillus clausii KSM-K16 | phage terminase-like protein large subunit [Bacillus clausii KSM-K16] dbj BAD03867.1 phage terminase-like protein large subunit [Bacillus clausii KSM-K16] | | | |
| 4820 | 56963101 | 25 | 2.00E-11 | Bacillus clausii KSM-K16 | phage terminase-like protein large subunit [Bacillus clausii KSM-K16] dbj BAD03867.1 phage terminase-like protein large subunit [Bacillus clausii KSM-K16] | | | |
| 4821, | 23127778 | 70 | 1.00E-107 | Nostoc punctiforme PCC 73102 | COG3033: Tryptophanase [Nostoc punctiforme PCC 73102] | C.freundii tpl gene for tyrosine phenol-lyase | 86 | 3.00E-18 |
| 4822 | 23127778 | 70 | 1.00E-107 | Nostoc punctiforme PCC 73102 | COG3033: Tryptophanase [Nostoc punctiforme PCC 73102] | | | 4.1.99.2 |
| 4823, | 48853579 | 53 | 8.00E-30 | Cytophaga hutchinsonii | COG1127: ABC-type transport system involved in resistance to organic solvents, ATPase component [Cytophaga hutchinsonii] | | | 1.8.-.- |
| 4824 | 48853579 | 53 | 8.00E-30 | Cytophaga hutchinsonii | COG1127: ABC-type transport system involved in resistance to organic solvents, ATPase component [Cytophaga hutchinsonii] | | | 1.8.-.- |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|---|----|------------------|
| 4825, 4826 | 46198917 | 28 | 3.00E-17 | Thermus thermophilus HB27 | transcriptional regulator, tatR family [Thermus thermophilus HB27] gb AA80957.1 transcriptional regulator, tatR family [Thermus thermophilus HB27] | | | |
| 4827, 4828 | 45521476 | 85 | 2.00E-65 | Methylobacillus flagellatus KT | COG0499: S-adenosylhomocysteine hydrolase [Methylobacillus flagellatus KT] | Bordetella pertussis strain Tohama I, complete genome; segment 10/12 | 87 | 2.00E-57 3.3.1.1 |
| 4829, 4830 | 48830870 | 40 | 1.00E-11 | Magnetococcus sp. MC-1 | COG0460: Homoserine dehydrogenase [Magnetococcus sp. MC-1] | | | 1.1.1.3 |
| 483, 484 | 20808896 | 37 | 7.00E-39 | Thermoanaerobact er tengcongensis MB4 | UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] gb AAM2567.1.1 UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] | | | 6.3.2.15 |
| 4833, 4834 | 23128506 | 47 | 2.00E-56 | Nostoc punctiforme PCC 73102 | COG0010: Arginase/agmatinase/formiminoglutamate hydrolase, arginase family [Nostoc punctiforme PCC 73102] | | | 3.5.3.11 |
| 4835, 4836 | 48853912 | 30 | 1.00E-25 | Cytophaga hutchinsonii | COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii] | | | 4.1.1.20 |
| 4837, 4838 | 32474556 | 33 | 2.00E-21 | Rhodopirellula ballica SH 1 | hypothetical protein RB6958 [Rhodopirellula ballica SH 1] emb CAD75097.1 conserved hypothetical protein [Pirellula sp.] | | | |
| 4839, 4840 | 32474556 | 33 | 2.00E-21 | Rhodopirellula ballica SH 1 | hypothetical protein RB6958 [Rhodopirellula ballica SH 1] emb CAD75097.1 conserved hypothetical protein [Pirellula sp.] | | | |
| 4847, 4848 | 48855210 | 24 | 3.00E-10 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | |
| 4849, 4850 | 48853964 | 44 | 3.00E-47 | Cytophaga hutchinsonii | COG0111: Phosphoglycerate dehydrogenase and related dehydrogenases [Cytophaga hutchinsonii] | | | 1.1.1.95 |
| 485, 486 | 20808896 | 39 | 2.00E-35 | Thermoanaerobact er tengcongensis MB4 | UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] gb AAM2567.1.1 UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] | | | 6.3.2.15 |
| 4853, 4854 | 21673003 | 59 | 2.00E-28 | Chlorobium tepidum TLS | alpha oxoglutarate ferredoxin oxidoreductase, beta subunit [Chlorobium tepidum TLS] gb AAM71410.1 alpha oxoglutarate ferredoxin oxidoreductase, beta subunit [Chlorobium tepidum TLS] | | | 1.2.7.3 |
| 4855, 4856 | 16124371 | 32 | 1.00E-09 | Caulobacter crescentus CB15 | hypothetical protein CC0116 [Caulobacter crescentus CB15] gb AAK22103.1 hypothetical protein [Caulobacter crescentus CB15] pir C87263 hypothetical protein CC0116 [imported] - Caulobacter crescentus | | | |
| 4861, 4862 | 53713899 | 39 | 2.00E-16 | Bacteroides fragilis YCH46 | hypothetical protein BF2607 [Bacteroides fragilis YCH46] dbj BAD49357.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |

[illegible]

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|----------|
| 4931, 4932 | 48854681 | 34 | 2.00E-09 | Cytophaga hutchinsonii | hypothetical protein Chut02002347 [Cytophaga hutchinsonii] | | | |
| 4933, 4934 | 48853375 | 48 | 2.00E-10 | Cytophaga hutchinsonii | COG4430: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 4935, 4936 | 15895033 | 40 | 3.00E-10 | Clostridium acetobutylicum ATCC 824 | Predicted nucleic acid binding protein, containing KH domain [Clostridium acetobutylicum ATCC 824] gb AAK79722.1 Predicted nucleic acid binding protein, containing KH domain [Clostridium acetobutylicum ATCC 824] pir G97116 probable nucleic acid binding protein, containing KH domain [imported] - Clostridium acetobutylicum sp Q97196 YH56_CLOAB Hypothetical UPF0109 protein CAC1756 | | | |
| 4941, 4942 | 20090716 | 30 | 1.00E-29 | Methanosarcina acetivorans C2A | hypothetical protein MA1866 [Methanosarcina acetivorans C2A] gb AAM0527.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | |
| 4943, 4944 | 30249879 | 44 | 2.00E-42 | Nitrosomonas europaea ATCC 19718 | Sulfate transporter [Nitrosomonas europaea ATCC 19718] emb CAD85838.1 Sulfate transporter [Nitrosomonas europaea ATCC 19718] | | | |
| 4945, 4946 | 53714523 | 27 | 5.00E-28 | Bacteroides fragilis YCH46 | hypothetical protein BF3236 [Bacteroides fragilis YCH46] db BAD49981.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 4949, 4950 | 48856903 | 38 | 1.00E-55 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | |
| 495, 496 | 5777601 | 44 | 1.00E-41 | Lampetra fluviatilis | polymerase polypeptide [Lampetra fluviatilis] | | | 3.4.23.- |
| 4951, 4952 | 48895505 | 42 | 5.00E-18 | Trichodesmium erythraeum IMS101 | COG3222: Uncharacterized protein conserved in bacteria [Trichodesmium erythraeum IMS101] | | | |
| 4953, 4954 | 48854204 | 43 | 3.00E-46 | Cytophaga hutchinsonii | COG0297: Glycogen synthase [Cytophaga hutchinsonii] | | | 2.4.1.21 |
| 4957, 4958 | 20094865 | 37 | 6.00E-45 | Methanopyrus kandleri AV19 | Fe-S oxidoreductase [Methanopyrus kandleri AV19] gb AAM02642.1 Fe-S oxidoreductase [Methanopyrus kandleri AV19] | | | |
| 4959, 4960 | 28854417 | 33 | 1.00E-13 | Pseudomonas syringae pv. tomato str. DC3000 | ferredoxin--NADP reductase [Pseudomonas syringae pv. tomato str. DC3000] ref NP_793786.1 ferredoxin--NADP reductase [Pseudomonas syringae pv. tomato str. DC3000] | | | 1.18.1.2 |
| 4963, 4964 | 9948447 | 28 | 2.00E-15 | Pseudomonas aeruginosa PAO1 | hypothetical protein PA2403 [Pseudomonas aeruginosa PAO1] ref ZP_00140125.1 COG3182: Uncharacterized iron-regulated membrane protein [Pseudomonas aeruginosa UCBBP-PA14] pir JA83344 hypothetical protein PA2403 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_251093.1 hypothetical protein PA2403 [Pseudomonas aeruginosa PAO1] | | | |
| 4967, 4968 | 53760034 | 52 | 2.00E-38 | Methylobacillus flagellatus KT | COG2870: ADP-heptose synthase, bifunctional sugar kinase/adenylyltransferase [Methylobacillus flagellatus KT] | | | 2.7.7.39 |

| | | | | | | | | | |
|---------------|--------------|----|----------|---|---|--|----|----------|----------|
| 4979, 4980 | 48846050 | 34 | 6.00E-23 | Geobacter metallireducens GS-15 | hypothetical protein Gmet02001503 [Geobacter metallireducens GS-15] | | | | |
| 4983, 4984 | 29349593 | 57 | 3.00E-66 | Bacteroides thetaiotaomicron VPI-5482 | xylosidase/arabinosidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79290.1 xylosidase/arabinosidase [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.2.1.37 |
| 4987, 4988 | 28262873 | 55 | 3.00E-91 | Rickettsia sibirica 246 | preprotein translocase secA subunit [Rickettsia sibirica 246] ref ZP_00142968.1 preprotein translocase secA subunit [Rickettsia sibirica 246] | Uncultured marine gamma proteobacterium EB000-45B06 fosmid clone | 91 | 2.00E-10 | |
| 4989, 4990 | 32307865 | 43 | 6.00E-53 | Rickettsia rickettsii | preprotein translocase SecA subunit [Rickettsia rickettsii] ref ZP_00153869.2 COG0653: Preprotein translocase subunit SecA (ATPase, RNA helicase) [Rickettsia rickettsii] | | | | |
| 499, 500 | 15893497 | 34 | 7.00E-10 | Clostridium acetobutylicum ATCC 824 | Sortase (surface protein transpeptidase), YHCS B subtilis ortholog [Clostridium acetobutylicum ATCC 824] gb AAK78186.1 Sortase (surface protein transpeptidase), YHCS B subtilis ortholog [Clostridium acetobutylicum ATCC 824] pir G96924 sortase (surface protein transpeptidase), YHCS B. subtilis ortholog [imported] - Clostridium acetobutylicum | | | | |
| 4991, 4992 | 29348249 | 51 | 9.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | O-methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77946.1 O-methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.1.1.- |
| 4993, 4994 | 50085810 | 42 | 2.00E-51 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD2753 [Acinetobacter sp. ADP1] emb CAG69498.1 hypothetical protein [Acinetobacter sp. ADP1] | | | | |
| 4995, 4996 | 48856863 | 39 | 2.00E-27 | Cytophaga hutchinsonii | COG1073: Hydrolases of the alpha/beta superfamily [Cytophaga hutchinsonii] | | | | |
| 4997, 4998 | 53711739 | 29 | 9.00E-25 | Bacteroides fragilis YCH46 | hypothetical protein BF0448 [Bacteroides fragilis YCH46] db BAD47197.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 4999, 5000 | ABP2662 0 | 31 | 4.00E-08 | | Desc:Streptococcus polypeptide SEQ ID NO 2416. Org:Streptococcus agalactiae | | | | |
| 5, 6 | 48855182 | 30 | 8.00E-13 | Cytophaga hutchinsonii | COG2911: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 5005, 5006 | 26991423 | 63 | 3.00E-87 | Pseudomonas putida KT2440 | type I restriction-modification system, R subunit [Pseudomonas putida KT2440] gb AAN70312.1 type I restriction-modification system, R subunit [Pseudomonas putida KT2440] | | | | 3.1.21.3 |
| 5007, 5008 | 48855480 | 60 | 7.00E-91 | Cytophaga hutchinsonii | COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Cytophaga hutchinsonii] | | | | 1.8.-.- |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|---------------|
| 501, 502 | 20808329 | 47 | 1.00E-38 | Thermoanaerobacter tengcongensis MB4 | hypothetical protein TTE1925 [Thermoanaerobacter tengcongensis MB4] gb AA025104.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4] | | | |
| 5011, 5012 | 50086533 | 40 | 6.00E-10 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD3581 [Acinetobacter sp. ADP1] emb CAG70221.1 conserved hypothetical protein [Acinetobacter sp. ADP1] | | | 2.3.1.- |
| 5015, 5016 | 16127503 | 47 | 8.00E-73 | Caulobacter crescentus CB15 | hypothetical protein CC3273 [Caulobacter crescentus CB15] gb AAK25235.1 hypothetical protein [Caulobacter crescentus CB15] pir G87654 hypothetical protein CC3273 [imported] - Caulobacter crescentus | | | |
| 5017, 5018 | 48854667 | 43 | 4.00E-42 | Cytophaga hutchinsonii | COG0072: Phenylalanyl-tRNA synthetase beta subunit [Cytophaga hutchinsonii] | | | 6.1.1.20 |
| 5021, 5022 | 48855525 | 39 | 1.00E-13 | Cytophaga hutchinsonii | hypothetical protein Chut020071868 [Cytophaga hutchinsonii] | | | |
| 5023, 5024 | 21226435 | 57 | 3.00E-56 | Methanosarcina mazei Go1 | Methyl-accepting chemotaxis protein [Methanosarcina mazei Go1] gb AAM30029.1 Methyl-accepting chemotaxis protein [Methanosarcina mazei Go1] | | | |
| 5029, 5030 | ABB5493 | 5 | 2.00E-34 | | Desc: Lactococcus lactis protein murG. Org: Lactococcus lactis IL1403 | | | 2.4.1.- |
| 5035, 5036 | 53712767 | 71 | 3.00E-75 | Bacteroides fragilis YCH46 | dioxygenase [Bacteroides fragilis YCH46] dbj BAD48225.1 dioxygenase [Bacteroides fragilis YCH46] | | | 1.3.1.9 |
| 5039, 5040 | 21672779 | 44 | 7.00E-16 | Buchnera aphidicola str. Sg (Schizaphis graminum) | FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor [Buchnera aphidicola str. Sg (Schizaphis graminum)] gb AAM68057.1 FKBP-type peptidyl-prolyl cis-trans isomerase [Buchnera aphidicola str. Sg (Schizaphis graminum)] sp Q8K943 FKBA_BUCAP FKBP-type peptidyl-prolyl cis-trans isomerase fkpA (PPIase) (Rotamase) | | | 5.2.1.8 |
| 5041, 5042 | 22657439 | 38 | 5.00E-14 | Streptomyces sp. 139 | putative bi-domain oxidoreductase [Streptomyces sp. 139] | | | 1.1.1.- |
| 5043, 5044 | 16265151 | 30 | 4.00E-07 | Sinorhizobium meliloti 1021 | hypothetical protein Smb20696 [Sinorhizobium meliloti 1021] pir C96017 | | | |
| 5045, 5046 | 34860755 | 21 | 5.00E-21 | Rattus norvegicus | hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb CAC49803.1 HYPOTHETICAL PROTEIN [Sinorhizobium meliloti 1021] | | | |
| 505, 506 | 29346948 | 29 | 5.00E-07 | Bacteroides thetaiotaomicron VPI-5482 | similar to hypothetical protein [Rattus norvegicus] | | | 3.1.11.- |
| 5051, 5052 | 17228491 | 73 | 9.00E-17 | Nostoc sp. PCC 7120 | hemagglutinin [Bacteroides thetaiotaomicron VPI-5482] gb AAO76645.1 hemagglutinin [Bacteroides thetaiotaomicron VPI-5482] | | | |
| | | | | | protease [Nostoc sp. PCC 7120] pir AI1930 proteinase [imported] - Nostoc sp. (strain PCC 7120) dbj BAB72953.1 protease [Nostoc sp. PCC 7120] | | | 3.4.21.4 8 |

| | | | | | | | | | |
|---------------|--------------|----|----------|------------------|---|---|--|--|----------|
| 5055, 5056 | 16081128 | 34 | 5.00E-26 | 168 | Bacillus subtilis subsp. subtilis str. | hypothetical protein BSU40760 [Bacillus subtilis subsp. subtilis str. 168] emb[CAB16113.1] yyaP [Bacillus subtilis subsp. subtilis str. 168] pir[S66001 conserved hypothetical protein yyaP - Bacillus subtilis sp P37508 YYAP_BACSU Hypothetical protein yyaP dbj BAA05207.1 unknown [Bacillus subtilis] | | | 3.4.24.- |
| 5059, 5060 | 48854514 | 44 | 7.00E-52 | hutchinsonii | Cytophaga hutchinsonii | COG1216: Predicted glycosyltransferases [Cytophaga hutchinsonii] | | | 2.4.1.- |
| 5061, 5062 | 7592812 | 45 | 1.00E-17 | itans | Actinobacillus actinomycetemcomitans | mannosyl transferase [Actinobacillus actinomycetemcomitans] | | | 2.4.1.- |
| 5063, 5064 | 48856118 | 50 | 2.00E-47 | hutchinsonii | Cytophaga hutchinsonii | COG0242: N-formylmethionyl-tRNA deformylase [Cytophaga hutchinsonii] | | | 3.5.1.88 |
| 5067, 5068 | 48854286 | 35 | 2.00E-25 | hutchinsonii | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 507, 508 | 48855576 | 27 | 2.00E-21 | hutchinsonii | Cytophaga hutchinsonii | COG4591: ABC-type transport system, involved in lipoprotein release, permease component [Cytophaga hutchinsonii] | | | |
| 5071, 5072 | 53795729 | 44 | 7.00E-72 | aurantiacus | Chloroflexus aurantiacus | COG0827: Adenine-specific DNA methylase [Chloroflexus aurantiacus] | | | 2.1.1.72 |
| 5073, 5074 | 53795729 | 43 | 7.00E-24 | aurantiacus | Chloroflexus aurantiacus | COG0827: Adenine-specific DNA methylase [Chloroflexus aurantiacus] | | | |
| 5075, 5076 | 53713856 | 31 | 3.00E-39 | YCH46 | Bacteroides fragilis YCH46 | phenylalanyl-tRNA synthetase beta chain [Bacteroides fragilis YCH46] dbj BAD49314.1 phenylalanyl-tRNA synthetase beta chain [Bacteroides fragilis YCH46] | | | 6.1.1.20 |
| 5077, 5078 | ABP2564 0 | 35 | 5.00E-08 | | | Desc:Streptococcus polypeptide SEQ ID NO 456. Org:Streptococcus pyogenes | | | 2.7.3.- |
| 5079, 5080 | 34396630 | 56 | 1.00E-43 | gingivalis W83 | Porphyromonas gingivalis W83 | SsrA-binding protein [Porphyromonas gingivalis W83] ref NP_904797.1 SsrA-binding protein [Porphyromonas gingivalis W83] sp Q7MWT5 SSRP_PORGI SsrA-binding protein | | | |
| 5081, 5082 | 52006884 | 44 | 2.00E-26 | 25259 | Thiobacillus denitrificans ATCC 25259 | COG0543: 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases [Thiobacillus denitrificans ATCC 25259] | | | |
| 5083, 5084 | 16127932 | 51 | 3.00E-70 | crenscentus CB15 | Caulobacter crenscentus CB15 | peptidyl-dipeptidase Dcp [Caulobacter crescentus CB15] gb AAK25864.1 peptidyl-dipeptidase Dcp [Caulobacter crescentus CB15] pir D87708 peptidyl-dipeptidase Dcp [Imported] - Caulobacter crescentus putative two-component system response regulator, no kinase domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO79223.1 putative two- component system response regulator, no kinase domain [Bacteroides thetaitaomicron VPI-5482] | | | 3.4.15.5 |
| 5089, 5090 | 29349526 | 44 | 4.00E-21 | VPI-5482 | Bacteroides thetaitaomicron VPI-5482 | | | | |

| | | | | | | | | |
|---|----------------------------------|----------------|----------------------------------|--|---|--|--|--------------------|
| 5091, 5092 5093, 5094 | 57159416 58460817 | 33 41 | 1.00E-15 1.00E-46 | Thermococcus kodakaraensis Idiomarina loihiensis L2TR | CDC48VCP homolog, AAA superfamily [Thermococcus kodakaraensis] ref YP_183570.1 CDC48VCP homolog, AAA superfamily [Thermococcus kodakaraensis] Predicted amidohydrolase [Idiomarina loihiensis L2TR] gb AAV82549.1 Predicted amidohydrolase [Idiomarina loihiensis L2TR] | | | 3.6.1.3 |
| 5095, 5096 | 15669515 | 37 | 4.00E-09 | Methanocaldococcus jannaschii DSM 2661 | cadmium resistance protein [Methanocaldococcus jannaschii DSM 2661] gb AAB99335.1 cadmium resistance protein [Methanocaldococcus jannaschii DSM 2661] sp Q58721 YD25_METJA Putative HTH-type transcriptional regulator MJ1325 pir D64465 hypothetical protein MJ1325 - Methanococcus jannaschii | | | |
| 5097, 5098 | 29349346 | 29 | 1.00E-09 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 5099, 5100 | 20089535 | 27 | 1.00E-10 | Methanosarcina acetivorans C2A | DNA primase [Methanosarcina acetivorans C2A] gb AAM04090.1 DNA primase [Methanosarcina acetivorans str. C2A] sp Q8TSZ5 PRIS_METAC Probable DNA primase small subunit | | | 2.7.7.- |
| 5101, 5102 | 15678984 | 35 | 6.00E-28 | Methanothermobacter thermautotrophicus str. Delta H | hypothetical protein MTH966 [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85462.1 conserved protein [Methanothermobacter thermautotrophicus str. Delta H] pir C69229 conserved hypothetical protein MTH966 - Methanobacterium thermautotrophicum (strain Delta H) | | | |
| 5105, 5106 5107, 5108 | 29348099 53715428 | 50 59 | 9.00E-57 3.00E-79 | Bacteroides thetaiotaomicron VPI-5482 Bacteroides fragilis YCH46 | histidine ammonia-lyase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77796.1 histidine ammonia-lyase [Bacteroides thetaiotaomicron VPI-5482] histidine ammonia-lyase [Bacteroides fragilis YCH46] dbj BAD50886.1 histidine ammonia-lyase [Bacteroides fragilis YCH46] | | | 4.3.1.3 4.3.1.3 |
| 511, 512 5111, 5112 5115, 5116 | 15606650 53713534 48863265 | 30 47 34 | 9.00E-09 1.00E-68 5.00E-09 | Aquifex aeolicus VF5 Bacteroides fragilis YCH46 Microbulbifer degradans 2-40 | DNA primase [Aquifex aeolicus VF5] gb AAC07430.1 DNA primase [Aquifex aeolicus VF5] pir G70429 DNA primase - Aquifex aeolicus sp Q67465 PRIM_AQUAE DNA primase probable oxidoreductase [Bacteroides fragilis YCH46] dbj BAD48992.1 probable oxidoreductase [Bacteroides fragilis YCH46] COG0402: Cytosine deaminase and related metal-dependent hydrolases [Microbulbifer degradans 2-40] | | | 2.7.7.- 1.-.-.- |
| 5121, 5122 | 34397903 | 46 | 2.00E-17 | Porphyromonas gingivalis W83 | exonuclease ABC, C subunit [Porphyromonas gingivalis W83] ref NP_906065.1 exonuclease ABC, C subunit [Porphyromonas gingivalis W83] | | | |
| 5123, 5124 | 56460818 | 30 | 9.00E-29 | Idiomarina loihiensis L2TR | Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihiensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihiensis L2TR] | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|--|--|----|------------------|
| 5125, 5126 | 57234544 | 27 | 1.00E-08 | Dehalococcoides ethenogenes 195 | D-ala D-ala ligase [Dehalococcoides ethenogenes 195] | | | 6.3.2.4 |
| 5129, 5130 | | | | Yersinia pseudotuberculosis | possible restriction modification enzyme [Yersinia pseudotuberculosis IP 32953] emb CAH23119.1 possible restriction modification enzyme [Yersinia pseudotuberculosis IP 32953] | | | 3.1.21.3 |
| 5131, 5132 | 51598166 | 39 | 4.00E-19 | Burkholderia cepacia R1808 | COG2856: Predicted Zn peptidase [Burkholderia cepacia R1808] | | | |
| 5133, 5134 | 46323894 | 23 | 1.00E-09 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | |
| 5135, 5136 | 48856037 | 45 | 9.00E-11 | Neisseria meningitidis Z2491 | DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] emb CAB85151.1 DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] pir A81821 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) NMA1931 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) | | | 3.2.2.20 |
| 5137, 5138 | 15794814 | 64 | 1.00E-51 | Bacteroides thetaiotaomicron VPI-5482 | NADH dehydrogenase I, chain I [Bacteroides thetaiotaomicron VPI-5482] gb AAO79168.1 NADH dehydrogenase I, chain I [Bacteroides thetaiotaomicron VPI-5482] | | | 1.6.5.3 |
| 5139, 5140 | 29349471 | 48 | 2.00E-37 | Nostoc sp. PCC 7120 | hypothetical protein alr8019 [Nostoc sp. PCC 7120] pir AD2553 hypothetical protein alr8019 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120gamma dbj BAB7349.1 ORF_ID:alr8019-transposase-unknown protein [Nostoc sp. PCC 7120] | | | |
| 5141, 5142 | 17227393 | 65 | 9.00E-35 | Methanocaldococcus jannaschii DSM 2661 | capsular polysaccharide biosynthesis protein M [Methanocaldococcus jannaschii DSM 2661] gb AAB99063.1 capsular polysaccharide biosynthesis protein M [Methanocaldococcus jannaschii DSM 2661] pir B64432 capsular polysaccharide biosynthesis protein M homolog - Methanocaldococcus jannaschii sp Q58459 YA59_METJA Hypothetical glycosyl transferase MJ1059 | | | 2.4.1.- |
| 5145, 5146 | 15669248 | 34 | 2.00E-28 | Cytophaga hutchinsonii | COG4251: Bacteriophytochrome (light-regulated signal transduction histidine kinase) [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 5151, 5152 | 48855659 | 37 | 6.00E-31 | Dechloromonas aromatica RCB | COG3385: FOG: Transposase and inactivated derivatives [Dechloromonas aromatica RCB] | | | |
| 5153, 5154 | 53730535 | 28 | 2.00E-18 | Bdellovibrio bacteriovorus HD100 | DNA-directed RNA polymerase beta chain [Bdellovibrio bacteriovorus HD100] emb CAE80754.1 DNA-directed RNA polymerase beta chain [Bdellovibrio bacteriovorus HD100] | Pseudomonas syringae pv. tomato str. DC3000 section 3 of 21 of the complete genome | 87 | 3.00E-12/2.7.7.6 |

| | | | | | | | | | |
|-------|----------|----|----------|--|--|--|----|----------|----------|
| 5157, | 21674733 | 33 | 3.00E-16 | Chlorobium tepidum TLS | cysteine synthase/cystathionine beta-synthase family protein [Chlorobium tepidum TLS] | | | | 4.2.1.22 |
| 5158 | 48856049 | 45 | 1.00E-31 | Cytophaga hutchinsonii | hypothetical protein Chut02001282 [Cytophaga hutchinsonii] | | | | |
| 5159, | | | | Thermoanaerobacter tengcongensis MB4 | DNA primase (bacterial type) [Thermoanaerobacter tengcongensis MB4] | | | | |
| 5160 | 20808175 | 38 | 6.00E-49 | Bacteroides thetaiotaomicron VPI-5482 | gb AA024950.1 DNA primase (bacterial type) [Thermoanaerobacter tengcongensis MB4] | | | | 2.7.7.- |
| 5161, | | | | Bacteroides thetaiotaomicron VPI-5482 | transcriptional regulator, AraC family [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 5162 | 29347766 | 33 | 1.00E-13 | Bacteroides fragilis YCH46 | putative transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 5163, | | | | Bacteroides fragilis YCH46 | putative transcriptional regulator [Bacteroides fragilis YCH46] | | | | |
| 5164 | 53715260 | 46 | 2.00E-32 | Cytophaga hutchinsonii | COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii] | | | | 6.1.1.4 |
| 5165, | 48855120 | 59 | 2.00E-76 | Geobacter sulfurreducens PCA | cytochrome c family protein [Geobacter sulfurreducens PCA] | | | | |
| 5166 | 39998349 | 47 | 1.00E-44 | uncultured crenarchaeote | gb AAR36650.1 cytochrome c family protein [Geobacter sulfurreducens PCA] | | | | |
| 5167, | | | | Cytophaga hutchinsonii | putative alpha/beta hydrolase [uncultured crenarchaeote] | | | | 3.1.1.1 |
| 5168 | 22797876 | 42 | 3.00E-29 | Cytophaga hutchinsonii | COG1033: Predicted exporters of the RND superfamily [Cytophaga hutchinsonii] | | | | |
| 5169, | | | | Legionella pneumophila str. Lens | hypothetical protein lp1211 [Legionella pneumophila str. Lens] | | | | |
| 5170 | 54295031 | 58 | 7.00E-99 | Oryza sativa (japonica cultivar-group) | emb CAH16351.1 hypothetical protein [Legionella pneumophila str. Lens] | | 88 | 2.00E-10 | 2.3.1.85 |
| 5171, | | | | Geobacter metallireducens GS-15 | ketose-bisphosphate aldolase class-II family-like [Oryza sativa (japonica cultivar-group)] | | | | |
| 5172 | 52077151 | 53 | 1.00E-26 | Geobacter metallireducens GS-15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | | 2.7.3.- |
| 5173, | 48845444 | 46 | 5.00E-52 | Lactobacillus plantarum bacteriophage LP65 | orf143 [Lactobacillus plantarum bacteriophage LP65] | | | | |
| 5174 | 56693191 | 62 | 5.00E-10 | Lactobacillus plantarum bacteriophage LP65 | orf143 [Lactobacillus plantarum bacteriophage LP65] | | | | |

| | | | | | | | | |
|-------|----------|----|----------|--|--|--|--|----------|
| 5185, | 53711742 | 55 | 2.00E-74 | Bacteroides fragilis YCH46 | UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides fragilis YCH46] | | | 6.3.2.15 |
| 5186 | | | | Cytophaga hutchinsonii | COG1843: Flagellar hook capping protein [Cytophaga hutchinsonii] | | | |
| 519, | 48853904 | 52 | 6.00E-32 | Bacteroides thetaiotaomicron VPI-5482 | integrase, site-specific recombinase [Bacteroides thetaiotaomicron VPI-5482] gblAAO77848.1 [integrase, site-specific recombinase [Bacteroides thetaiotaomicron VPI-5482]] | | | |
| 5191, | 29348151 | 34 | 5.00E-38 | Cytophaga hutchinsonii | COG1544: Ribosome-associated protein Y (PSrp-1) [Cytophaga hutchinsonii] | | | |
| 5192 | 48853519 | 42 | 3.00E-12 | Chloroflexus aurantiacus | COG0438: Glycosyltransferase [Chloroflexus aurantiacus] | | | 2.4.1.- |
| 5193, | 53797263 | 30 | 6.00E-39 | Cytophaga hutchinsonii | COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] | | | 2.-.-.- |
| 5194 | 48856035 | 40 | 2.00E-20 | Cytophaga hutchinsonii | COG0196: FAD synthase [Cytophaga hutchinsonii] | | | 2.7.1.26 |
| 5195, | 48854843 | 46 | 2.00E-22 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 5196 | 48831856 | 50 | 1.00E-48 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC10117 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gblAAS68750.1 [conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]] | | | |
| 520, | 45656027 | 40 | 6.00E-50 | Saccharopolyspora spinosa | multi-domain regulatory protein, LuxR family [Saccharopolyspora spinosa] | | | |
| 5201, | 41350162 | 29 | 5.00E-15 | Bacteroides fragilis YCH46 | UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides fragilis YCH46] | | | 6.3.2.15 |
| 521, | 53711742 | 33 | 4.00E-11 | Cytophaga hutchinsonii | COG1251: NAD(P)H-nitrite reductase [Cytophaga hutchinsonii] | | | 1.6.6.4 |
| 5211, | 48855076 | 58 | 3.00E-65 | Cytophaga hutchinsonii | hypothetical protein Chut02002697 [Cytophaga hutchinsonii] | | | |
| 5212 | 48854498 | 55 | 7.00E-96 | Cytophaga hutchinsonii | | | | |

| | | | | | | |
|---------------|----------|----|----------|---|---|----------|
| 5221, 5222 | 12517826 | 57 | 3.00E-48 | Escherichia coli O157:H7 | putative peptidoglycan enzyme [Escherichia coli O157:H7 ref NP_289782.1 putative peptidoglycan enzyme [Escherichia coli O157:H7 EDL933] ref NP_312114.1 putative peptidoglycan enzyme [Escherichia coli O157:H7] pir B85985 probable peptidoglycan enzyme mtgA [imported] - Escherichia coli (strain O157:H7, substrain EDL933) db B837510.1 putative peptidoglycan enzyme [Escherichia coli O157:H7] pir G91139 probable peptidoglycan enzyme [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050952) sp Q8X91 MTGA_ECO57 Monofunctional biosynthetic peptidoglycan transglycosylase (Monofunctional TGase) | 2.4.2.- |
| 5223, 5224 | 30250418 | 31 | 2.00E-21 | Nitrosomonas europaea ATCC 19718 | DEAD/DEAH box helicase [Nitrosomonas europaea ATCC 19718] emb CAD8641.1 DEAD/DEAH box helicase [Nitrosomonas europaea ATCC 19718] | 3.1.21.3 |
| 5229, 5230 | | | | | | 3.4.24.- |
| 523, 524 | 28262674 | 47 | 2.00E-48 | Rickettsia sibirica 246 | DNA ligase [Rickettsia sibirica 246] ref ZP_00142769.1 DNA ligase [Rickettsia sibirica 246] | 6.5.1.2 |
| 5237, 5238 | 42523059 | 54 | 5.00E-58 | Bdellovibrio bacteriovorus HD100 | probable zinc proteinase [Bdellovibrio bacteriovorus HD100] emb CAE79432.1 probable zinc proteinase [Bdellovibrio bacteriovorus HD100] | 3.4.99.- |
| 5245, 5246 | 53711500 | 53 | 3.00E-37 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] db BAD46958.1 two-component system response regulator [Bacteroides fragilis YCH46] | 2.7.3.- |
| 5247, 5248 | 48891723 | 32 | 7.00E-16 | Trichodesmium erythraeum IMS101 | COG0515: Serine/threonine protein kinase [Trichodesmium erythraeum IMS101] | 2.7.1.- |
| 5251, 5252 | 48854312 | 36 | 3.00E-41 | Cytophaga hutchinsonii | COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii] | |
| 5253, 5254 | 29347685 | 61 | 2.00E-61 | Bacteroides thetaiotaomicron VPI-5482 | thymidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77382.1 thymidine kinase [Bacteroides thetaiotaomicron VPI-5482] | 2.7.1.21 |
| 5259, 5260 | 23613218 | 25 | 7.00E-13 | Plasmodium falciparum 3D7 | hypothetical protein [Plasmodium falciparum 3D7] emb CAD51560.1 hypothetical protein [Plasmodium falciparum 3D7] | 3.1.11.- |
| 5263, 5264 | 23128321 | 33 | 4.00E-21 | Nostoc punctiforme PCC 73102 | COG4886: Leucine-rich repeat (LRR) protein [Nostoc punctiforme PCC 73102] | 4.6.1.1 |
| 5265, 5266 | 20807353 | 31 | 7.00E-21 | Thermoanaerobact er tengcongensis MB4 | DNA-directed RNA polymerase specialized sigma subunits, sigma24 homologs [Thermoanaerobacter tengcongensis MB4] gb AAM24128.1 DNA- directed RNA polymerase specialized sigma subunits, sigma24 homologs [Thermoanaerobacter tengcongensis MB4] | |

| | | | | | | | | |
|---------------|----------|----|-----------|---|--|--|-------|-------------------|
| 5267, 5268 | 21674062 | 51 | 2.00E-57 | Chlorobium tepidum TLS | preprotein translocase SecA subunit [Chlorobium tepidum TLS] gb AA072469.1 preprotein translocase SecA subunit [Chlorobium tepidum TLS] | | | |
| 5269, 5270 | 6460190 | 30 | 1.00E-13 | Deinococcus radiodurans | transcriptional regulator, TetR family [Deinococcus radiodurans] pir F75261 transcription regulator, TetR family - Deinococcus radiodurans (strain R1) ref NP_296097.1 transcriptional regulator, TetR family [Deinococcus radiodurans R1] | | | |
| 5271, 5272 | 56476406 | 51 | 5.00E-57 | Azoarcus sp. EbN1 | hypothetical protein ebA1785 [Azoarcus sp. EbN1] emb CAI07094.1 conserved hypothetical protein [Azoarcus sp. EbN1] | | | |
| 5273, 5274 | 48854227 | 51 | 4.00E-13 | Cytophaga hutchinsonii | COG2908: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 5275, 5276 | 17229012 | 67 | 3.00E-40 | Nostoc sp. PCC 7120 | hypothetical protein air1520 [Nostoc sp. PCC 7120] pir AB1996 hypothetical protein air1520 [imported] - Nostoc sp. (strain PCC 7120) db BAB77886.1 air1520 [Nostoc sp. PCC 7120] | | | |
| 5277, 5278 | 15893463 | 59 | 2.00E-54 | Clostridium acetobutylicum ATCC 824 | ABC transporter (ATP-binding protein) [Clostridium acetobutylicum ATCC 824] gb AAK78152.1 ABC transporter (ATP-binding protein) [Clostridium acetobutylicum ATCC 824] pir E96920 ABC transporter (ATP-binding protein) CAC0169 [imported] - Clostridium acetobutylicum | | 1.8-- | |
| 5281, 5282 | 37528152 | 71 | 1.00E-103 | Photobacterium luminescens subsp. laumondii TTO1 | Type I site-specific deoxyribonuclease HsdR [Photobacterium luminescens subsp. laumondii TTO1] emb CAE16694.1 Type I site-specific deoxyribonuclease HsdR [Photobacterium luminescens subsp. laumondii TTO1] | | 81 | 3.00E-18 3.1.21.3 |
| 5287, 5288 | 48855091 | 36 | 2.00E-22 | Cytophaga hutchinsonii | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii] | | | |
| 5291, 5292 | 53713908 | 65 | 2.00E-29 | Bacteroides fragilis YCH46 | hypothetical protein BF2616 [Bacteroides fragilis YCH46] db BAD49366.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 5293, 5294 | 48862321 | 26 | 1.00E-16 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02002532 [Microbulbifer degradans 2-40] putative ABC transporter permease [Bacteroides fragilis YCH46] | | | |
| 5295, 5296 | 53712889 | 30 | 4.00E-09 | Bacteroides fragilis YCH46 | db BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46] | | | |
| 53, 54 | AAW9886 | 7 | 4.00E-13 | | Desc.H. pylori GHPO 1695 protein. Org:Helicobacter pylori | | | 2.1.1.72 |

| | | | | | | | | |
|-------|----------|----|----------|--|---|--|--|----------|
| 5301, | 18311381 | 46 | 4.00E-20 | Clostridium perfringens str. 13 | 30S ribosomal protein S3 [Clostridium perfringens str. 13] dbj BAB82105.1] | | | |
| 5302 | | | | | 30S ribosomal protein S3 [Clostridium perfringens str. 13] sp Q8XHS9 RS3_CLOPE 30S ribosomal protein S3 | | | |
| 5305, | 48853434 | 67 | 2.00E-40 | Cytophaga hutchinsonii | COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] | | | 2.7.7.24 |
| 5306 | | | | | arsenate reductase [Rhodopirellula baltica SH 1] emb CAD77194.1] | | | |
| 5309, | 32476822 | 53 | 2.00E-24 | Rhodopirellula baltica SH 1 | arsenate reductase [Pirellula sp.] | | | 1.97.1.5 |
| 5310 | | | | | | | | |
| | | | | Bacillus thuringiensis serovar konkukian str. 97-27 | hypothetical protein BT9727_1747 [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA62754.1] hypothetical protein BT9727_1747 [Bacillus thuringiensis serovar konkukian str. 97-27] | | | |
| 531, | 49480552 | 32 | 4.00E-16 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 5311, | 48855191 | 48 | 6.00E-53 | | | | | |
| 5312 | | | | Bacteroides fragilis YCH46 | putative two-component system sensor protein without kinase domain [Bacteroides fragilis YCH46] dbj BAD48617.1] putative two-component system sensor protein without kinase domain [Bacteroides fragilis YCH46] | | | 2.7.3.- |
| 5321, | 53713159 | 37 | 6.00E-25 | | hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD36698.1] conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | |
| 5322 | | | | Thermotoga maritima MSB8 | | | | |
| 5323, | 15644379 | 38 | 1.00E-09 | Cytophaga hutchinsonii | COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii] | | | 3.4.24.- |
| 5325, | 48856042 | 56 | 4.00E-39 | | | | | |
| 5326 | | | | Cytophaga hutchinsonii | COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii] | | | 3.4.24.- |
| 5327, | 48856042 | 58 | 3.00E-55 | | putative carbamoyl-phosphate synthase large chain [Clostridium tetani E88] gb AAO36241.1] putative carbamoyl-phosphate synthase large chain [Clostridium tetani E88] | | | 6.3.4.13 |
| 5328 | | | | Clostridium tetani E88 | hypothetical protein mli7009 [Mesorhizobium loti MAFF303099] dbj BAB53194.1] mli7009 [Mesorhizobium loti MAFF303099] | | | |
| 5333, | 28211360 | 38 | 4.00E-26 | Mesorhizobium loti MAFF303099 | COG1112: Superfamily I DNA and RNA helicases and helicase subunits [Ralstonia eutropha JMP134] | | | 2.7.7.- |
| 5334 | | | | Ralstonia eutropha JMP134 | COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulifer degradans 2-40] | | | |
| 5335, | 13475838 | 35 | 1.00E-26 | | | | | |
| 5336 | | | | | | | | |
| 5341, | 53761281 | 35 | 8.00E-18 | Microbulifer degradans 2-40 | | | | |
| 5342 | | | | | | | | |
| 5345, | 48864231 | 28 | 1.00E-15 | | | | | |
| 5346 | | | | | | | | |

| | | | | | | | | | |
|-------|----------|----|----------|--|--|--|--|--|-----------|
| 5347, | 20808572 | 49 | 3.00E-62 | Thermoanaerobacter tengcongensis | Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains [Thermoanaerobacter tengcongensis MB4] gb AAM25347.1 Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains [Thermoanaerobacter tengcongensis MB4] sp Q8R841 GLMS_THETN | | | | 2.6.1.16 |
| 5348 | | | | | Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase) | | | | |
| 5349, | 48856843 | 50 | 5.00E-73 | Cytophaga hutchinsonii | COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases | | | | 6.2.1.1 |
| 5350 | | | | | | | | | |
| 5351, | 48732838 | 46 | 1.00E-20 | Pseudomonas fluorescens PfO-1 | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Pseudomonas fluorescens PfO-1] | | | | |
| 5352 | | | | | hypothetical protein MJ0570 [Methanocaldococcus jannaschii DSM 2661] gb AAB98564.1 conserved hypothetical protein [Methanocaldococcus jannaschii DSM 2661] pir B64371 hypothetical protein MJ0570 - Methanococcus jannaschii sp Q57990 Y570_METJA Hypothetical protein MJ0570 | | | | |
| 5355, | 15668750 | 34 | 6.00E-26 | Methanocaldococcus jannaschii DSM 2661 | | | | | |
| 5356 | | | | | | | | | |
| 5357, | | | | Chromobacterium violaceum ATCC 12472 | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_900582.1 hypothetical protein CV0912 [Chromobacterium violaceum ATCC 12472] | | | | 1.14.13.- |
| 5358 | 34102220 | 36 | 6.00E-29 | | succinoglycan biosynthesis protein exoA [Clostridium tetani E88] gb AAO36740.1 succinoglycan biosynthesis protein exoA [Clostridium tetani E88] | | | | |
| 5359, | | | | Clostridium tetani E88 | | | | | |
| 5360 | 28211859 | 41 | 9.00E-27 | Bacteriophage RM | putative glycosyltransferases [Bacteriophage RM 378] | | | | 2.4.1.- |
| 5365, | 30044003 | 25 | 2.00E-12 | | | | | | |
| 5366 | | | | | | | | | |
| 5367, | | | | Chloroflexus aurantiacus | COG0438: Glycosyltransferase [Chloroflexus aurantiacus] | | | | |
| 5368 | 53794669 | 25 | 7.00E-10 | | | | | | |
| | | | | | | | | | |
| 5369, | | | | | At5g28460/F21B23_120 [Arabidopsis thaliana] gb AAK97697.1 AT5g28460/F21B23_120 [Arabidopsis thaliana] ref NP_680234.1 pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] gb AAF88002.1 contains similarity to PPR family PF01535 (Domain of unknown function), score=340.5, E=1.9e-98, N=2 [Arabidopsis thaliana] | | | | |
| 5370 | 27363272 | 26 | 1.00E-15 | Arabidopsis thaliana | | | | | |
| 537, | | | | Psychrobacter sp. 273-4 | COG2352: Phosphoenolpyruvate carboxylase [Psychrobacter sp. 273-4] | | | | 4.1.1.31 |
| 538 | 52853863 | 37 | 6.00E-25 | Microbulifer degradans 2-40 | COG2755: Lysophospholipase L1 and related esterases [Microbulifer degradans 2-40] | | | | |
| 5371, | | | | | | | | | |
| 5372 | 48863713 | 61 | 8.00E-22 | Bacteroides fragilis | peptide deformylase [Bacteroides fragilis YCH46] dbj BAD48431.1 peptide deformylase [Bacteroides fragilis YCH46] | | | | 3.5.1.88 |
| 5373, | | | | | | | | | |
| 5374 | 53712973 | 42 | 1.00E-27 | YCH46 | | | | | |

| | | | | | | | | |
|-------|----------|----|----------|----------------------------------|--|---|-------------|----------|
| 5375, | 53714080 | 36 | 5.00E-32 | Bacteroides fragilis YCH46 | tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | |
| 5376 | | | | | dbj BAD49538.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | |
| 5377, | 48854369 | 38 | 1.00E-28 | Cytophaga hutchinsonii | COG0608: Single-stranded DNA-specific exonuclease [Cytophaga hutchinsonii] | | | 3.1.- |
| 5378 | | | | | hypothetical protein MA1679 [Methanosarcina acetivorans C2A] | | | |
| 5379, | | | | | gb AAM05086.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | | | |
| 5380 | 20090531 | 42 | 2.00E-20 | Microbulbifer degradans 2-40 | COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulbifer degradans 2-40] | | | |
| 5383, | 48864231 | 31 | 1.00E-22 | Wolinella succinogenes DSM 1740 | ADP-HEPTOSE-LPS HEPTOSYLTRANSFERASE II (RFAF) [Wolinella succinogenes DSM 1740] emb CAE10509.1 ADP-HEPTOSE-LPS HEPTOSYLTRANSFERASE II (RFAF) [Wolinella succinogenes] | | | |
| 5384 | | | | | | | | |
| 5389, | 34557794 | 31 | 1.00E-14 | | | | | |
| 5390 | | | | | | | | |
| 539, | | | | | | | | |
| 540 | 48855609 | 77 | 2.00E-63 | Cytophaga hutchinsonii | COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii] | Bacteroides fragilis YCH46 DNA, complete genome | 93 4.00E-07 | |
| 5395, | | | | | hypothetical protein aq_1006 [Aquifex aeolicus VF5] gb AAC07092.1 | | | |
| 5396 | | | | | hypothetical protein [Aquifex aeolicus VF5] pir A70387 conserved | | | |
| 5399, | 15606308 | 22 | 1.00E-08 | Aquifex aeolicus VF5 | hypothetical protein aq_1006 - Aquifex aeolicus sp O67124 RA50_AQUAE Probable DNA double-strand break repair rad50 ATPase | | | |
| 5400 | 48856125 | 37 | 2.00E-28 | Cytophaga hutchinsonii | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] | | | |
| 5401, | | | | | MutT/NUDIX family protein [Burkholderia pseudomallei K96243] | | | |
| 5402 | 53717978 | 30 | 3.00E-10 | Burkholderia pseudomallei K96243 | emb CAH34326.1 MutT/NUDIX family protein [Burkholderia pseudomallei K96243] | | | 3.6.1.- |
| 5405, | | | | | | | | |
| 5406 | 48854498 | 55 | 5.00E-39 | Cytophaga hutchinsonii | COG0325: Predicted enzyme with a TIM-barrel fold [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 5413, | | | | | | | | |
| 5414 | 15384032 | 32 | 4.00E-12 | uncultured crenarchaeote 74A4 | xanthine-guanine phosphoribosyltransferase [uncultured crenarchaeote 74A4] | | | 2.4.2.- |
| 5415, | | | | | | | | |
| 5416 | 48854158 | 52 | 2.00E-31 | Cytophaga hutchinsonii | COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii] | | | 1.11.1.1 |
| 5419, | | | | | | | | |
| 5420 | 48855100 | 55 | 1.00E-27 | Cytophaga hutchinsonii | COG0424: Nucleotide-binding protein implicated in inhibition of septum formation [Cytophaga hutchinsonii] | | | 0 |
| 5421, | | | | | | | | |
| 5422 | 48855348 | 26 | 4.00E-09 | Cytophaga hutchinsonii | hypothetical protein Chut02001679 [Cytophaga hutchinsonii] | | | |
| 5427, | | | | | deoxyribonuclease, TatD family [Geobacter sulfurreducens PCA] | | | |
| 5428 | 39997584 | 43 | 3.00E-57 | Geobacter sulfurreducens PCA | gb AAR35862.1 deoxyribonuclease, TatD family [Geobacter sulfurreducens PCA] | | | 3.1.21.- |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|----|----------|
| 543, 544 | 29346396 | 32 | 5.00E-23 | Bacteroides thetaiotaomicron VPI-5482 | conserved hypothetical protein, putative DNA-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76093.1 conserved hypothetical protein, putative DNA-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 5437, 5438 | 53715101 | 35 | 2.00E-31 | Bacteroides fragilis YCH46 | hypothetical protein BF3817 [Bacteroides fragilis YCH46] dbj BAD50559.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 5439, 5440 | 48853176 | 35 | 5.00E-38 | Ferroplasma acidarmanus | COG0624: Acetylornithine deacetylase/Succinyl-L-diaminopimelate desuccinylase and related deacylases [Ferroplasma acidarmanus] | | | 3.5.1.16 |
| 5441, 5442 | 52550513 | 36 | 2.00E-08 | uncultured archaeon GZfos9D8 | conserved hypothetical protein [uncultured archaeon GZfos9D8] | | | |
| 5443, 5444 | 48855541 | 79 | 2.00E-62 | Cytophaga hutchinsonii | COG1875: Predicted ATPase related to phosphate starvation-inducible protein PhoH [Cytophaga hutchinsonii] | Chlamydia muridarum section 27 of 85 of the complete genome | 93 | 1.00E-06 |
| 545, 546 | 48853731 | 41 | 2.00E-22 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 5453, 5454 | 17231921 | 40 | 3.00E-53 | Nostoc sp. PCC 7120 | hypothetical protein al4429 [Nostoc sp. PCC 7120] dbj BAB76128.1 hlpA (Nostoc sp. PCC 7120) pir AE2359 hypothetical protein hlpA [imported] - Nostoc sp. (strain PCC 7120) | | | |
| 5455, 5456 | 23016842 | 40 | 8.00E-47 | Magnetospirillum magnetotacticum MS-1 | COG0367: Asparagine synthase (glutamine-hydrolyzing) [Magnetospirillum magnetotacticum MS-1] | | | 6.3.5.4 |
| 5457, 5458 | 48855191 | 48 | 2.00E-53 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] | | | 2.7.3.- |

| | | | | | | | | |
|--|--|----------------------|--|--|---|--|--|---------------------------|
| 5459, 5460 5461, 5462 5463, 5464 5465, 5466 | 37528266 48856605 48853925 48853434 | 28 67 39 69 | 3.00E-11 4.00E-69 3.00E-25 1.00E-85 | Photorhabdus luminescens subsp. laumondii TTO1 Cytophaga hutchinsonii Cytophaga hutchinsonii Cytophaga hutchinsonii | Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930575.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930493.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930331.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928792.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928083.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_927821.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16814.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15731.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15643.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15473.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE13790.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE13033.1 Transposase, IS630 COG2171: Tetrahydrodipicolinate N-succinyltransferase [Cytophaga hutchinsonii] COG3124: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] | | | 2.3.1.11 7 2.7.7.24 |
| 5467, 5468 | 52840856 | 50 | 3.00E-31 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | glyoxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123011.1 hypothetical protein [pp0673 [Legionella pneumophila str. Paris] gb AAU26708.1 glyoxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH11821.1 hypothetical protein [Legionella pneumophila str. Paris] ABC transporter, ATP-binding/permease protein [Brucella suis 1330] gb AAN29385.1 ABC transporter, ATP-binding/permease protein [Brucella suis 1330] COG0026: Phosphoribosylaminimidazole carboxylase (NCAIR synthetase) [Cytophaga hutchinsonii] | | | |
| 5469, 5470 547, 548 | 23501343 48854305 | 31 44 | 2.00E-29 2.00E-27 | Brucella suis 1330 Cytophaga hutchinsonii | | | | 4.1.1.21 |
| 5475, 5476 | 53715782 | 62 | 1.00E-79 | Bacteroides fragilis YCH46 | methionyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD51240.1 methionyl-tRNA synthetase [Bacteroides fragilis YCH46] | | Mus musculus cDNA clone IMAGE:30025832 | 81 1.00E-41 6.1.1.10 |
| 5477, 5478 | 23126368 | 51 | 3.00E-61 | Nostoc punctiforme PCC 73102 | COG3391: Uncharacterized conserved protein [Nostoc punctiforme PCC 73102] | | | |

| | | | | | | | | |
|-------|----------|----|----------|---|---|--|--|----------|
| 5481, | 48860370 | 41 | 2.00E-30 | Clostridium thermocellum ATCC 27405 | COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Clostridium thermocellum ATCC 27405] | | | 2.7.3.- |
| 5482 | | | | Thermoanaerobacter tengcongensis MB4 | hypothetical protein TTE0217 [Thermoanaerobacter tengcongensis MB4] | | | |
| 5485, | 20806743 | 43 | 4.00E-60 | MB4 | gb AAAM23518.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4] | | | |
| 5486 | | | | Shewanella oneidensis MR-1 | peptidase, M16 family [Shewanella oneidensis MR-1] | | | 3.4.-.- |
| 5487, | 24375064 | 40 | 6.00E-48 | oneidensis MR-1 | peptidase, M16 family [Shewanella oneidensis MR-1] | | | |
| 5489, | 45526941 | 53 | 4.00E-36 | Crocospaera watsonii WH 8501 | COG0058: Glucan phosphorylase [Crocospaera watsonii WH 8501] | | | 2.4.1.1 |
| 5490 | | | | Cytophaga hutchinsonii | COG1530: Ribonucleases G and E [Cytophaga hutchinsonii] | | | 3.1.4.- |
| 5493, | 48854348 | 46 | 1.00E-32 | Cytophaga hutchinsonii | | | | |
| 5494 | | | | Cytophaga hutchinsonii | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | | | |
| 5499, | 48853518 | 38 | 2.00E-41 | Ralstonia solanacearum | hypothetical protein RS02260 [Ralstonia solanacearum GMI1000] | | | |
| 5500 | | | | Ralstonia solanacearum GMI1000 | emb CAD13614.1 CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] | | | |
| 5503, | 17544805 | 58 | 1.00E-18 | Clostridium tetani | DNA mismatch repair protein mutS [Clostridium tetani E88] gb AAO35868.1 | | | |
| 5504 | | | | Clostridium tetani E88 | DNA mismatch repair protein mutS [Clostridium tetani E88] | | | |
| 551, | 28210987 | 47 | 3.00E-42 | Clostridium thermocellum ATCC 27405 | sp Q895H2 MUTS_CLOTE DNA mismatch repair protein mutS | | | |
| 552 | | | | Clostridium thermocellum ATCC 27405 | COG0417: DNA polymerase elongation subunit (family B) [Clostridium thermocellum ATCC 27405] | | | |
| 5511, | 48860541 | 25 | 2.00E-12 | Cytophaga hutchinsonii | COG1796: DNA polymerase IV (family X) [Cytophaga hutchinsonii] | | | 2.7.7.7 |
| 5512 | | | | Cytophaga hutchinsonii | hypothetical protein CE0259 [Corynebacterium efficiens YS-314] | | | |
| 5515, | 48853823 | 39 | 4.00E-36 | Corynebacterium efficiens YS-314 | dbj BAC17069.1 conserved hypothetical protein [Corynebacterium efficiens YS-314] | | | 3.1.21.3 |
| 5517, | 25026815 | 38 | 1.00E-23 | Pyrococcus furiosus DSM 3638 | transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638] | | | |
| 5518 | | | | Pyrococcus furiosus DSM 3638 | gb AAL80615.1 transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638] | | | |
| 5519, | 18976863 | 40 | 5.00E-30 | Pyrococcus furiosus DSM 3638 | transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638] | | | |
| 5520 | | | | Pyrococcus furiosus DSM 3638 | gb AAL80615.1 transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638] | | | |
| 5521, | 18976863 | 40 | 5.00E-30 | Pyrococcus furiosus DSM 3638 | transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638] | | | |
| 5522 | | | | Methanothermobacter thermautotrophicus str. Delta H | phytoene dehydrogenase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB86273.1 phytoene dehydrogenase [Methanothermobacter thermautotrophicus str. Delta H] pir E59108 phytoene dehydrogenase - Methanothermobacter thermautotrophicum (strain Delta H) | | | |
| 5525, | 15679795 | 42 | 2.00E-55 | str. Delta H | | | | |
| 5526 | | | | | | | | |

| | | | | | | | | | |
|-------|----------|----|----------|---|--|--|--|--|----------|
| 5527, | 29348887 | 39 | 8.00E-33 | Bacteroides thetataoamicon | integrase [Bacteroides thetataoamicon VPI-5482] gb AAO78584.1 | | | | |
| 5528 | | | | VPI-5482 | Integrase [Bacteroides thetataoamicon VPI-5482] | | | | |
| 5529, | | | | Cytophaga | hypothetical protein Chut02003027 [Cytophaga hutchinsonii] | | | | |
| 5530 | 48854354 | 47 | 7.00E-26 | hutchinsonii | | | | | |
| 5531, | | | | | GALACTOSYL TRANSFERASE, GDP-MANNOSE | | | | |
| 5532 | 34556501 | 42 | 1.00E-47 | Wolinella succinogenes DSM | PYROPHOSPHORYLASE, PHOSPHOMANNOMUTASE, UDP-GALACTOSE 4-EPIMERASE, GALACTOSYL TRANSFERASE, NUCLEOTIDE SUGAR DEHYDROGENASE, NUCLEOTIDE SUGAR EPIMERASE, AND PUTATIVE EPIMERASE/DEHYDRATASE GENES; AND UNKNOWN GENES [Wolinella succinogenes DSM 1740] emb CAE09216.1 GALACTOSYL TRANSFERASE, GDP-MANNOSE | | | | 6.3.5.4 |
| 5533, | | | | | PYROPHOSPHORYLASE, PHOSPHOMANNOMUTASE, UDP-GALACTOSE | | | | |
| 5534 | 42523194 | 41 | 3.00E-45 | Bdellovibrio bacteriovorus HD100 | 4-EPIMERASE, GALACTOSYL TRANSFERASE, NUCLEOTIDE SUGAR DEHYDROGENASE, NUCLEOTIDE SUGAR EPIMERASE, AND PUTATIVE EPIMERASE/DEHYDRATASE GENES; AND UNKNOWN GENES [Wolinella succinogenes] | | | | 5.1.3.- |
| 5535, | | | | | UDP-N-acetyl-D-quinovosamine 4-epimerase [Bdellovibrio bacteriovorus HD100] emb CAE79567.1 UDP-N-acetyl-D-quinovosamine 4-epimerase [Bdellovibrio bacteriovorus HD100] | | | | |
| 5536 | 15894081 | 34 | 6.00E-29 | Clostridium acetobutylicum ATCC 824 | Nucleoside-diphosphate-sugar epimerase (UDP-glucose 4-epimerase) [Clostridium acetobutylicum ATCC 824] gb AAK78770.1 Nucleoside- diphosphate-sugar epimerase (UDP-glucose 4-epimerase) [Clostridium acetobutylicum ATCC 824] pir [G96997 nucleoside-diphosphate-sugar epimerase (UDP-glucose 4-epimerase) [imported] - Clostridium acetobutylicum] | | | | 5.1.3.2 |
| 5541, | | | | | arsenate reductase [Rhodopirella baltica SH 1] emb CAD77194.1 | | | | 1.97.1.5 |
| 5542 | 32476822 | 53 | 2.00E-24 | Rhodopirella baltica SH 1 | arsenate reductase [Pirella sp.] | | | | |
| 5545, | | | | | putative GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD48795.1 | | | | |
| 5546 | 53713337 | 66 | 2.00E-39 | Bacteroides fragilis YCH46 | putative GTP-binding protein [Bacteroides fragilis YCH46] | | | | |
| 5547, | | | | | COG0774: UDP-3-O-acyl-N-acetylglucosamine deacetylase [Cytophaga hutchinsonii] | | | | 3.5.1.- |
| 5548 | 48854755 | 56 | 7.00E-65 | Cytophaga hutchinsonii | | | | | |
| 5551, | | | | | COG5368: Uncharacterized protein conserved in bacteria [Xylella fastidiosa Ann-1] | | | | |
| 5552 | 52856886 | 49 | 4.00E-19 | Xylella fastidiosa Ann-1 | hypothetical protein BF0783 [Bacteroides fragilis YCH46] dbj BAD47534.1 | | | | |
| 5553, | | | | | hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 5554 | 53712076 | 32 | 1.00E-15 | Bacteroides fragilis YCH46 | | | | | |
| 5555, | | | | | COG0594: RNase P protein component [Cytophaga hutchinsonii] | | | | |
| 5556 | 48853808 | 36 | 6.00E-11 | Cytophaga hutchinsonii | | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|--|----------|
| 5559, 5560 | 25026974 | 42 | 2.00E-24 | Corynebacterium efficiens YS-314 | hypothetical protein CE0418 [Corynebacterium efficiens YS-314] dbj BAC17228.1 hypothetical protein [Corynebacterium efficiens YS-314] | | | | |
| 5561, 5562 | 53712631 | 55 | 4.00E-40 | Bacteroides fragilis YCH46 | tyrosine type site-specific recombinase [Bacteroides fragilis dbj BAD48089.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] | | | | |
| 5569, 5570 | 54296325 | 30 | 3.00E-19 | Legionella pneumophila str. Paris | hypothetical protein lpp0354 [Legionella pneumophila str. Paris] emb CAH11502.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | |
| 557, 558 | 48853718 | 37 | 1.00E-19 | Cytophaga hutchinsonii | COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii] | | | | |
| 5577, 5578 | 48855087 | 32 | 6.00E-18 | Cytophaga hutchinsonii | COG1773: Rubredoxin [Cytophaga hutchinsonii] | | | | |
| 5583, 5584 | 48855659 | 40 | 2.00E-47 | Cytophaga hutchinsonii | COG4251: Bacteriophytochrome (light-regulated signal transduction histidine kinase) [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 5585, 5586 | 22996431 | 29 | 5.00E-16 | Xylella fastidiosa Ann-1 | COG4924: Uncharacterized protein conserved in bacteria [Xylella fastidiosa Ann-1] | | | | |
| 5589, 5590 | 48846049 | 41 | 2.00E-38 | Geobacter metallireducens GS-15 | COG0587: DNA polymerase III, alpha subunit [Geobacter metallireducens GS-15] | | | | 2.7.7.7 |
| 5591, 5592 | 32471828 | 52 | 1.00E-44 | Rhodopirellula baltica SH 1 | glutathione peroxidase [Rhodopirellula baltica SH 1] emb CAD72506.1 glutathione peroxidase [Pirellula sp.] | | | | 1.11.1.9 |
| 5595, 5596 | 9715733 | 36 | 9.00E-13 | Anabaena sp. 90 | peptide synthetase [Anabaena sp. 90] | | | | |
| 5597, 5598 | 52842392 | 37 | 8.00E-41 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | peptide synthetase, non-ribosomal [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gbj AAU28244.1 peptide synthetase, non- ribosomal [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | | 2.1.2.9 |
| 5599, 5600 | 55379401 | 28 | 1.00E-19 | Haloarcula marismortui ATCC 43049 | N(2)N(2)-dimethylguanosine tRNA methyltransferase [Haloarcula marismortui ATCC 43049] gbj AAV47545.1 N(2)N(2)-dimethylguanosine tRNA methyltransferase [Haloarcula marismortui ATCC 43049] | | | | 2.1.1.32 |
| 5601, 5602 | 15644050 | 38 | 3.00E-15 | Thermotoga maritima MSB8 | hypothetical protein TM1295 [Thermotoga maritima MSB8] gbj AAD36369.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir F72272 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | | |
| 5603, 5604 | 48855841 | 52 | 1.00E-62 | Cytophaga hutchinsonii | COG0380: Trehalose-6-phosphate synthase [Cytophaga hutchinsonii] | | | | 2.4.1.15 |
| 5605, 5606 | 48856924 | 29 | 4.00E-25 | Cytophaga hutchinsonii | COG1538: Outer membrane protein [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|--|--|----------------------|--|--|--|--|--|--|---------------------|
| 5609, 5610 5615, 5616 5617, 5618 5619, 5620 | 48477477 37222112 1711282 46019862 | 41 54 39 33 | 2.00E-41 2.00E-83 9.00E-21 2.00E-23 | Picrophilus torridus DSM 9790 uncultured bacterium Bacillus circulans Streptococcus thermophilus | protein translation initiation factor 2 subunit alpha [Picrophilus torridus DSM 9790] gb AAT42990.1 protein translation initiation factor 2 subunit alpha [Picrophilus torridus DSM 9790] Uvs063 [uncultured bacterium] chitinase C [Bacillus circulans] putative endonuclease [Streptococcus thermophilus] UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Thermosynechococcus elongatus BP-1] dbj BAC09361.1 UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Thermosynechococcus elongatus BP-1] sp Q8DHY4 MURG_SYNEL UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (Undecaprenyl-PP-MurNAc-pentapeptide-UDP-GlcNAc GlcNAc transferase) | | | | 3.2.1.14 |
| 5621, 5622 5623, 5624 5627, 5628 563, 564 | 22299352 48855461 48855703 48855887 | 31 26 33 57 | 5.00E-10 2.00E-08 2.00E-25 4.00E-24 | Thermosynechococcus elongatus BP-1 Cytophaga hutchinsonii Cytophaga hutchinsonii Cytophaga hutchinsonii | COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Cytophaga hutchinsonii] COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii] COG0261: Ribosomal protein L21 [Cytophaga hutchinsonii] | | | | 2.4.1.- 2.7.3.- |
| 5633, 5634 5637, 5638 | 29345869 48854339 | 31 55 | 6.00E-27 4.00E-86 | Bacteroides thetaiotaomicron VPI-5482 Cytophaga hutchinsonii | beta-hexosaminidase precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO75566.1 beta-hexosaminidase precursor [Bacteroides thetaiotaomicron VPI-5482] COG0178: Exonuclease ATPase subunit [Cytophaga hutchinsonii] | | | | 3.2.1.52 |
| 5639, 5640 5649, 5650 | 53714567 29348537 | 46 55 | 4.00E-43 9.00E-36 | Bacteroides fragilis YCH46 Bacteroides thetaiotaomicron VPI-5482 | septum formation protein Maf [Bacteroides fragilis YCH46] dbj BAD50025.1 septum formation protein Maf [Bacteroides fragilis YCH46] putative xanthosine triphosphate pyrophosphatase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78234.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides thetaiotaomicron VPI-5482] sensory transduction histidine kinase [Methanothermobacter thermoautotrophicus str. Delta H] gb AAB85400.1 sensory transduction histidine kinase [Methanothermobacter thermoautotrophicus str. Delta H] pir G69220 sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Delta H) | | | | 2.7.7.56 2.7.3.- |
| 5651, 5652 | 15678922 | 37 | 7.00E-34 | thermoautotrophicus str. Delta H | | | | | 2.7.3.- |

| | | | | | | | | | |
|---------------|--------------|----|----------|---|--|--|--|--|----------|
| 5653, 5654 | 55978296 | 32 | 3.00E-10 | Thermus thermophilus HB8 | hypothetical protein TTHB113 [Thermus thermophilus HB8] dbj[BAD71909.1] conserved hypothetical protein [Thermus thermophilus HB8] | | | | |
| 5655, 5656 | 23124336 | 48 | 2.00E-56 | Nostoc punctiforme PCC 73102 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 5657, 5658 | 48854565 | 42 | 2.00E-26 | Cytophaga hutchinsonii | COG0431: Predicted flavoprotein [Cytophaga hutchinsonii] | | | | |
| 5659, 5660 | 56962495 | 38 | 9.00E-25 | Bacillus clausii KSM-K16 | two-component response regulator of nitrate reduction [Bacillus clausii KSM-K16] dbj[BAD63260.1] two-component response regulator of nitrate reduction [Bacillus clausii KSM-K16] | | | | |
| 5661, 5662 | 29349422 | 56 | 4.00E-45 | Bacteroides thetaiotaomicron VPI-5482 | putative type II restriction endonuclease [Bacteroides thetaiotaomicron VPI-5482] gb[AAO79119.1] putative type II restriction endonuclease [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.1.21.4 |
| 5669, 5670 | 52550550 | 37 | 4.00E-35 | uncultured archaeon GZfos9E5 | two-component hybrid sensor and regulator [uncultured archaeon GZfos9E5] | | | | 2.7.3.- |
| 5671, 5672 | 53714385 | 42 | 5.00E-18 | Bacteroides fragilis YCH46 | putative glycosylhydrolase [Bacteroides fragilis YCH46] dbj[BAD49843.1] putative glycosylhydrolase [Bacteroides fragilis YCH46] | | | | 3.2.1.17 |
| 5673, 5674 | 9837394 | 40 | 1.00E-07 | Flavobacterium johnsoniae | Flo10 [Flavobacterium johnsoniae] | | | | 3.6.3.4 |
| 5675, 5676 | 9837394 | 40 | 1.00E-07 | Flavobacterium johnsoniae | Flo10 [Flavobacterium johnsoniae] | | | | 3.6.3.4 |
| 5685, 5686 | 33595845 | 50 | 3.00E-28 | Bordetella parapertussis 12822 | hypothetical protein BPP1172 [Bordetella parapertussis 12822] ref[NP_887934.1] hypothetical protein BB1388 [Bordetella bronchiseptica RB50] emb[CAE36473.1] conserved hypothetical protein [Bordetella parapertussis] emb[CAE31886.1] conserved hypothetical protein [Bordetella bronchiseptica RB50] | | | | |
| 5687, 5688 | ABB8477 1 | 46 | 9.00E-57 | | Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org: Cytophaga hutchinsonii | | | | 2.7.7.7 |
| 5689, 5690 | 15383990 | 60 | 2.00E-59 | uncultured crenarchaeote 74A4 | cysteinyI-tRNA synthetase [uncultured crenarchaeote 74A4] | | | | 6.1.1.16 |
| 5691, 5692 | 48855366 | 69 | 2.00E-23 | Cytophaga hutchinsonii | COG3209: Rhs family protein [Cytophaga hutchinsonii] | | | | |
| 5695, 5696 | 29349387 | 50 | 1.00E-28 | Bacteroides thetaiotaomicron VPI-5482 | putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb[AAO79084.1] putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.1.1.- |
| 5697, 5698 | 48853518 | 40 | 7.00E-31 | Cytophaga hutchinsonii | COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|------------------------------------|---|--|--|--|----------|
| 57, 58 | 2281663 | 54 | 3.00E-60 | Flavobacterium johnsoniae | gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [imported] - Flavobacterium johnsoniae | | | | 1.8.-.- |
| 5701, | | | | Cytophaga | COG4867: Uncharacterized protein with a von Willebrand factor type A (VWA) domain [Cytophaga hutchinsonii] | | | | |
| 5702 | 48854298 | 58 | 4.00E-87 | hutchinsonii | COG1083: CMP-N-acetylneuraminic acid synthetase [Cytophaga hutchinsonii] | | | | 2.7.7.43 |
| 5705, | 48854593 | 51 | 2.00E-58 | Cytophaga hutchinsonii | COG1875: Predicted ATPase related to phosphate starvation-inducible protein PhoH [Cytophaga hutchinsonii] | | | | |
| 5706 | | | | Cytophaga hutchinsonii | putative helicase [Acinetobacter sp. ADP1] emb CAG68837.1 putative helicase [Acinetobacter sp. ADP1] | | | | |
| 5707 | 48855541 | 73 | 1.00E-115 | hutchinsonii | COG0196: FAD synthase [Cytophaga hutchinsonii] | | | | 2.7.1.26 |
| 5708 | 50085149 | 41 | 1.00E-27 | ADP1 | COG2166: SufE protein probably involved in Fe-S center assembly [Cytophaga hutchinsonii] | | | | |
| 5711, | 48854843 | 44 | 4.00E-47 | Cytophaga hutchinsonii | hypothetical protein ST2175 [Sulfolobus tokodaii str. 7] dbj BAB67280.1 245aa long conserved hypothetical protein [Sulfolobus tokodaii str. 7] | | | | 2.1.1.79 |
| 5712 | 15922502 | 27 | 1.00E-13 | str. 7 | COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | | 1.8.-.- |
| 5713, | 48856329 | 54 | 1.00E-51 | Cytophaga hutchinsonii | COG1109: Phosphomannomutase [Cytophaga hutchinsonii] | | | | 5.4.2.8 |
| 5714 | 48854793 | 56 | 2.00E-97 | Cytophaga hutchinsonii | hypothetical protein Bd0790 [Bdellovibrio bacteriovorus HD100] emb CAE78740.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100] | | | | |
| 5715, | | | | Sulfolobus tokodaii | sensory transduction histidine kinase [Methanosarcina acetivorans C2A] | | | | 2.7.3.- |
| 5716 | 42522367 | 53 | 2.00E-20 | HD100 | hypothetical protein Meth02003909 [Methanosarcina barkeri str. fusaro] | | | | |
| 5719, | | | | Methanosarcina acetivorans C2A | hypothetical protein SSO3050 [Sulfolobus solfataricus P2] gb AAK43150.1 | | | | |
| 5720 | 20089441 | 35 | 2.00E-29 | acetivorans C2A | Hypothetical protein SSO3050 [Sulfolobus solfataricus P2] pir G90486 | | | | |
| 5725, | | | | Methanosarcina barkeri str. fusaro | hypothetical protein SSO3050 [imported] - Sulfolobus solfataricus | | | | |
| 5726 | | | | Sulfolobus solfataricus P2 | probable pilin biogenesis protein [Clostridium perfringens str. 13] dbj BAB81991.1 probable pilin biogenesis protein [Clostridium perfringens str. 13] | | | | |
| 573, | | | | Clostridium perfringens str. 13 | COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii] | | | | |
| 574 | 18311267 | 34 | 5.00E-24 | perfringens str. 13 | transcription-repair coupling factor [Chlorobium tepidum TLS] | | | | |
| 5731, | | | | Cytophaga hutchinsonii | transcription-repair coupling factor [Chlorobium tepidum TLS] | | | | |
| 5732 | 48854732 | 25 | 8.00E-18 | hutchinsonii | transcription-repair coupling factor [Chlorobium tepidum TLS] | | | | |
| 5733, | | | | Chlorobium tepidum TLS | transcription-repair coupling factor [Chlorobium tepidum TLS] | | | | |
| 5734 | 21673485 | 25 | 1.00E-20 | tepidum TLS | transcription-repair coupling factor [Chlorobium tepidum TLS] | | | | |

| | | | | | | | | |
|---------------|----------|----|-----------|---|--|--|--|----------|
| 5751, 5752 | 53715815 | 31 | 2.00E-42 | Bacteroides fragilis YCH46 | two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] dbj BAD51273.1 two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] | | | 2.7.3.- |
| 5753, 5754 | 29347164 | 37 | 3.00E-42 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482] gb AAO76861.1 two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 5757, 5758 | 48856549 | 66 | 1.00E-104 | Cytophaga hutchinsonii | COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Cytophaga hutchinsonii] | | | |
| 5759, 5760 | 48856079 | 62 | 1.00E-66 | Cytophaga hutchinsonii | COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] | | | 1.8.- |
| 5761, 5762 | 48891723 | 32 | 6.00E-16 | Trichodesmium erythraeum IMS101 | COG0515: Serine/threonine protein kinase [Trichodesmium erythraeum IMS101] | | | 2.7.1.- |
| 5767, 5768 | 48855464 | 38 | 8.00E-25 | Cytophaga hutchinsonii | COG1999: Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems [Cytophaga hutchinsonii] | | | |
| 5769, 5770 | 16802005 | 37 | 2.00E-35 | Listeria innocua Clip11262 | hypothetical protein lin2946 [Listeria innocua Clip11262] emb CAC98171.1 lin2946 [Listeria innocua] pir AC1800 hypothetical protein lin2946 [imported] [Listeria innocua (strain Clip11262)] | | | |
| 577, 578 | 53715867 | 51 | 4.00E-37 | Bacteroides fragilis YCH46 | putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46] dbj BAD51325.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46] | | | 2.7.7.56 |
| 5777, 5778 | 2995399 | 36 | 3.00E-17 | Bacillus megaterium | regulatory protein [Bacillus megaterium] gb AA83973.1 mercury resistance operon negative regulator MerR1 [Bacillus sp. RC607] | | | |
| 5781, 5782 | 53797309 | 45 | 1.00E-60 | Chloroflexus aurantiacus | sp P22853 MERR_BACCE Mercuric resistance operon regulatory protein pir T44501 merR1 protein [imported] - Clostridium butyricum dbj BAB62429.1 mercury-responsive transcriptional regulator protein [Bacillus cereus] dbj BAA86113.1 MerR1 [Clostridium butyricum] | | | 6.1.1.16 |
| 5783, 5784 | 15605808 | 37 | 3.00E-18 | Aquifex aedificus VF5 | hypothetical protein aq_268 [Aquifex aedificus VF5] gb AAC06590.1 hypothetical protein [Aquifex aedificus VF5] pir E70324 conserved hypothetical protein aq_268 - Aquifex aedificus | | | |
| 5787, 5788 | 53711500 | 51 | 1.00E-53 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD46958.1 two-component system response regulator [Bacteroides fragilis YCH46] | | | 2.7.3.- |

| | | | | | | | | | |
|-------|----------|----|----------|--|--|--|--|--|----------|
| 5789, | 48895439 | 31 | 9.00E-16 | Trichodesmium erythraeum IMS101 | COG0431: Predicted flavoprotein [Trichodesmium erythraeum IMS101] | | | | |
| 5790 | | | | Cytophaga hutchinsonii | COG1748: Saccharopine dehydrogenase and related proteins [Cytophaga hutchinsonii] | | | | 1.5.1.10 |
| 5791, | 48854542 | 45 | 4.00E-23 | Streptomyces avermitilis MA-4680 | hypothetical protein [Streptomyces avermitilis MA-4680] ref[NP_824022.1] | | | | |
| 5792 | 29606495 | 47 | 1.00E-43 | Streptomyces avermitilis MA-4680 | hypothetical protein SAV2846 [Streptomyces avermitilis MA-4680] | | | | |
| 5793, | 29606495 | 43 | 1.00E-24 | Streptomyces avermitilis MA-4680 | hypothetical protein [Streptomyces avermitilis MA-4680] ref[NP_824022.1] | | | | |
| 5794 | | | | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein SAV2846 [Streptomyces avermitilis MA-4680] | | | | |
| 5799, | 29349512 | 28 | 9.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | DNA helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79209.1] | | | | |
| 5800 | | | | Bdellovibrio bacteriovorus HD100 | DNA helicase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 5805, | 42523943 | 38 | 9.00E-35 | Bacteroides fragilis YCH46 | Redox-sensitive transcriptional activator [Bdellovibrio bacteriovorus HD100] | | | | |
| 5806 | | | | Bacteroides fragilis YCH46 | emb CAE80316.1] Redox-sensitive transcriptional activator [Bdellovibrio bacteriovorus HD100] | | | | |
| 5807, | 53713469 | 50 | 9.00E-72 | Bacteroides fragilis YCH46 | putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1] putative helicase [Bacteroides fragilis YCH46] | | | | |
| 5808 | | | | Nostoc punctiforme PCC 73102 | COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 581, | 23129412 | 31 | 1.00E-14 | Synechococcus elongatus PCC 6301 | two-component response regulator [Synechococcus elongatus PCC 6301] dbj BAD78390.1] two-component response regulator [Synechococcus elongatus PCC 6301] ref ZP_00202158.1] COG2200: FOG: EAL domain [Synechococcus elongatus PCC 7942] | | | | 2.7.3.- |
| 5813, | 56750209 | 40 | 2.00E-34 | Clostridium thermocellum ATCC 27405 | COG0124: Histidyl-tRNA synthetase [Clostridium thermocellum ATCC 27405] | | | | 6.1.1.21 |
| 5814 | 48860303 | 42 | 3.00E-53 | Clostridium perfringens str. 13 | histidine-tRNA ligase [Clostridium perfringens str. 13] dbj BAB81640.1] | | | | |
| 5815, | | | | Clostridium perfringens str. 13 | histidine-tRNA ligase [Clostridium perfringens str. 13] sp Q8XJ27 SYH_CLOPE Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS) | | | | 6.1.1.21 |
| 5816 | 18310916 | 50 | 6.00E-34 | Bacteroides thetaiotaomicron VPI-5482 | DNA replication and repair protein RecF, ABC family ATPase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79360.1] DNA replication and repair protein RecF, ABC family ATPase [Bacteroides thetaiotaomicron VPI-5482] sp Q89ZW6 REC_F_BACTN DNA replication and repair protein recF | | | | |
| 5817, | | | | | | | | | |
| 5818 | | | | | | | | | |
| 5821, | 29349663 | 39 | 5.00E-20 | | | | | | |
| 5822 | | | | | | | | | |

| | | | | | | | | | |
|-------|----------|----|----------|--|---|--|--|--|----------|
| 5829, | 9948447 | 28 | 5.00E-17 | Pseudomonas aeruginosa PAO1 | hypothetical protein PA2403 [Pseudomonas aeruginosa PAO1] ref ZP_00140125.1 COG3182: Uncharacterized iron-regulated membrane protein [Pseudomonas aeruginosa UCBCPP-PA14] pir A83344 hypothetical protein PA2403 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_251093.1 hypothetical protein PA2403 [Pseudomonas aeruginosa PAO1] | | | | 1.8.1.2 |
| 5830, | ABP0492 | 63 | 4.00E-43 | | Desc:Human ORFX protein sequence SEQ ID NO:9824. Org:Homo sapiens polyphosphate glucokinase [Nostoc sp. PCC 7120] pir AH1977 | | | | |
| 5831, | | | | | polyphosphate glucokinase [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73328.1 polyphosphate glucokinase [Nostoc sp. PCC 7120] | | | | 2.7.1.63 |
| 5832, | 17228866 | 50 | 2.00E-51 | Nostoc sp. PCC 7120 | COG0304: 3-oxoacyl-(acyl-carrier-protein) synthase [Cytophaga hutchinsonii] | | | | |
| 5833, | 48856692 | 50 | 3.00E-23 | Cytophaga hutchinsonii | two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] dbj BAD51273.1 two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] | | | | 2.7.3.- |
| 5834, | 53715815 | 33 | 4.00E-38 | Bacteroides fragilis YCH46 | COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 5835, | 48857007 | 53 | 4.00E-67 | Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 5836, | 48857007 | 47 | 6.00E-75 | Cytophaga hutchinsonii | hypothetical protein BT3209 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78315.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 5837, | 29348618 | 41 | 9.00E-54 | Bacteroides thetaiotaomicron VPI-5482 | ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76293.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 5838, | 29346596 | 74 | 4.00E-36 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein Chte02000708 [Clostridium thermocellum ATCC 27405] | | | | |
| 5839, | 48859986 | 31 | 3.00E-25 | Clostridium thermocellum ATCC 27405 | hypothetical protein MAP1660 [Mycobacterium avium subsp. paratuberculosis str. k10] gb AAS03977.1 hypothetical protein MAP1660 [Mycobacterium avium subsp. paratuberculosis str. k10] | | | | 2.1.1.- |
| 5840, | 41407758 | 36 | 8.00E-39 | Mycobacterium avium subsp. paratuberculosis str. k10 | peptidase (M20/M25/M40 family) [Xylella fastidiosa Temecula1] gb AAO29682.1 peptidase (M20/M25/M40 family) [Xylella fastidiosa Temecula1] | | | | 3.4.17.2 |
| 5841, | 28199718 | 33 | 2.00E-25 | Xylella fastidiosa Temecula1 | 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579] gb AAO7321.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579] | | | | 1.13.11. |
| 5842, | 30018489 | 52 | 1.00E-41 | Bacillus cereus ATCC 14579 | | | | | 27 |

| | | | | | | | | |
|---------------|--------------|----|----------|------------------------------------|--|--|----|-------------------|
| 5865, 5866 | 48853959 | 46 | 8.00E-27 | Cytophaga hutchinsonii | COG0416: Fatty acid/phospholipid biosynthesis enzyme [Cytophaga hutchinsonii] | | | |
| 5867, 5868 | 53715112 | 28 | 2.00E-21 | Bacteroides fragilis YCH46 | 4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4- alpha-glucanotransferase [Bacteroides fragilis YCH46] | | | |
| 5869, 5870 | ABB8477 1 | 44 | 1.00E-56 | | Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org: Cytophaga hutchinsonii | | | |
| 587, 588 | 17231112 | 69 | 1.00E-51 | Nostoc sp. PCC 7120 | type I restriction modification enzyme M subunit [Nostoc sp. PCC 7120] dbj BAB75319.1 type I restriction modification enzyme M subunit [Nostoc sp. PCC 7120] pir JAE2258 type I restriction modification enzyme M chain [Imported] - Nostoc sp. (strain PCC 7120) | Nostoc sp. PCC 7120 DNA, complete genome | 87 | 7.00E-12 2.1.1.72 |
| 5873, 5874 | 13508372 | 39 | 4.00E-27 | Mycoplasma pneumoniae M129 | hypothetical protein MPN633 [Mycoplasma pneumoniae M129] gb AAB95857.1 conserved hypothetical protein, see: MPN635 [Mycoplasma pneumoniae M129] pir S73535 hypothetical protein C12_orf247 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75164 YG33_MYCPN Hypothetical protein MPN633 (C12_orf247) | | | |
| 5875, 5876 | 48856042 | 52 | 4.00E-32 | Cytophaga hutchinsonii | COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii] | | | 3.4.24.- |
| 5879, 5880 | 17231112 | 68 | 4.00E-42 | Nostoc sp. PCC 7120 | type I restriction modification enzyme M subunit [Nostoc sp. PCC 7120] dbj BAB75319.1 type I restriction modification enzyme M subunit [Nostoc sp. PCC 7120] pir JAE2258 type I restriction modification enzyme M chain [Imported] - Nostoc sp. (strain PCC 7120) | Nostoc sp. PCC 7120 DNA, complete genome | 87 | 5.00E-12 2.1.1.72 |
| 5881, 5882 | 15606196 | 33 | 3.00E-08 | Aquifex aeolicus VF5 | (p)ppGpp 3-pyrophosphohydrolase [Aquifex aeolicus VF5] gb AAC06975.1 (p)ppGpp 3-pyrophosphohydrolase [Aquifex aeolicus VF5] pir J70373 (p)ppGpp 3-pyrophosphohydrolase - Aquifex aeolicus sp O67012 SPOT_AQUAE Guanosine-3',5'-bis(diphosphate) 3'- pyrophosphohydrolase ((ppGpp)ase) (Penta-phosphate guanosine-3'- pyrophosphohydrolase) | | | 3.1.7.2 |
| 5883, 5884 | 57160028 | 30 | 5.00E-09 | Thermococcus kodakaraensis | predicted transcription regulator, DUF118 helix-turn-helix family [Thermococcus kodakaraensis] ref YP_184182.1 predicted transcription regulator, DUF118 helix-turn-helix family [Thermococcus kodakaraensis] | | | |
| 5885, 5886 | 23125101 | 35 | 1.00E-12 | Nostoc punctiforme PCC 73102 | COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Nostoc punctiforme PCC 73102] | | | |
| 5887, 5888 | 23474779 | 24 | 7.00E-07 | Desulfovibrio desulfuricans G20 | COG4564: Signal transduction histidine kinase [Desulfovibrio desulfuricans G20] | | | 2.7.3.- |
| 5889, 5890 | 48854298 | 60 | 1.00E-71 | Cytophaga hutchinsonii | COG4867: Uncharacterized protein with a von Willebrand factor type A (vWA) domain [Cytophaga hutchinsonii] | | | |

| | | | | | | | | |
|--------|----------|----|----------|---|---|---|----|----------|
| 589, | 48854139 | 59 | 5.00E-44 | Cytophaga hutchinsonii | COG1066: Predicted ATP-dependent serine protease [Cytophaga hutchinsonii] | | | 3.4.21.- |
| 590 | | | | Geobacillus kaustophilus | hypothetical protein GK0592 [Geobacillus kaustophilus HTA426] | | | |
| 5891, | | | | | dbj BAD74877.1 hypothetical conserved protein [Geobacillus kaustophilus HTA426] | | | 2.1.1.- |
| 5892 | 56419127 | 62 | 4.00E-60 | HTA426 | | | | |
| 5893, | | | | Cytophaga hutchinsonii | hypothetical protein Chut02001715 [Cytophaga hutchinsonii] | | | |
| 5894 | 48855383 | 61 | 5.00E-55 | hutchinsonii | hypothetical protein CTC00544 [Clostridium tetani E88] gb AAO35164.1 | | | |
| 5895, | | | | Clostridium tetani | conserved protein [Clostridium tetani E88] | | | |
| 5896 | 28210283 | 28 | 2.00E-17 | E88 | | | | |
| | | | | | | Leptospira interrogans serovar lai str. 56601 chromosome I, section 300 of 397 of the complete sequence | 88 | 7.00E-21 |
| 5897, | | | | Leptospira interrogans serovar lai str. 56601 | hypothetical protein LA3317 [Leptospira interrogans serovar Lai str. 56601] gb AAN50515.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] | | | |
| 5898 | 24216016 | 69 | 1.00E-61 | | | | | 2.3.1.- |
| 5899, | | | | Anopheles gambiae | ENSANGP00000000470 [Anopheles gambiae] | | | |
| 5900 | 31195995 | 54 | 3.00E-41 | Bacteroides thetaiotaomicron VPI-5482 | ABC transporter, ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75801.1 ABC transporter, ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] | | | 1.8.- |
| 59, 60 | 29346104 | 48 | 2.00E-33 | | | | | |
| 5903, | | | | Cytophaga hutchinsonii | COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] | | | 2.7.7.24 |
| 5904 | 48853434 | 68 | 1.00E-50 | | | | | |
| 5907, | | | | Microbulbifer degradans 2-40 | COG0784: FOG: CheY-like receiver [Microbulbifer degradans 2-40] | | | 2.7.3.- |
| 5908 | 48864299 | 41 | 4.00E-12 | | hypothetical protein TTC1430 [Thermus thermophilus HB27] | | | |
| 5909, | | | | Thermus thermophilus HB27 | gb AAS81772.1 hypothetical protein TTC1430 [Thermus thermophilus HB27] | | | |
| 5910 | 46199732 | 48 | 4.00E-71 | | | | | |
| 591, | | | | | glutamate synthase, small subunit [Azoarcus sp. EbN1] emb CAI07366.1 | | | 1.4.1.13 |
| 592 | 56476678 | 64 | 5.00E-84 | Azoarcus sp. EbN1 | Glutamate synthase, small subunit [Azoarcus sp. EbN1] | | | |
| | | | | | conserved hypothetical protein-putative sodium:solute symporter [Rhodopirellula ballica SH 1] emb CAD73139.1 conserved hypothetical protein-putative sodium:solute symporter [Pirellula sp.] | | | |
| 5911, | | | | Rhodopirellula ballica SH 1 | putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79825.1 putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 5912 | 32472461 | 32 | 2.00E-18 | | | | | |
| 5915, | | | | Bacteroides thetaiotaomicron VPI-5482 | COG1181: D-alanine-D-alanine ligase and related ATP-grasp enzymes [Cytophaga hutchinsonii] | | | 6.3.2.4 |
| 5916 | 29350128 | 36 | 6.00E-25 | | | | | |
| 5919, | | | | Cytophaga hutchinsonii | | | | |
| 5920 | 48854866 | 49 | 2.00E-74 | | | | | |

| | | | | | | | | | |
|-------|----------|----|----------|------------------------|---|--|--|--|--|
| 5921, | 48855764 | 39 | 7.00E-25 | Cytophaga hutchinsonii | COG5316: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 5922 | | | | Tetraodon | uncharacterized conserved protein [Tetraodon nigroviridis] | | | | |
| 5929, | 47212116 | 56 | 3.00E-17 | nigroviridis | uncharacterized conserved protein [Tetraodon nigroviridis] | | | | |
| 5930 | | | | Pyrococcus | hypothetical acylaminoacyl-peptidase [Pyrococcus furiosus DSM 3638] | | | | |
| 593, | 18976690 | 30 | 7.00E-07 | furiosus DSM 3638 | hypothetical acylaminoacyl-peptidase [Pyrococcus furiosus DSM 3638] | | | | |
| 594 | | | | Pyrococcus | hypothetical acylaminoacyl-peptidase [Pyrococcus furiosus DSM 3638] | | | | |
| 5931, | 34397422 | 40 | 7.00E-09 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5932 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5933, | 48855192 | 43 | 2.00E-52 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5934 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5939, | 34397422 | 40 | 7.00E-09 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5940 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5941, | 48855192 | 43 | 2.00E-52 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5942 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5945, | 34397903 | 44 | 2.00E-62 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5946 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5949, | 48854708 | 24 | 5.00E-19 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5950 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 595, | 49236276 | 22 | 3.00E-17 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 596 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5951, | 48846288 | 51 | 1.00E-26 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5952 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5955, | 53711793 | 27 | 5.00E-08 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5956 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5959, | 22797891 | 32 | 2.00E-15 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5960 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5961, | 15644384 | 25 | 8.00E-14 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5962 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5961, | 29348148 | 45 | 2.00E-22 | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |
| 5962 | | | | Pyrococcus | DNA-binding response regulator, LuxR family [Pyrococcus gingivalis W83] | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|-------------|----------|
| 5963, 5964 | 29349252 | 53 | 1.00E-98 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO78949.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | 3.6.1.- |
| 5967, 5968 | 24214475 | 32 | 1.00E-11 | Leptospira interrogans serovar Lai str. 56601 | hypothetical protein LA1775 [Leptospira interrogans serovar Lai str. 56601] gb AAN48974.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] | | | |
| 5969, 5970 | 22797889 | 36 | 3.00E-19 | uncultured crenarchaeote | putative histidine kinase [uncultured crenarchaeote] | | | 2.7.3.- |
| 5971, 5972 | 41205694 | 41 | 8.00E-56 | Geobacillus stearothermophilus | putative rhamnosyltransferase [Geobacillus stearothermophilus] | | | 2.4.- |
| 5973, 5974 | 48855182 | 29 | 2.00E-22 | Cytophaga hutchinsonii | COG2911: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 5977, 5978 | 16802005 | 38 | 3.00E-24 | Listeria innocua Clp11262 | hypothetical protein lin2946 [Listeria innocua Clp11262] emb CAC98171.1 lin2946 [Listeria innocua] pir AC1800 hypothetical protein lin2946 [Imported] Listeria innocua (strain Clp11262) | | | |
| 5979, 5980 | 48839666 | 78 | 2.00E-80 | Methanosarcina barkeri str. fusaro | COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro] | Methanosarcina acetivorans str. C2A, section 503 of 534 of the complete genome | 83 1.00E-47 | |
| 5981, 5982 | 20091607 | 36 | 5.00E-44 | Methanosarcina acetivorans C2A | sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AAM06162.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A] | | | 2.7.3.- |
| 5983, 5984 | 53715101 | 33 | 2.00E-26 | Bacteroides fragilis YCH46 | hypothetical protein BF3817 [Bacteroides fragilis YCH46] db BAD50559.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 5987, 5988 | 10956006 | 53 | 1.00E-77 | Coxiella burnetii | hypothetical protein [Coxiella burnetii] emb CAA63678.1 orf 410 [Coxiella burnetii] emb CAA53126.1 unnamed protein product [Coxiella burnetii] pir S38238 hypothetical protein - Coxiella burnetii | | | |
| 5989, 5990 | 48838087 | 27 | 1.00E-08 | Methanosarcina barkeri str. fusaro | COG0608: Single-stranded DNA-specific exonuclease [Methanosarcina barkeri str. fusaro] | | | 3.1.- |
| 599, 600 | 34398083 | 48 | 4.00E-47 | Porphyromonas gingivalis W83 | polypeptide deformylase [Porphyromonas gingivalis W83] ref NP_906244.1 polypeptide deformylase [Porphyromonas gingivalis W83] spiQ7MT07 DEF_PORGI Peptide deformylase (PDF) (Polypeptide deformylase) | | | 3.5.1.88 |
| 5993, 5994 | 48833949 | 48 | 4.00E-66 | Magnetococcus sp. MC-1 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Magnetococcus sp. MC-1] | | | 2.4.1.- |
| 5995, 5996 | 48854977 | 61 | 6.00E-87 | Cytophaga hutchinsonii | COG0685: 5,10-methylenetetrahydrofolate reductase [Cytophaga hutchinsonii] | | | 1.5.1.20 |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|---------------|
| 6003, 6004 | 48839274 | 56 | 3.00E-79 | Methanosarcina barkeri str. fusaro | COG4096: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Methanosarcina barkeri str. fusaro] | | | 3.1.21.3 |
| 6005, 6006 | 37519843 | 56 | 6.00E-66 | Gloeobacter violaceus PCC 7421 | hypothetical protein gl0274 [Gloeobacter violaceus PCC 7421] dbj BAC88215.1 gl0274 [Gloeobacter violaceus PCC 7421] UDP-N-acetylmuramate dehydrogenase [Thermoanaerobacter tengcongensis MB4] gb AAM25027.1 UDP-N-acetylmuramate dehydrogenase [Thermoanaerobacter tengcongensis MB4] sp Q8R8Z6 MURB_THETN UDP-N-acetylenolpyruvoylglucosamine reductase (UDP-N-acetylmuramate dehydrogenase) | | | 3.4.19.1 |
| 6011, 6012 | 20808252 | 26 | 2.00E-12 | Thermoanaerobact er tengcongensis MB4 | signal-transducing histidine kinase [Archaeoglobus fulgidus DSM 4304] gb AAB90464.1 signal-transducing histidine kinase [Archaeoglobus fulgidus DSM 4304] pir B69346 signal-transducing histidine kinase homolog - Archaeoglobus fulgidus | | | 1.1.1.15 8 |
| 6013, 6014 | 11498376 | 32 | 1.00E-32 | Archaeoglobus fulgidus DSM 4304 | hypothetical protein ABC4087 [Bacillus clausii KSM-K16] dbj BAD66618.1 conserved hypothetical protein [Bacillus clausii KSM-K16] hypothetical protein aii4429 [Nostoc sp. PCC 7120] dbj BAB76128.1 hlpA [Nostoc sp. PCC 7120] pir AE2359 hypothetical protein hlpA [imported] - Nostoc sp. (strain PCC 7120) | | | 2.7.3.- |
| 6017, 6018 | 56955845 | 37 | 5.00E-27 | Bacillus clausii KSM-K16 | hypothetical protein STH2259 [Symbiobacterium thermophilum IAM 14863] dbj BAD41244.1 hypothetical protein [Symbiobacterium thermophilum IAM 14863] | | | |
| 6019, 6020 | 17231921 | 42 | 2.00E-54 | Nostoc sp. PCC 7120 | hypothetical protein TTC1428 [Thermus thermophilus HB27] gb AAS81770.1 hypothetical protein TTC1428 [Thermus thermophilus HB27] | | | |
| 6021, 6022 | 51893397 | 25 | 4.00E-11 | Symbiobacterium thermophilum IAM 14863 | putative glycosylhydrolase [Bacteroides fragilis YCH46] dbj BAD49843.1 putative glycosylhydrolase [Bacteroides fragilis YCH46] | | | 3.2.1.17 |
| 6023, 6024 | 46199730 | 37 | 5.00E-12 | Thermus thermophilus HB27 | COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] transcriptional regulator, Crp family [Porphyromonas gingivalis W83] ref NP_905705.1 transcriptional regulator, Crp family [Porphyromonas gingivalis W83] | | | |
| 6025, 6026 | 53714385 | 34 | 2.00E-20 | Bacteroides fragilis YCH46 | COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] | | | 2.7.3.- |
| 6027, 6028 | 48855612 | 42 | 4.00E-47 | Cytophaga hutchinsonii | | | | |
| 6029, 6030 | 34397542 | 33 | 1.00E-31 | Porphyromonas gingivalis W83 | | | | |
| 6033, 6034 | 23128539 | 39 | 3.00E-16 | Nostoc punctiforme PCC 73102 | | | | |

| | | | | | | | | |
|-------|----------|----|----------|---|---|--|--|----------|
| 6035, | 24214122 | 31 | 4.00E-29 | Leptospira interrogans serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] | | | |
| 6036 | | | | | | | | |
| 6037, | 13516917 | 28 | 5.00E-16 | Myxococcus xanthus | hybrid sensor [Myxococcus xanthus] | | | |
| 6038 | | | | | | | | |
| 6039, | 47826745 | 27 | 6.00E-17 | Prevotella intermedia | dipeptidyl peptidase IV [Prevotella intermedia] | | | 3.4.14.- |
| 6040 | | | | | | | | |
| 6045, | | | | Xanthomonas axonopodis pv. citri str. 306 | endonuclease [Xanthomonas axonopodis pv. citri str. 306] gb AAM35495.1 endonuclease [Xanthomonas axonopodis pv. citri str. 306] | | | 3.2.- |
| 6046 | 21241377 | 58 | 4.00E-44 | | Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 65409. | | | |
| 6047, | AAG5152 | 50 | 5.00E-44 | | Org:Arabidopsis thaliana | | | 1.17.4.1 |
| 6048 | | | | | Desc:isoprenoid related protein sequence SEQ ID No 28. | | | |
| 6049, | AAO2185 | 46 | 2.00E-60 | | Org:Synechococcus sp | | | 4.1.3.37 |
| 6050 | 7 | | | | | | | |
| 605, | | | | Cytophaga hutchinsonii | COG0504: CTP synthase (UTP-ammonia lyase) [Cytophaga hutchinsonii] | | | 6.3.4.2 |
| 606 | 48856944 | 63 | 3.00E-60 | | hypothetical protein SO2930 [Shewanella oneidensis MR-1] gb AAN55944.1 | | | |
| 6051, | | | | Shewanella oneidensis MR-1 | hypothetical protein [Shewanella oneidensis MR-1] | | | |
| 6052 | 24374457 | 42 | 5.00E-60 | | | | | |
| 6053, | | | | Cytophaga hutchinsonii | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 6054 | 48854564 | 53 | 5.00E-67 | | sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gb AAN51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gb AAS71912.1 sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | 2.7.7.4 |
| 6055, | | | | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | | | | |
| 6056 | 45659189 | 52 | 8.00E-89 | | hypothetical protein Chut02003091 [Cytophaga hutchinsonii] | | | |
| 6063, | | | | Cytophaga hutchinsonii | | | | |
| 6064 | 48854003 | 28 | 1.00E-25 | | DNA polymerase [Podovirus SOG] | | | 2.7.7.7 |
| 6065, | | | | Podovirus SOG | | | | |
| 6066 | 32442287 | 28 | 2.00E-11 | | | | | |
| 6067, | | | | Ralstonia metallidurans CH34 | hypothetical protein Reut02003175 [Ralstonia metallidurans CH34] | | | |
| 6068 | 48766633 | 33 | 9.00E-11 | | | | | |

| | | | | | | | | |
|-------|----------|----|----------|--|--|--|--|---------|
| 6069, | 16264609 | 29 | 5.00E-07 | Sinorhizobium meliloti 1021 | putative oligopeptide uptake ABC transporter periplasmic solute-binding protein precursor [Sinorhizobium meliloti 1021] emb CAC33589.1 | | | |
| 6070 | | | | | oligopeptide ABC transporter [Sinorhizobium meliloti] pir E95949 probable oligopeptide uptake ABC transporter periplasmic solute-binding protein precursor oppA; [imported] - Sinorhizobium meliloti (strain 1021) | | | |
| 607, | 53795203 | 44 | 6.00E-25 | Chloroflexus aurantiacus | magaplasmid pSymB emb CAC49261.1 putative oligopeptide uptake ABC transporter periplasmic solute-binding protein precursor [Sinorhizobium meliloti 1021] | | | 3.5.2.6 |
| 6071, | 27262180 | 57 | 1.00E-27 | Hellobacillus | COG1680: Beta-lactamase class C and other penicillin binding proteins [Chloroflexus aurantiacus] | | | 2.7.7.7 |
| 6072 | AA78012 | | | | exonuclease ABC subunit C [Hellobacillus mobilis] | | | |
| 6073, | | 29 | 2.00E-17 | | Desc: Sphaerotilus natans SnaBI endonuclease protein SEQ ID NO:4. | | | |
| 6074 | 53717831 | 48 | 2.00E-48 | Burkholderia pseudomallei K96243 | Org: Sphaerotilus natans | | | |
| 6075, | | | | | glutamyl-tRNA amidotransferase subunit B [Burkholderia pseudomallei K96243] emb CAH34176.1 glutamyl-tRNA amidotransferase subunit B | | | 6.3.5.- |
| 6076 | 24374986 | 44 | 5.00E-46 | Shewanella oneidensis MR-1 | [Burkholderia pseudomallei K96243] hypothetical protein phosphatase [Shewanella oneidensis MR-1] gb AAN56473.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | |
| 6077, | | | | | two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator | | | 2.7.3.- |
| 6078 | 27377973 | 48 | 5.00E-25 | Bradyrhizobium japonicum USDA 110 | [Bradyrhizobium japonicum USDA 110] | | | |
| 6081, | 48853721 | 33 | 3.00E-13 | Cytophaga hutchinsonii | hypothetical protein Chut02003580 [Cytophaga hutchinsonii] | | | |
| 6082 | 56477873 | 32 | 9.00E-24 | Azoarcus sp. EbN1 | glycosyl transferase, family 2 [Azoarcus sp. EbN1] emb CAI08561.1 | | | 2.4.1.- |
| 6085, | | | | | Glycosyl transferase, family 2 [Azoarcus sp. EbN1] | | | |
| 6086 | 20808429 | 38 | 2.00E-16 | Thermoanaerobacter tengcongensis MB4 | antirestriction protein [Thermoanaerobacter tengcongensis MB4] gb AAM25204.1 antirestriction protein [Thermoanaerobacter tengcongensis MB4] | | | |
| 6087, | | | | | COG0458: Carbamoylphosphate synthase large subunit (split gene in MJ) | | | 6.3.5.5 |
| 6088 | 48855433 | 62 | 8.00E-42 | Cytophaga hutchinsonii | [Cytophaga hutchinsonii] | | | 6.2.1.3 |
| 609, | 48854120 | 58 | 1.00E-56 | Cytophaga hutchinsonii | COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] | | | |
| 6091, | | | | | COG1321: Mn-dependent transcriptional regulator [Cytophaga hutchinsonii] | | | |
| 6092 | 48856607 | 48 | 3.00E-16 | Bacteroides thetaiotaomicron | TonB [Bacteroides thetaiotaomicron VP1-5482] gb AAO77166.1 TonB [Bacteroides thetaiotaomicron VP1-5482] | | | |
| 6093, | | | | | | | | |
| 6094 | 29347469 | 34 | 1.00E-13 | Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 6099, | | | | | | | | |
| 6100 | 48853766 | 35 | 8.00E-41 | | | | | |
| 6103, | | | | | | | | |
| 6104 | | | | | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|----------|
| 6105, 6106 | 48839924 | 57 | 6.00E-45 | Methanosarcina barkeri str. fusaro | COG5316: Uncharacterized conserved protein [Methanosarcina barkeri str. fusaro] | | | |
| 6107, 6108 | 48891840 | 33 | 3.00E-29 | Trichodesmium erythraeum IMS101 | COG1232: Protoporphyrinogen oxidase [Trichodesmium erythraeum IMS101] | | | 1.3.3.4 |
| 6109, 6110 | 53797309 | 45 | 1.00E-60 | Chloroflexus aurantiacus | COG0215: Cysteinyl-tRNA synthetase [Chloroflexus aurantiacus] transposase [Bacteroides thetaiotaomicron VPI-5482] ref[NP_812706.1] transposase [Bacteroides thetaiotaomicron VPI-5482] ref[NP_811980.1] transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] ref[NP_810669.1] transposase, invertase [Bacteroides thetaiotaomicron VPI- 5482] ref[NP_810516.1] transposase [Bacteroides thetaiotaomicron VPI- 5482] ref[NP_809398.1] transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO79845.1] transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78900.1] transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78174.1] transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76863.1] transposase, invertase [Bacteroides thetaitotaomicron VPI-5482] gb AAO76710.1] transposase [Bacteroides thetaitotaomicron VPI-5482] gb AAO75592.1] transposase [Bacteroides thetaitotaomicron VPI-5482] | | | 6.1.1.16 |
| 611, 612 | 29350148 | 34 | 2.00E-23 | Bacteroides thetaitotaomicron VPI-5482 | putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79084.1] putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 6111, 6112 | 29349387 | 41 | 6.00E-17 | Bacteroides thetaitotaomicron VPI-5482 | | | | |
| 6113, 6114 | 13508087 | 33 | 2.00E-14 | Mycoplasma pneumoniae M129 | 5-formyl tetrahydrofolate cyclo-ligase (H10858) homolog [Mycoplasma pneumoniae M129] gb AAB96136.1] 5-formyl tetrahydrofolate cyclo-ligase (H10858) homolog; similar to GenBank Accession Number D64160, from H. Influenzae [Mycoplasma pneumoniae M129] pir S73814 probable 5-formyl tetrahydrofolate cyclo-ligase H10858 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75430 Y245_MYCPN Hypothetical protein MG245 homolog (H91_orf164) | | | 6.3.3.2 |
| 6115, 6116 | 48856028 | 47 | 1.00E-39 | Cytophaga hutchinsonii | COG1057: Nicotinic acid mononucleotide adenylyltransferase [Cytophaga hutchinsonii] | | | 2.7.7.18 |
| 6119, 6120 | 48855616 | 26 | 5.00E-24 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |
| 6121, 6122 | | | | | | | | 2.7.3.- |
| 6123, 6124 | 47551295 | 29 | 2.00E-08 | Strongylocentrotus purpuratus | egg bindin receptor 1 [Strongylocentrotus purpuratus] gb AAR03494.1] egg bindin receptor 1 precursor [Strongylocentrotus purpuratus] | | | |

| | | | | | | | | |
|-------|----------|----|----------|--|---|--|--|---------------|
| 6127, | 34397354 | 69 | 6.00E-19 | Porphyrromonas gingivalis W83 | orotate phosphoribosyltransferase [Porphyrromonas gingivalis W83] ref NP_905518.1 orotate phosphoribosyltransferase [Porphyrromonas gingivalis W83] sp Q7MUX4 PYRE_PORGI Orotate phosphoribosyltransferase (OPRT) (OPRTase) | | | 2.4.2.10 |
| 6128, | 48854506 | 39 | 9.00E-15 | Cytophaga hutchinsonii | hypothetical protein Chut02002705 [Cytophaga hutchinsonii] | | | 3.6.1.- |
| 6129, | | | | Symbiobacterium thermophilum IAM 14863 | RNA polymerase ECF-type sigma factor [Symbiobacterium thermophilum IAM 14863] dbj BAD39830.1 RNA polymerase ECF-type sigma factor [Symbiobacterium thermophilum IAM 14863] | | | |
| 613, | 51891983 | 36 | 4.00E-15 | Thermosynechococcus elongatus BP-1 | phosphoenolpyruvate synthase [Thermosynechococcus elongatus BP-1] dbj BAC08316.1 phosphoenolpyruvate synthase [Thermosynechococcus elongatus BP-1] | | | 2.7.9.2 |
| 6135, | 22298307 | 62 | 3.00E-90 | Helicobacter pylori J99 | hypothetical protein jhp0094 [Helicobacter pylori J99] gb AAD05675.1 putative [Helicobacter pylori J99] pir E71975 hypothetical protein [jhp0094 - Helicobacter pylori (strain J99)] | | | 2.4.- |
| 6136 | 15611164 | 44 | 3.00E-39 | Desulfotalea psychrophila Lsv54 | hypothetical protein DP2762 [Desulfotalea psychrophila Lsv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila Lsv54] | | | 2.1.1.14 4 |
| 6141, | 51246614 | 29 | 3.00E-19 | Desulfotalea psychrophila Lsv54 | hypothetical protein DP2762 [Desulfotalea psychrophila Lsv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila Lsv54] | | | 2.1.1.14 4 |
| 6143, | 51246614 | 29 | 1.00E-21 | Bacillus halodurans C-125 | cardiolipin synthetase [Bacillus halodurans C-125] dbj BAB06577.1 cardiolipin synthetase [Bacillus halodurans C-125] pir B84007 cardiolipin synthetase BH2858 [imported] - Bacillus halodurans (strain C-125) | | | |
| 6145, | 15615421 | 36 | 1.00E-33 | Mannheimia succiniciproducens MBEL55E | sp Q9K8Z4 CLS_BACHD Cardiolipin synthetase (Cardiolipin synthase) (CL synthase) | | | 2.7.8.- |
| 6147, | | | | Mycobacterium tuberculosis H37Rv | CarB protein [Mannheimia succiniciproducens MBEL55E] gb AAU38098.1 CarB protein [Mannheimia succiniciproducens MBEL55E] | | | 6.3.5.5 |
| 6148 | 52425546 | 26 | 2.00E-13 | uncultured archaeon GZfos3D4 | hypothetical protein Rv0329c [Mycobacterium tuberculosis H37Rv] ref NP_334753.1 MitM-related protein [Mycobacterium tuberculosis CDC1551] gb AAK44567.1 MitM-related protein [Mycobacterium tuberculosis CDC1551] pir B70527 hypothetical protein Rv0329c - Mycobacterium tuberculosis (strain H37Rv) emb CAB09577.1 CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv] | | | |
| 615, | 15607470 | 27 | 4.00E-07 | uncultured archaeon GZfos3D4 | alpha-mannosidase [uncultured archaeon GZfos3D4] | | | 3.2.1.24 |
| 6153, | 52550389 | 39 | 3.00E-47 | uncultured crenarchaeote | putative translation elongation factor EF Tu-like protein [uncultured crenarchaeote] | | | |
| 6154 | 42557720 | 44 | 7.00E-23 | | | | | |
| 6155, | | | | | | | | |
| 6156 | | | | | | | | |

| | | | | | | | | |
|---------------|----------|----|-----------|---|--|---|----------|---------------|
| 6157, 6158 | 48855337 | 63 | 5.00E-93 | Cytophaga hutchinsonii | COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii] | : | | |
| 6159, 6160 | 1185191 | 57 | 4.00E-64 | Odontella sinensis | ORF 644 [Odontella sinensis] pir S78301 hypothetical protein 644 - Odontella sinensis chloroplast ref NP_043642.1 ORF 844 [Odontella sinensis] sp P49825 FTSH_ODOSI Cell division protein ftsH homolog ATP phosphoribosyltransferase [Bacteroides fragilis YCH46] dbj BAD49935.1 ATP phosphoribosyltransferase [Bacteroides fragilis YCH46] | Odontella sinensis complete chloroplast genome 89 | 1.00E-07 | 3.4.24.- |
| 6161, 6162 | 53714477 | 58 | 4.00E-66 | Bacteroides fragilis YCH46 | | | | 2.4.2.17 |
| 6165, 6166 | 48853743 | 67 | 1.00E-118 | Cytophaga hutchinsonii | COG0188: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit [Cytophaga hutchinsonii] | | | 5.99.1.- |
| 6167, 6168 | 48893692 | 30 | 2.00E-35 | Trichodesmium erythraeum IMS101 | COG2317: Zn-dependent carboxypeptidase [Trichodesmium erythraeum IMS101] | | | 3.4.17.1 9 |
| 6169, 6170 | 48854510 | 56 | 5.00E-51 | Cytophaga hutchinsonii | COG0622: Predicted phosphoesterase [Cytophaga hutchinsonii] | | | |
| 6173, 6174 | 54032283 | 33 | 3.00E-10 | Polaromonas sp. JS666 | COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Polaromonas sp. JS666] | | | |
| 6177, 6178 | 42525886 | 44 | 1.00E-27 | Treponema denticola ATCC 35405 | UDP-N-acetylmuramoylalanine-D-glutamate ligase [Treponema denticola ATCC 35405] gb AAS10865.1 UDP-N-acetylmuramoylalanine-D-glutamate ligase [Treponema denticola ATCC 35405] | | | 6.3.2.9 |
| 6179, 6180 | 48851974 | 31 | 5.00E-12 | Ferroplasma acidarmanus | hypothetical protein Faci02001417 [Ferroplasma acidarmanus] | | | |
| 6181, 6182 | 48864233 | 35 | 6.00E-22 | Microbulbifer degradans 2-40 | COG0845: Membrane-fusion protein [Microbulbifer degradans 2-40] | | | |
| 6183, 6184 | 48853832 | 60 | 2.00E-45 | Cytophaga hutchinsonii | COG0484: DnaJ-class molecular chaperone with C-terminal Zn finger domain [Cytophaga hutchinsonii] | | | |
| 6187, 6188 | 48853636 | 33 | 1.00E-24 | Cytophaga hutchinsonii | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 619, 620 | 29346219 | 29 | 1.00E-07 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT0809 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75916.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482] | | | |
| 6195, 6196 | 39995659 | 23 | 2.00E-14 | Geobacter sulfurreducens PCA | hypothetical protein GSU0552 [Geobacter sulfurreducens PCA] gb AAR33883.1 conserved domain protein [Geobacter sulfurreducens PCA] | | | |
| 6201, 6202 | 46120890 | 38 | 1.00E-33 | Methylobacillus flagellatus KT | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Methylobacillus flagellatus KT] | | | 2.7.3.- |
| 6203, 6204 | 48855896 | 41 | 4.00E-50 | Cytophaga hutchinsonii | COG0557: Exoribonuclease R [Cytophaga hutchinsonii] | | | 3.1.-.- |

| | | | | | | | | | |
|---------------|----------|----|-----------|---|---|---|----|----------|----------|
| 6209, 6210 | 53713098 | 64 | 1.00E-39 | Bacteroides fragilis YCH46 | GAF domain-containing protein involved in signal transduction [Bacteroides fragilis YCH46] dbj BAD48556.1 GAF domain-containing protein involved in signal transduction [Bacteroides fragilis YCH46] | | | | |
| 6213, 6214 | 29349346 | 30 | 6.00E-13 | Bacteroides thetataoamicron VPI-5482 | ATP-dependent DNA helicase recQ [Bacteroides thetataoamicron VPI-5482] gb AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetataoamicron VPI-5482] | | | | 3.6.1.- |
| 6215, 6216 | 56808880 | 31 | 4.00E-17 | Streptococcus pyogenes M49 591 | hypothetical protein SpyOM01000106 [Streptococcus pyogenes M49 591] | | | | |
| 6217, 6218 | 48853520 | 66 | 1.00E-118 | Cytophaga hutchinsonii | COG0192: S-adenosylmethionine synthetase [Cytophaga hutchinsonii] | Bacteroides thetataoamicron VPI-5482, section 14 of 21 of the complete genome | 83 | 6.00E-20 | 2.5.1.6 |
| 6219, 6220 | 53711352 | 64 | 2.00E-91 | Bacteroides fragilis YCH46 | S-adenosylmethionine synthetase [Bacteroides fragilis YCH46] dbj BAD46810.1 S-adenosylmethionine synthetase [Bacteroides fragilis YCH46] | Bacteroides thetataoamicron VPI-5482, section 14 of 21 of the complete genome | 83 | 4.00E-20 | 2.5.1.6 |
| 6221, 6222 | 29347668 | 42 | 2.00E-19 | Bacteroides thetataoamicron VPI-5482 | GTP-binding protein [Bacteroides thetataoamicron VPI-5482] gb AAO77365.1 GTP-binding protein [Bacteroides thetataoamicron VPI-5482] | | | | |
| 6225, 6226 | 31195773 | 45 | 6.00E-22 | Anopheles gambiae | ENSANGP00000000136 [Anopheles gambiae] hypothetical protein BPSS0056 [Burkholderia pseudomallei K96243] | | | | 2.3.1.- |
| 623, 624 | 53721095 | 35 | 7.00E-10 | Burkholderia pseudomallei K96243 | emb CAH37499.1 conserved hypothetical protein [Burkholderia pseudomallei K96243] | | | | |
| 6231, 6232 | 21672859 | 38 | 8.00E-16 | Chlorobium tepidum TLS | ATP synthase F1, delta subunit [Chlorobium tepidum TLS] gb AAM71266.1 ATP synthase F1, delta subunit [Chlorobium tepidum TLS] | | | | 3.6.3.15 |
| 6237, 6238 | 23501247 | 37 | 1.00E-29 | Brucella suis 1330 Nitrosomonas europaea ATCC | DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M) | | | | |
| 6243, 6244 | 30249879 | 39 | 4.00E-27 | 19718 | Sulfate transporter [Nitrosomonas europaea ATCC 19718] emb CAD85838.1 Sulfate transporter [Nitrosomonas europaea ATCC 19718] | | | | |

| | | | | | | | | |
|-------|----------|----|-----------|--|--|--|-------------|----------|
| 6251, | 48854662 | 24 | 5.00E-15 | Cytophaga hutchinsonii | COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Cytophaga hutchinsonii] | | | |
| 6252, | | | | | COG0071: Molecular chaperone (small heat shock protein) [Cytophaga hutchinsonii] | | | |
| 6253, | 48855680 | 58 | 2.00E-35 | Cytophaga hutchinsonii | | | | |
| 6254, | | | | Anopheles gambiae | | | | 3.1.- |
| 6255, | 31194811 | 47 | 2.00E-33 | Wolfinella succinogenes DSM 1740 | ENSANGP00000002016 [Anopheles gambiae] | | | |
| 6256, | | | | | ADP-HEPTOSE-LPS HEPTOSYLTRANSFERASE II (RFAF) [Wolfinella succinogenes DSM 1740] emb[CAE10509.1] ADP-HEPTOSE-LPS HEPTOSYLTRANSFERASE II (RFAF) [Wolfinella succinogenes] | | | |
| 6257, | 34557794 | 31 | 3.00E-15 | Shewanella oneidensis MR-1 | peptidase, M13 family [Shewanella oneidensis MR-1] gb AA56820.1 | | | 3.4.24.7 |
| 6258, | | | | | peptidase, M13 family [Shewanella oneidensis MR-1] | | | 1 |
| 6259, | 24375333 | 34 | 1.00E-20 | Methanosarcina mazei Go1 | | | | |
| 6260, | | | | | Ferredoxin [Methanosarcina mazei Go1] gb AAM32910.1 Ferredoxin [Methanosarcina mazei Go1] | | 84 1.00E-11 | 1.6.4.- |
| 6265, | 21229316 | 67 | 1.00E-108 | Microbulifer degradans 2-40 | COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulifer degradans 2-40] | | | |
| 6266, | 48864231 | 29 | 1.00E-12 | Cytophaga hutchinsonii | COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] | | | |
| 6267, | 48855210 | 27 | 4.00E-15 | Cytophaga hutchinsonii | COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] | | | 2.7.7.24 |
| 6273, | 48853434 | 68 | 1.00E-50 | Cytophaga hutchinsonii | COG1250: 3-hydroxyacyl-CoA dehydrogenase [Cytophaga hutchinsonii] | | | 1.1.1.35 |
| 6274, | | | | | COG2942: N-acyl-D-glucosamine 2-epimerase [Anabaena variabilis ATCC 29413] | | | 5.1.3.8 |
| 6277, | 48854116 | 65 | 1.00E-108 | Anabaena variabilis ATCC 29413 | type I restriction-modification system, M subunit [Desulfovibrio vulgaris subsp. vulgare str. Hildenborough] gb AAS96186.1 type I restriction-modification system, M subunit [Desulfovibrio vulgaris subsp. vulgare str. Hildenborough] | | | 2.1.1.72 |
| 6278, | | | | | Uvs062 [uncultured bacterium] | | | |
| 6279, | 46135554 | 32 | 6.00E-09 | Desulfovibrio vulgaris subsp. vulgare str. Hildenborough | RecQ [Pasteurella multocida subsp. multocida str. Pm70] gb AAK03511.1 | | | |
| 6280, | | | | | RecQ [Pasteurella multocida subsp. multocida str. Pm70] sp Q9CL21 RECQ_PASMU ATP-dependent DNA helicase recQ | | | 3.6.1.- |
| 6281, | 46580119 | 50 | 3.00E-68 | Cytophaga hutchinsonii | COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] | | | |
| 6282, | | | | | | | | |
| 6283, | 37222111 | 48 | 2.00E-74 | Pasteurella multocida subsp. multocida str. Pm70 | | | | |
| 6284, | | | | | | | | |
| 6285, | 15603292 | 42 | 5.00E-17 | Cytophaga hutchinsonii | | | | |
| 6286, | | | | | | | | |
| 6289, | 48856559 | 36 | 5.00E-18 | | | | | |
| 6290, | | | | | | | | |

| | | | | | | | | |
|---------------|----------|----|-----------|--|--|--|----|----------|
| 6291, 6292 | 57167915 | 42 | 6.00E-21 | Campylobacter coli RM2228 | para-aminobenzoate synthetase (pabB) [Campylobacter coli RM2228] gb EAL57701.1 para-aminobenzoate synthetase (pabB) [Campylobacter coli RM2228] | | | 4.1.3.- |
| 6293, 6294 | 42521895 | 69 | 1.00E-125 | Bdellovibrio bacteriovorus HD100 | preprotein translocase SecA subunit [Bdellovibrio bacteriovorus HD100] emb CAE77929.1 preprotein translocase SecA subunit [Bdellovibrio bacteriovorus HD100] | Haemophilus ducreyi strain 35000HP section 5 of 6 of the complete genome | 89 | 1.00E-11 |
| 6295, 6296 | 42521895 | 69 | 1.00E-125 | Bdellovibrio bacteriovorus HD100 | preprotein translocase SecA subunit [Bdellovibrio bacteriovorus HD100] emb CAE77929.1 preprotein translocase SecA subunit [Bdellovibrio bacteriovorus HD100] | Haemophilus ducreyi strain 35000HP section 5 of 6 of the complete genome | 89 | 1.00E-11 |
| 6297, 6298 | 48854534 | 38 | 7.00E-19 | Cytophaga hutchinsonii | COG2834: Outer membrane lipoprotein-sorting protein [Cytophaga hutchinsonii] | | | |
| 6299, 6300 | 48854534 | 38 | 7.00E-19 | Cytophaga hutchinsonii | COG2834: Outer membrane lipoprotein-sorting protein [Cytophaga hutchinsonii] | | | |
| 63, 64 | 15644112 | 35 | 6.00E-07 | Thermotoga maritima MSB8 | response regulator [Thermotoga maritima MSB8] gb AAD36430.1 response regulator [Thermotoga maritima MSB8] pir A72263 response regulator - Thermotoga maritima (strain MSB8) | | | |
| 6301, 6302 | ABB5290 | 50 | 4.00E-72 | | Desc:Escherichia coli polypeptide SEQ ID NO 1226. Org:Escherichia coli | | | |
| 6303, 6304 | ABB5290 | 50 | 4.00E-72 | | Desc:Escherichia coli polypeptide SEQ ID NO 1226. Org:Escherichia coli | | | |
| 6305, 6306 | 53715355 | 27 | 2.00E-20 | Bacteroides fragilis YCH46 | hypothetical protein BF4071 [Bacteroides fragilis YCH46] dbj BAD50813.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 631, 632 | 53711742 | 45 | 5.00E-46 | Bacteroides fragilis YCH46 | UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides fragilis YCH46] | | | 3.1.3.15 |
| 6311, 6312 | 48854498 | 54 | 2.00E-60 | Cytophaga hutchinsonii | hypothetical protein Chut02002697 [Cytophaga hutchinsonii] | | | |
| 6313, 6314 | 45656929 | 50 | 1.00E-58 | Leptospira interrogans serovar Copenhageni str. Ficruz L1-130 | adenylate or guanylate cyclase [Leptospira interrogans serovar Copenhageni str. Ficruz L1-130] ref NP_713221.1 adenylate cyclase [Leptospira interrogans serovar Lai str. 56601] gb AAN50239.1 adenylate cyclase [Leptospira interrogans serovar lai str. 56601] gb AAS69652.1 adenylate or guanylate cyclase [Leptospira interrogans serovar Copenhageni str. Ficruz L1-130] | | | 4.6.1.2 |
| 6319, 6320 | 48855775 | 23 | 8.00E-08 | Cytophaga hutchinsonii | hypothetical protein Chut02000984 [Cytophaga hutchinsonii] | | | |

| | | | | | | | | |
|---------------|----------|----|-----------|--|---|--|-------------|----------|
| 6325, 6326 | 56675038 | 43 | 8.00E-19 | uncultured bacterium | cellulase [uncultured bacterium] | | | |
| 6333, 6334 | 48845443 | 39 | 1.00E-47 | Geobacter metallireducens GS-15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 6335, 6336 | 12515380 | 43 | 2.00E-64 | Escherichia coli O157:H7 | unknown protein encoded within prophage CP-933R [Escherichia coli O157:H7] ref NP_287814.1 unknown protein encoded within prophage CP-933R [Escherichia coli O157:H7 EDL933] ref NP_309982.1 hypothetical protein ECs1955 [Escherichia coli O157:H7] dbj BAB35378.1 hypothetical protein [Escherichia coli O157:H7] pir C90873 hypothetical protein ECs1855 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) pir H85745 unknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain O157:H7, substrain EDL933) | | | |
| 6337, 6338 | 15678563 | 60 | 8.00E-51 | Methanothermobacter thermautotrophicus str. Delta H | peptide methionine sulfoxide reductase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85041.1 peptide methionine sulfoxide reductase [Methanothermobacter thermautotrophicus str. Delta H] pir F69170 peptide methionine sulfoxide reductase - Methanobacterium thermoautotrophicum (strain Delta H) sp O26635 MSRA_METTH Peptide methionine sulfoxide reductase msrA (Protein-methionine-S-oxide reductase) (Peptide Met(O) reductase) | Methanosarcina acetivorans str. C2A, section 349 of 534 of the complete genome | 83 6.00E-66 | 1.8.4.6 |
| 6339, 6340 | 48838915 | 75 | 1.00E-125 | Methanosarcina barkeri str. fusaro | COG0449: Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains [Methanosarcina barkeri str. fusaro] | | | |
| 6341, 6342 | 48853602 | 60 | 7.00E-98 | Cytophaga hutchinsonii | COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii] | | | |
| 6343, 6344 | 18309430 | 22 | 5.00E-07 | Clostridium perfringens str. 13 | probable transcriptional regulator [Clostridium perfringens str. 13] dbj BAB80154.1 probable transcriptional regulator [Clostridium perfringens str. 13] | | | |
| 6345, 6346 | 48860240 | 35 | 3.00E-15 | Clostridium thermocellum ATCC 27405 | COG2207: AraC-type DNA-binding domain-containing proteins [Clostridium thermocellum ATCC 27405] | Cytophaga sp. KUC-1 alcdh gene for alcohol dehydrogenase, complete cds | 85 1.00E-15 | 2.1.1.63 |
| 6347, 6348 | 11345445 | 34 | 1.00E-07 | Acinetobacter baumannii | unknown [Acinetobacter baumannii] | | | |

| | | | | | | | | | |
|-------|----------|----|----------|--------------------------------------|---|---|-------------|----------|--|
| 6353, | 48859423 | 30 | 6.00E-09 | Clostridium thermocellum ATCC 27405 | hypothetical protein Cht02001311 [Clostridium thermocellum ATCC 27405] | | | | |
| 6354 | | | | Cytophaga hutchinsonii | hypothetical protein Cht02003884 [Cytophaga hutchinsonii] | | | | |
| 6357, | 48853385 | 45 | 2.00E-18 | | | Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence | ## 5.00E-30 | | |
| 6358 | | | | | | Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence | ## 5.00E-30 | | |
| 6359, | | | | | | | | | |
| 6360 | | | | | | | | | |
| 6361, | | | | | | | | | |
| 6362 | | | | | | | | | |
| 6365, | 29605540 | 49 | 1.00E-13 | Streptomyces avermitilis MA-4680 | putative arginase [Streptomyces avermitilis MA-4680] ref NP_823071.1 | | | 3.5.3.1 | |
| 6366 | | | | | putative arginase [Streptomyces avermitilis MA-4680] | | | | |
| 6369, | | | | | translation elongation factor G, putative [Porphyromonas gingivalis W83] | | | 3.6.1.48 | |
| 6370 | 34397003 | 44 | 1.00E-74 | Porphyromonas gingivalis W83 | ref NP_905168.1 translation elongation factor G, putative [Porphyromonas gingivalis W83] | | | | |
| 637, | | | | Magnetospirillum magnetotacticum | | | | | |
| 638 | 46201417 | 36 | 2.00E-18 | MS-1 | COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1] | | | 2.7.3.- | |
| 6375, | | | | Cytophaga hutchinsonii | | | | 4.1.1.23 | |
| 6376 | 48854533 | 66 | 2.00E-84 | | COG0284: Oratidine-5'-phosphate decarboxylase [Cytophaga hutchinsonii] | | | | |
| 6377, | | | | Chromobacterium violaceum ATCC 12472 | conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] | | | | |
| 6378 | 34103796 | 30 | 6.00E-07 | | ref NP_902156.1 hypothetical protein CV2486 [Chromobacterium violaceum ATCC 12472] | | | | |
| 6381, | | | | Vibrio vulnificus | DNA polymerase I [Vibrio vulnificus CMCP6] gbl AAO09403.1 DNA polymerase I [Vibrio vulnificus CMCP6] | | | 2.7.7.7 | |
| 6382 | 27364348 | 25 | 2.00E-11 | CMCP6 | response regulator [Porphyromonas gingivalis W83] ref NP_905164.1 | | | | |
| 6383, | | | | Porphyromonas gingivalis W83 | response regulator [Porphyromonas gingivalis W83] | | | | |
| 6384 | 34396999 | 57 | 7.00E-63 | | | | | | |
| 6385, | | | | | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] | | | 2.7.3.- | |
| 6386 | 48854752 | 50 | 5.00E-90 | Cytophaga hutchinsonii | | | | | |

| | | | | | | | | | |
|---------------------------------|----------------------|----------|----------------------|---|--|--|--|--|---------|
| 6387, 6388, 6393, 6394 | 28854897 18481484 | 37 36 | 1.00E-23 1.00E-06 | Pseudomonas syringae pv. tomato str. DC3000 Tetrahymena thermophila | ISPsy11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794264.1 ISPsy11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000] | | | | |
| 6395, 6396 | 29347576 | 37 | 3.00E-40 | Bacteroides thetaiotaomicron VPI-5482 | endonuclease [Tetrahymena thermophila] two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77273.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.3.- |
| 6397, 6398 | 29346363 | 33 | 5.00E-16 | Bacteroides thetaiotaomicron VPI-5482 | Integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76060.1 Integrase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 6401, 6402 | 48855725 | 29 | 2.00E-16 | Cytophaga hutchinsonii | hypothetical protein Chut02000929 [Cytophaga hutchinsonii] | | | | |
| 6403, 6404 | 48895816 | 39 | 1.00E-16 | Trichodesmium erythraeum IMS101 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Trichodesmium erythraeum IMS101] | | | | 2.7.3.- |
| 6405, 6406 | 20090869 | 29 | 1.00E-08 | Methanosarcina acetivorans C2A Clostridium thermocellum | hypothetical protein MA2021 [Methanosarcina acetivorans C2A] gb AAM05424.1 hypothetical protein [Methanosarcina acetivorans str. C2A] | | | | |
| 6407, 6408 | 48858046 | 40 | 7.00E-51 | ATCC 27405 | COG0178: Excinuclease ATPase subunit [Clostridium thermocellum ATCC 27405] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|-----------------------------------|---|---|----|----------|----------|
| 6409, 6410 | 20808983 | 32 | 6.00E-16 | MB4 | Thermoanaerobacter tengcongensis | transposase [Thermoanaerobacter tengcongensis MB4] ref NP_623590.1 transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622797.1 transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622779.1 transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622700.1 transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622094.1 transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622043.1 transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622035.1 transposase [Thermoanaerobacter tengcongensis MB4] ref NP_621726.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM25194.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM23647.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM25758.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM24401.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM24383.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM24304.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM23698.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM23639.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM23330.1 trans | | | |
| 641, 642 | 48854524 | 63 | 2.00E-67 | Cytophaga hutchinsonii | COG1217: Predicted membrane GTPase involved in stress response | | | | 3.6.1.48 |
| 6411, 6412 | 42523011 | 35 | 7.00E-20 | Bdellovibrio bacteriovorus HD100 | ADP-heptose:LPS heptosyltransferase II [Bdellovibrio bacteriovorus HD100] emb CAE79384.1 ADP-heptose:LPS heptosyltransferase II [Bdellovibrio bacteriovorus HD100] | | | | |
| 6415, 6416 | 28211584 | 38 | 4.00E-19 | Clostridium tetani E88 | histidyl-tRNA synthetase [Clostridium tetani E88] gb AAO36465.1 histidyl-tRNA synthetase [Clostridium tetani E88] sp Q892X7 SYH_CLOTE Histidyl-tRNA synthetase [Histidine-tRNA ligase] (HisRS) | | | | 6.1.1.21 |
| 6417, 6418 | 18313085 | 33 | 2.00E-37 | Pyrobaculum aerophilum str. IM2 | branched-chain amino acid binding protein [Pyrobaculum aerophilum str. IM2] gb AAL63934.1 branched-chain amino acid binding protein [Pyrobaculum aerophilum str. IM2] | | | | |
| 6419, 6420 | 48894700 | 44 | 1.00E-28 | Trichodesmium erythraeum IMS101 | COG1523: Type II secretory pathway, pullulanase PulA and related glycosidases [Trichodesmium erythraeum IMS101] | Treponema denticola ATCC 35405, section 1 of 10 of the complete genome | 92 | 3.00E-14 | 3.2.1.- |
| 6423, 6424 | 54296294 | 37 | 7.00E-34 | Legionella pneumophila str. Paris | hypothetical protein lpp0323 [Legionella pneumophila str. Paris] emb CAH11471.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | 2.3.1.- |

| | | | | | | | | | |
|-------|----------|----|----------|---|--|--|--|--|----------|
| 6427, | 32469352 | 50 | 1.00E-07 | Francisella tularensis subsp. novicida | unknown [Francisella tularensis subsp. novicida] | | | | |
| 6428 | | | | | conserved hypothetical protein [Porphyromonas gingivalis W83] | | | | |
| 6429, | 34397310 | 42 | 2.00E-30 | Porphyromonas gingivalis W83 | ref NP_905474.1 hypothetical protein PG1300 [Porphyromonas gingivalis W83] | | | | 2.1.1.- |
| 6431, | | | | | tRNA delta(2)-isopentenylpyrophosphate transferase [Treponema denticola ATCC 35405] | | | | |
| 6432 | 42526955 | 40 | 2.00E-16 | Treponema denticola ATCC 35405 | transferase [Treponema denticola ATCC 35405] | | | | 2.5.1.8 |
| 6435, | | | | | putative restriction enzyme modulator protein [Staphylococcus aureus subsp. aureus MRSA252] | | | | |
| 6436 | 49482330 | 39 | 1.00E-24 | Staphylococcus aureus subsp. aureus MRSA252 | modulator protein [Staphylococcus aureus subsp. aureus MRSA252] | | | | |
| 6437, | | | | | histidyl-tRNA synthetase [Clostridium tetani E88] | | | | |
| 6438 | 28211584 | 31 | 4.00E-22 | Clostridium tetani E88 | tRNA synthetase [Clostridium tetani E88] | | | | 6.1.1.21 |
| 6439, | 51573655 | 56 | 2.00E-25 | Borrelia garinii PBI | isoleucyl-tRNA synthetase [Borrelia garinii PBI] | | | | |
| 6440 | | | | Cytophaga hutchinsonii | tRNA synthetase [Borrelia garinii PBI] | | | | 6.1.1.5 |
| 6441, | 48854681 | 34 | 8.00E-13 | Cytophaga hutchinsonii | hypothetical protein Chut02002347 [Cytophaga hutchinsonii] | | | | |
| 6442 | | | | | hypothetical protein Chut02002840 [Cytophaga hutchinsonii] | | | | |
| 6443, | 48854173 | 28 | 1.00E-25 | Clostridium thermocellum | hypothetical protein Cite02000708 [Clostridium thermocellum ATCC 27405] | | | | |
| 6444 | 48859986 | 31 | 3.00E-25 | ATCC 27405 | | | | | |
| 6449, | | | | | COG2202: FOG: PAS/PAC domain [Anabaena variabilis ATCC 29413] | | | | 2.7.3.- |
| 6450 | 53765108 | 32 | 4.00E-25 | Anabaena variabilis ATCC 29413 | hypothetical protein LIC13227 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714224.1 hypothetical protein LA4044 | | | | |
| 645, | | | | | [Leptospira interrogans serovar Lai str. 56601] gb AA51242.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] | | | | |
| 6453, | | | | | gb AA571772.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | |
| 6454 | 45659049 | 37 | 2.00E-21 | Fiocruz L1-130 | | | | | |
| | | | | Thiobacillus denitrificans ATCC 25259 | COG1309: Transcriptional regulator [Thiobacillus denitrificans ATCC 25259] | | | | |
| 6455, | 52006061 | 35 | 9.00E-28 | ATCC 25259 | COG0774: UDP-3-O-acetyl-N-acetylglucosamine deacetylase [Cytophaga hutchinsonii] | | | | 4.2.1.- |
| 6456 | | | | | | | | | |
| 6457, | 48854755 | 59 | 1.00E-74 | Cytophaga hutchinsonii | | | | | |
| 6458 | | | | | | | | | |

| | | | | | | | | | |
|-------|----------|----|-----------|--|--|--|--|--|---------------|
| 6459, | 53797309 | 45 | 1.00E-60 | Chloroflexus aurantiacus | COG0215: CysteinyI-tRNA synthetase [Chloroflexus aurantiacus] | | | | 6.1.1.16 |
| 6460 | | | | Gloeobacter violaceus PCC 7421 | hypothetical protein glr2879 [Gloeobacter violaceus PCC 7421] dbj BAC90820.1 glr2879 [Gloeobacter violaceus PCC 7421] | | | | |
| 6461, | 37522448 | 28 | 3.00E-08 | | | | | | |
| 6462 | | | | Desulfotalea psychrophila LSv54 | hypothetical protein DP2762 [Desulfotalea psychrophila LSv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila LSv54] | | | | 2.1.1.14 4 |
| 6463, | 51246614 | 30 | 3.00E-21 | Desulfotalea psychrophila LSv54 | hypothetical protein DP2762 [Desulfotalea psychrophila LSv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila LSv54] | | | | 2.1.1.14 4 |
| 6464 | | | | Cytophaga hutchinsonii | COG0337: 3-dehydroquinase synthetase [Cytophaga hutchinsonii] signal transduction histidine kinase [Vibrio vulnificus YJ016] dbj BAC94870.1 signal transduction histidine kinase [Vibrio vulnificus YJ016] | | | | 4.2.3.4 |
| 6465, | 51246614 | 30 | 9.00E-21 | Desulfotalea psychrophila LSv54 | hypothetical protein DP2762 [Desulfotalea psychrophila LSv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila LSv54] | | | | 2.1.1.14 4 |
| 6466 | | | | Vibrio vulnificus YJ016 | | | | | 2.7.3.- |
| 6467, | 48856143 | 37 | 2.00E-18 | | | | | | 2.4.1.- |
| 6468 | 37680290 | 40 | 2.00E-13 | | | | | | |
| 6471, | | | | | | | | | |
| 6472 | | | | Geobacillus stearothermophilus | endo-1,4-beta-xylanase (EC 3.2.1.8) - Bacillus stearothermophilus sp P45703 XYN2_BACST Endo-1,4-beta-xylanase precursor (Xylanase) (1,4-beta-D-xylan xylanohydrolase) dbj BAA05668.1 xylanase [Geobacillus stearothermophilus] | | | | 3.2.1.8 |
| 6473, | 2126856 | 51 | 1.00E-48 | Geobacillus stearothermophilus | uroporphyrinogen-III synthase HemD, putative [Porphyromonas gingivalis W83] ref NP_904537.1 uroporphyrinogen-III synthase HemD, putative [Porphyromonas gingivalis W83] | | | | |
| 6475, | 34396369 | 50 | 1.00E-38 | Porphyromonas gingivalis W83 | | | | | |
| 6476 | | | | Geobacter sulfurreducens PCA | GTP pyrophosphokinase [Geobacter sulfurreducens PCA] gb AAR35612.1 GTP pyrophosphokinase [Geobacter sulfurreducens PCA] | | | | 2.7.6.5 |
| 6477, | 39997334 | 63 | 1.00E-125 | Geobacter sulfurreducens PCA | | | | | |
| 6478 | | | | Bdellovibrio bacteriovorus HD100 | GTP pyrophosphokinase [Bdellovibrio bacteriovorus HD100] emb CAE79448.1 GTP pyrophosphokinase [Bdellovibrio bacteriovorus HD100] | | | | 2.7.6.5 |
| 6479, | 42523075 | 51 | 1.00E-90 | Bdellovibrio bacteriovorus HD100 | | | | | |
| 6480 | | | | Methanosarcina mazei Go1 | Methyl-accepting chemotaxis protein [Methanosarcina mazei Go1] gb AAM30029.1 Methyl-accepting chemotaxis protein [Methanosarcina mazei Go1] | | | | |
| 6481, | 21226435 | 56 | 4.00E-35 | Methanosarcina mazei Go1 | | | | | |
| 6482 | | | | Deinococcus radiodurans | conserved hypothetical protein [Deinococcus radiodurans] pir H75297 conserved hypothetical protein - Deinococcus radiodurans (strain R1) ref NP_295956.1 hypothetical protein DR2234 [Deinococcus radiodurans R1] | | | | |
| 6483, | 6460039 | 32 | 5.00E-21 | Deinococcus radiodurans | | | | | |
| 6484 | | | | Symbiobacterium thermophilum IAM 14863 | two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863] dbj BAD40025.1 two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863] | | | | 2.7.3.- |
| 6485, | 51892178 | 29 | 1.00E-14 | | | | | | |
| 6486 | | | | | | | | | |

| | | | | | | | | | |
|-------|----------|----|----------|---|--|--|--|--|------------|
| 649, | 48856580 | 48 | 2.00E-31 | Cytophaga hutchinsonii | hypothetical protein Chut02000314 [Cytophaga hutchinsonii] | | | | |
| 650 | | | | Geobacter sulfurreducens PCA | trehalose-phosphatase [Geobacter sulfurreducens PCA] gb AAR35711.1 | | | | 3.1.3.12 |
| 6491, | 39997433 | 37 | 3.00E-21 | | trehalose-phosphatase [Geobacter sulfurreducens PCA] | | | | |
| 6492 | | | | | putative histidine ammonia-lyase [Staphylococcus aureus subsp. aureus MRSA252] emb CAG39036.1 putative histidine ammonia-lyase [Staphylococcus aureus subsp. aureus MRSA252] sp Q6GKT7 HUTH_STAAR Histidine ammonia-lyase (Histidase) | | | | 4.3.1.3 |
| 6495, | 49482261 | 40 | 2.00E-20 | Staphylococcus aureus subsp. aureus MRSA252 | thiamine biosynthesis protein [Pyrococcus horikoshii OT3] dbj BAA30255.1 | | | | |
| 6496 | | | | | 446aa long hypothetical thiamine biosynthesis protein [Pyrococcus horikoshii OT3] pir E71057 probable thiamin biosynthesis protein - Pyrococcus horikoshii | | | | 2.7.4.7 |
| 6503, | 14590982 | 43 | 7.00E-35 | Pyrococcus horikoshii OT3 | | | | | |
| 6504 | | | | | | | | | |
| 651, | 48856481 | 69 | 3.00E-55 | Cytophaga hutchinsonii | COG1225: Peroxiredoxin [Cytophaga hutchinsonii] | | | | 1.6.4.- |
| 652 | | | | | hypothetical protein mir4723 [Mesorhizobium loti MAFF303099] dbj BAB51313.1 mir4723 [Mesorhizobium loti MAFF303099] | | | | |
| 6511, | 13473959 | 37 | 5.00E-15 | Mesorhizobium loti MAFF303099 | | | | | |
| 6512 | | | | | | | | | |
| 6513, | 48854274 | 41 | 7.00E-47 | Cytophaga hutchinsonii | COG3239: Fatty acid desaturase [Cytophaga hutchinsonii] | | | | 1.14.99.25 |
| 6514 | | | | | | | | | |
| 6515, | 56675038 | 43 | 2.00E-15 | uncultured bacterium | cellulase [uncultured bacterium] | | | | |
| 6516 | | | | | | | | | |
| 6521, | 50287657 | 44 | 1.00E-18 | Candida glabrata | unnamed protein product [Candida glabrata] emb CAG59182.1 unnamed protein product [Candida glabrata CBS138] | | | | |
| 6522 | | | | | | | | | |
| 6527, | 52698490 | 45 | 5.00E-14 | Rickettsia akari str. Hartford | COG0080: Ribosomal protein L11 [Rickettsia akari str. Hartford] | | | | |
| 6528 | | | | | | | | | |
| 6529, | | | | Wolbachia endosymbiont of Drosophila melanogaster | ferrochelatase [Wolbachia endosymbiont of Drosophila melanogaster] gb AAS14832.1 ferrochelatase [Wolbachia endosymbiont of Drosophila melanogaster] | | | | 4.99.1.1 |
| 6530 | 42520983 | 57 | 3.00E-73 | melanogaster | | | | | |
| 653, | | | | | | | | | |
| 654 | 53759377 | 34 | 7.00E-14 | Methylobacillus flagellatus KT | COG2010: Cytochrome c, mono- and diheme variants [Methylobacillus flagellatus KT] | | | | 1.7.99.3 |
| 6533, | | | | | | | | | |
| 6534 | 53714870 | 42 | 6.00E-14 | Bacteroides fragilis YCH46 | RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD50328.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] | | | | |
| 6535, | | | | | | | | | |
| 6536 | 34396896 | 61 | 4.00E-48 | Porphyromonas gingivalis W83 | polyA polymerase family protein [Porphyromonas gingivalis W83] ref NP_905062.1 polyA polymerase family protein [Porphyromonas gingivalis W83] | | | | 2.7.7.19 |
| 6537, | | | | | | | | | |
| 6538 | 53712197 | 32 | 5.00E-13 | Bacteroides fragilis YCH46 | hypothetical protein BF0904 [Bacteroides fragilis YCH46] dbj BAD47655.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |

| | | | | | | | | |
|---------------|----------|----|-----------|--|---|--|-------------|---------|
| 6539, 6540 | 32477219 | 38 | 2.00E-18 | Rhodopirellula baltica SH 1 | hypothetical acetyltransferase [Rhodopirellula baltica SH 1] emb CAD77288.1 hypothetical acetyltransferase [Pirellula sp.] | | | |
| 6541, 6542 | 56750395 | 35 | 2.00E-07 | Synechococcus elongatus PCC 6301 | hypothetical protein syc0386_c [Synechococcus elongatus PCC 6301] dbj BAD78576.1 unknown protein [Synechococcus elongatus PCC 6301] | | | |
| 6543, 6544 | 17547951 | 31 | 1.00E-14 | Ralstonia solanacearum GMI1000 | PUTATIVE BACTERIOPHAGE-RELATED PROTEIN [Ralstonia solanacearum GMI1000] emb CAD17020.1 PUTATIVE BACTERIOPHAGE- RELATED PROTEIN [Ralstonia solanacearum] | | | |
| 6549, 6550 | 34396235 | 53 | 1.00E-64 | Porphyromonas gingivalis W83 | sensor histidine kinase [Porphyromonas gingivalis W83] ref NP_904403.1 | | | 2.7.3.- |
| 6551, 6552 | 48862211 | 47 | 5.00E-33 | Microbulbifer degradans 2-40 | sensor histidine kinase [Porphyromonas gingivalis W83] COG2989: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] | | | |
| 6553, 6554 | 53758638 | 37 | 2.00E-31 | Methylococcus capsulatus str. Bath | conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_113480.1 hypothetical protein MCA1003 [Methylococcus capsulatus str. Bath] | | | |
| 6555, 6556 | 48854335 | 41 | 8.00E-28 | Cytophaga hutchinsonii | COG3762: Predicted membrane protein [Cytophaga hutchinsonii] hypothetical protein MA4122 [Methanosarcina acetivorans C2A] ref NP_616740.1 hypothetical protein MA1814 [Methanosarcina acetivorans C2A] ref NP_615925.1 hypothetical protein MA0973 [Methanosarcina acetivorans C2A] gb AAM07470.1 predicted protein [Methanosarcina acetivorans str. C2A] gb AAM05220.1 predicted protein [Methanosarcina acetivorans str. C2A] gb AAM04405.1 predicted protein [Methanosarcina acetivorans str. C2A] | Methanosarcina acetivorans str. C2A, section 319 of 534 of the complete genome | 85 4.00E-57 | |
| 6565, 6566 | 20092915 | 74 | 1.00E-106 | Methanosarcina acetivorans C2A | 19 kDa subunit of the signal recognition particle [Methanopyrus kandleri AV19] gb AAM02764.1 19 kDa subunit of the signal recognition particle [Methanopyrus kandleri AV19] sp Q8TV49 SR19_METKA Signal recognition particle 19 kDa protein (SRP19) | | | |
| 6567, 6568 | 20094987 | 34 | 1.00E-07 | Methanopyrus kandleri AV19 | BpmI endonuclease-methyltransferase fusion protein type IIg [uncultured archaeon GZfos9D8] | | | |
| 6569, 6570 | 52550522 | 45 | 9.00E-54 | GZfos9D8 | glucose-inhibited division protein B [Porphyromonas gingivalis W83] ref NP_905481.1 glucose-inhibited division protein B [Porphyromonas gingivalis W83] sp Q7MV10 GIDB_PORGI Methyltransferase gldB (Glucose inhibited division protein B) | | | 3.1.- |
| 657, 658 | 31194811 | 45 | 1.00E-33 | Anopheles gambiae | glucose-inhibited division protein B [Porphyromonas gingivalis W83] ref NP_905481.1 glucose-inhibited division protein B [Porphyromonas gingivalis W83] sp Q7MV10 GIDB_PORGI Methyltransferase gldB (Glucose inhibited division protein B) | | | |
| 657, 658 | 34397317 | 41 | 2.00E-18 | Porphyromonas gingivalis W83 | glucose-inhibited division protein B [Porphyromonas gingivalis W83] ref NP_905481.1 glucose-inhibited division protein B [Porphyromonas gingivalis W83] sp Q7MV10 GIDB_PORGI Methyltransferase gldB (Glucose inhibited division protein B) | | | |

| | | | | | | | | |
|-------|----------|----|----------|---|--|--|--|----------|
| 6571, | 29349974 | 42 | 4.00E-38 | Bacteroides thetalaotomicron VPI-5482 | two-component system response regulator protein [Bacteroides thetalaotomicron VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetalaotomicron VPI-5482] | | | |
| 6572 | | | | | two-component response regulator [Bacillus halodurans C-125] dbj BAB07561.1 two-component response regulator [Bacillus halodurans C- 125] pir B84130 two-component response regulator BH3842 [imported] - Bacillus halodurans (strain C-125) | | | |
| 6575, | 15616404 | 42 | 7.00E-10 | Bacillus halodurans C-125 | | | | |
| 6581, | | | | Cytophaga hutchinsonii | COG0167: Dihydroorotate dehydrogenase [Cytophaga hutchinsonii] | | | 1.3.3.1 |
| 6582 | 48854536 | 55 | 5.00E-64 | Cytophaga hutchinsonii | COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Cytophaga hutchinsonii] | | | 2.3.1.51 |
| 6589, | 48853682 | 29 | 9.00E-20 | Clostridium thermocellum | COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | 2.7.3.- |
| 659, | 48860416 | 43 | 1.00E-28 | Chlorobium tepidum TLS | ATP-dependent Clp protease, ATP-binding subunit ClpC [Chlorobium tepidum TLS] gb AAM71439.1 ATP-dependent Clp protease, ATP-binding subunit ClpC [Chlorobium tepidum TLS] | | | |
| 6591, | 21673032 | 67 | 2.00E-17 | Nostoc sp. PCC 7120 | two-component sensor histidine kinase [Nostoc sp. PCC 7120] pir JAG1909 two-component sensor histidine kinase all0825 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB72782.1 two-component sensor histidine kinase [Nostoc sp. PCC 7120] | | | 2.7.3.- |
| 6593, | 17228320 | 34 | 8.00E-18 | | | | | |
| 6594 | ABP0398 | 1 | | Geobacter metallireducens GS | Desc: Human ORFX protein sequence SEQ ID NO:7944. Org: Homo sapiens | | | |
| 6595, | | | | | | | | |
| 6596 | 1 | 36 | 8.00E-11 | Geobacter metallireducens GS | COG2804: Type II secretory pathway, ATPase Pule/Tfp pilus assembly pathway, ATPase PilB [Geobacter metallireducens GS-15] | | | |
| 6601, | 48846577 | 55 | 3.00E-79 | Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 6602 | 48856489 | 45 | 4.00E-61 | | | | | |
| 6603, | | | | Leptospira interrogans serovar Lai str. 56601 | Para-aminobenzoate synthetase [Leptospira interrogans serovar Lai str. 56601] gb AAN47309.1 Para-aminobenzoate synthetase [Leptospira interrogans serovar lai str. 56601] | | | 4.1.3.- |
| 6604 | 24212810 | 38 | 3.00E-17 | | | | | |
| 6605, | | | | Idiomarina lohiensis L2TR | Secreted enzyme, contains two amidohydrolase related domains [Idiomarina lohiensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina lohiensis L2TR] | | | |
| 6609, | 56460818 | 49 | 1.00E-61 | Idiomarina lohiensis L2TR | Predicted hydrolase of the alpha/beta superfamily [Idiomarina lohiensis L2TR] gb AAV83358.1 Predicted hydrolase of the alpha/beta superfamily | | | 3.2.1.41 |
| 6610 | | | | | | | | |
| 6613, | | | | | | | | |
| 6614 | 56461626 | 36 | 7.00E-28 | Burkholderia cepacia R18194 | COG0604: NADPH:quinone reductase and related Zn-dependent oxidoreductases [Burkholderia cepacia R18194] | | | 1.6.5.5 |
| 6615, | 46311319 | 50 | 2.00E-18 | | | | | |
| 6616 | | | | | | | | |

| | | | | | | | | | |
|---------------|----------|----|-----------|---|--|--|--|--|----------|
| 6617, 6618 | 28211857 | 26 | 2.00E-16 | Clostridium tetani E88 | glycosyl transferase [Clostridium tetani E88] | | | | 2.4.1.- |
| 6619, 6620 | 53765041 | 28 | 1.00E-17 | Anabaena variabilis ATCC 29413 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Anabaena variabilis ATCC 29413] | | | | 2.-.-.- |
| 6623, 6624 | 48855616 | 67 | 1.00E-112 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | | |
| 6629, 6630 | 48854463 | 52 | 5.00E-49 | Cytophaga hutchinsonii | COG0193: Peptidyl-RNA hydrolase [Cytophaga hutchinsonii] | | | | 3.1.1.29 |
| 6631, 6632 | 53796261 | 74 | 5.00E-45 | Chloroflexus aurantiacus | COG4898: Uncharacterized protein conserved in bacteria [Chloroflexus aurantiacus] | | | | |
| 6637, 6638 | 21672859 | 38 | 8.00E-16 | Chlorobium tepidum TLS | ATP synthase F1, delta subunit [Chlorobium tepidum TLS] gb AAM71266.1 ATP synthase F1, delta subunit [Chlorobium tepidum TLS] | | | | 3.6.3.15 |
| 6643, 6644 | 48855342 | 39 | 7.00E-18 | Cytophaga hutchinsonii | COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii] | | | | 3.4.99.- |
| 6645, 6646 | 48854662 | 24 | 2.00E-19 | Cytophaga hutchinsonii | COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Cytophaga hutchinsonii] | | | | |
| 6647, 6648 | 48854272 | 43 | 2.00E-40 | Cytophaga hutchinsonii | COG0564: Pseudouridylylase synthases, 23S RNA-specific [Cytophaga hutchinsonii] | | | | 4.2.1.70 |
| 6649, 6650 | 47569655 | 58 | 1.00E-10 | Bacillus cereus G9241 | prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241] gb EAL12072.1 prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241] | | | | |
| 665, 666 | 17547951 | 31 | 1.00E-14 | Ralstonia solanacearum GMI1000 | PUTATIVE BACTERIOPHAGE-RELATED PROTEIN [Ralstonia solanacearum GMI1000] emb CAD17020.1 PUTATIVE BACTERIOPHAGE-RELATED PROTEIN [Ralstonia solanacearum] | | | | |
| 6651, 6652 | 31194343 | 51 | 9.00E-38 | Anopheles gambiae | ENSANGP00000000181 [Anopheles gambiae] | | | | |
| 6653, 6654 | 30020326 | 47 | 1.00E-40 | Bacillus cereus ATCC 14579 | Dihydrofolate reductase [Bacillus cereus ATCC 14579] gb AAP09158.1 Dihydrofolate reductase [Bacillus cereus ATCC 14579] | | | | 1.5.1.3 |
| 6655, 6656 | 53715360 | 48 | 1.00E-60 | Bacteroides fragilis YCH46 | ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] | | | | 3.6.1.- |
| 6657, 6658 | 48856124 | 44 | 3.00E-22 | Cytophaga hutchinsonii | COG0770: UDP-N-acetylmuramyl pentapeptide synthase [Cytophaga hutchinsonii] | | | | 6.3.2.15 |
| 6659, 6660 | 27382562 | 24 | 2.00E-18 | Bradyrhizobium japonicum USDA 110 | hypothetical protein bir7451 [Bradyrhizobium japonicum USDA 110] dbj BAC52716.1 bir7451 [Bradyrhizobium japonicum USDA 110] | | | | 6.3.2.4 |
| 6665, 6666 | 52006523 | 55 | 3.00E-40 | Thiobacillus denitrificans ATCC 25259 | COG0532: Translation initiation factor 2 (IF-2; GTPase) [Thiobacillus denitrificans ATCC 25259] | | | | |

| | | | | | | | | | |
|--------|----------|----|-----------|---|--|--|--|--|----------|
| 6667, | 23123559 | 30 | 7.00E-14 | Nostoc punctiforme PCC 73102 | COG5485: Predicted ester cyclase [Nostoc punctiforme PCC 73102] | | | | |
| 6668 | | | | Cytophaga hutchinsonii | | | | | 1.5.3.- |
| 6677, | 48856145 | 42 | 3.00E-37 | | COG0506: Proline dehydrogenase [Cytophaga hutchinsonii] | | | | |
| 6679, | | | | Pyrococcus furiosus DSM 3638 | glycosyl transferase [Pyrococcus furiosus DSM 3638] gb AAL81483.1 | | | | |
| 6680 | 18977731 | 34 | 4.00E-30 | Francisella tularensis subsp. tularensis Schu 4 | glycosyl transferase [Pyrococcus furiosus DSM 3638] | | | | |
| 6681, | | | | | hypothetical protein FTT0522 [Francisella tularensis subsp. tularensis Schu 4] emb CAG45155.1 conserved hypothetical protein [Francisella tularensis subsp. tularensis] | | | | 2.1.1.72 |
| 6682 | 56707657 | 52 | 1.00E-28 | | | | | | |
| 6683, | | | | synthetic construct | hypothetical protein FTT0520 [synthetic construct] | | | | |
| 6684 | 57339644 | 49 | 9.00E-50 | Bdellovibrio bacteriovorus HD100 | putative potassium/proton antiporter [Bdellovibrio bacteriovorus HD100] | | | | |
| 6687, | | | | | emb CAE80097.1 putative potassium/proton antiporter [Bdellovibrio bacteriovorus HD100] | | | | |
| 6688 | 42523724 | 44 | 4.00E-18 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT2008 [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 6689, | | | | | gb AAO77115.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 6690 | 29347418 | 43 | 1.00E-46 | Cytophaga hutchinsonii | COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Cytophaga hutchinsonii] | | | | 2.7.6.5 |
| 6693, | 48856298 | 58 | 1.00E-109 | | | | | | |
| 6694 | | | | Cytophaga hutchinsonii | | | | | |
| 6695, | | | | | COG1522: Transcriptional regulators [Cytophaga hutchinsonii] | | | | |
| 6696 | 48856980 | 50 | 5.00E-39 | Thermoanaerobacter tengcongensis MB4 | Response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain [Thermoanaerobacter tengcongensis MB4] | | | | |
| 6697, | | | | | gb AAM25604.1 Response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain [Thermoanaerobacter tengcongensis MB4] | | | | 2.7.3.- |
| 6698 | 20808829 | 36 | 8.00E-11 | Clostridium thermocellum ATCC 27405 | COG1040: Predicted amidophosphoribosyltransferases [Clostridium thermocellum ATCC 27405] | | | | |
| 6699, | | | | Legionella pneumophila str. Paris | hypothetical protein plpp0078 [Legionella pneumophila str. Paris] | | | | |
| 6700. | 48859351 | 31 | 4.00E-19 | | emb CAH17255.1 hypothetical protein [Legionella pneumophila str. Paris] | | | | |
| 67, 68 | 54295921 | 38 | 3.00E-11 | Cytophaga hutchinsonii | hypothetical protein Chut02003551 [Cytophaga hutchinsonii] | | | | |
| 6701, | | | | | | | | | |
| 6702 | 48853695 | 55 | 6.00E-65 | Nostoc punctiforme PCC 73102 | hypothetical protein Npun02006402 [Nostoc punctiforme PCC 73102] | | | | |
| 6703, | | | | | COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] | | | | 6.2.1.3 |
| 6704 | 23125186 | 36 | 4.00E-22 | Cytophaga hutchinsonii | | | | | |
| 6707, | | | | | | | | | |
| 6708 | 48854120 | 51 | 2.00E-74 | | | | | | |

| | | | | | | | | | |
|-------|----------|----|-----------|---|--|--|--|--|----------|
| 6709, | 48855792 | 38 | 3.00E-25 | Cytophaga hutchinsonii | COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | | |
| 6710 | | | | Ralstonia solanacearum | PUTATIVE BACTERIOPHAGE-RELATED PROTEIN [Ralstonia solanacearum GM11000] emb CAD17020.1 PUTATIVE BACTERIOPHAGE-RELATED PROTEIN [Ralstonia solanacearum] | | | | |
| 671, | 17547951 | 30 | 2.00E-13 | | two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 672 | | | | Bacteroides thetaiotaomicron | gb AAO78783.1 two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 6721, | 29349086 | 24 | 1.00E-12 | VPI-5482 | putative two-component system sensor protein histidine kinase [Bacteroides fragilis YCH46] dbj BAD50632.1 putative two-component system sensor protein histidine kinase [Bacteroides fragilis YCH46] | | | | 2.7.3.- |
| 6723, | 53715174 | 39 | 3.00E-38 | YCH46 | COG2137: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 6724 | | | | Cytophaga hutchinsonii | | | | | |
| 6727, | 48854316 | 45 | 4.00E-32 | | | | | | |
| 6728 | | | | Leptospira interrogans serovar Lai str. 56601 | methylmalonyl-CoA mutase [Leptospira interrogans serovar Lai str. 56601] gb AAN50154.1 methylmalonyl-CoA mutase [Leptospira interrogans serovar lai str. 56601] | | | | 5.4.99.2 |
| 6729, | 24215655 | 56 | 2.00E-93 | Cytophaga hutchinsonii | COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins [Cytophaga hutchinsonii] | | | | |
| 673, | 48854535 | 73 | 1.00E-101 | Bacteroides thetaiotaomicron | transcriptional regulator, TetR family [Bacteroides thetaiotaomicron VPI-5482] gb AAO76513.1 transcriptional regulator, TetR family [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 6731, | 29346816 | 31 | 3.00E-12 | VPI-5482 | hypothetical protein Atu0403 [Agrobacterium tumefaciens str. C58] gb AAL41424.1 conserved hypothetical protein [Agrobacterium tumefaciens str. C58] gb AAK86218.1 AGR_C_710p [Agrobacterium tumefaciens str. C58] pir AB2626 conserved hypothetical protein Atu0403 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir A97408 hypothetical protein AGR_C_710 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) ref NP_353433.1 hypothetical protein AGR_C_710 [Agrobacterium tumefaciens str. C58] | | | | |
| 6732 | | | | Agrobacterium tumefaciens str. C58 | | | | | |
| 6735, | 17934318 | 33 | 8.00E-14 | | hypothetical protein BF3507 [Bacteroides fragilis YCH46] dbj BAD50250.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 6736 | | | | Bacteroides fragilis YCH46 | COG0188: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit [Cytophaga hutchinsonii] | | | | 5.99.1.- |
| 6737, | 53714792 | 43 | 8.00E-17 | Cytophaga hutchinsonii | Desc.H3 homologue of prolyl-tripeptidyl peptidase DPP. Org: Porphyromonas gingivalis | | | | |
| 6738 | | | | | | | | | |
| 6739, | 48853743 | 60 | 2.00E-91 | | | | | | |
| 6740 | AA1851 | 35 | 2.00E-08 | | | | | | |
| 6741, | | | | | | | | | |
| 6742 | 2 | | | | | | | | |

| | | | | | | | | |
|-------|----------|----|----------|--|--|--|----|----------|
| 6749, | 53715862 | 53 | 2.00E-54 | Bacteroides fragilis YCH46 | DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] | | | |
| 6750 | | | | | dbj BAD51320.1 DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] | | | |
| 675, | 21226234 | 63 | 2.00E-38 | Methanosarcina mazel Go1 | hypothetical protein MM0132 [Methanosarcina mazel Go1] gb AAM29828.1 conserved protein [Methanosarcina mazel Goe1] | | | |
| 6751, | 48854843 | 38 | 5.00E-45 | Cytophaga hutchinsonii | COG0196: FAD synthase [Cytophaga hutchinsonii] | | | 2.7.1.26 |
| 6753, | 48855703 | 33 | 4.00E-27 | Cytophaga hutchinsonii | COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii] | | | 2.7.3.- |
| 6754 | | | | | | | | |
| 6757, | 48853840 | 32 | 9.00E-25 | Cytophaga hutchinsonii | COG0438: Glycosyltransferase [Cytophaga hutchinsonii] | | | |
| 6758 | | | | | hypothetical protein ebA3316 [Azoarcus sp. EbN1] emb CAI07993.1 conserved hypothetical protein [Azoarcus sp. EbN1] | | | |
| 6763, | 56477305 | 34 | 3.00E-11 | Azoarcus sp. EbN1 | | | | |
| 6764 | | | | Leuconostoc mesenteroides subsp. mesenteroides | | | | |
| 6765, | 23025125 | 54 | 1.00E-57 | ATCC 8293 | COG4974: Site-specific recombinase XerD [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293] | | 84 | 1.00E-10 |
| 6767, | 53760034 | 52 | 2.00E-38 | Methylobacillus flagellatus KT | COG2870: ADP-heptose synthase, bifunctional sugar kinase/adenylyltransferase [Methylobacillus flagellatus KT] | | | 2.7.7.39 |
| 6768 | | | | Thermoanaerobacter tengcongensis MB4 | UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] gb AAM25671.1 UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] | | | 6.3.2.15 |
| 6769, | 20808896 | 39 | 2.00E-35 | Microbulbifer degradans 2-40 | | | | |
| 6770 | | | | | | | | |
| 677, | 53714426 | 60 | 5.00E-50 | Bacteroides fragilis YCH46 | hypothetical protein BF3139 [Bacteroides fragilis YCH46] dbj BAD49884.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 678 | | | | Thermoanaerobacter tengcongensis MB4 | UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] gb AAM25671.1 UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] | | | 6.3.2.15 |
| 6771, | | | | | | | | |
| 6772 | 20808896 | 38 | 4.00E-36 | Microbulbifer degradans 2-40 | COG0216: Protein chain release factor A [Microbulbifer degradans 2-40] | | | |
| 6773, | 48863872 | 52 | 1.00E-81 | | | | | |
| 6774 | ABB5552 | 37 | 1.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | Desc: Lactococcus lactis protein yweC, Org: Lactococcus lactis IL1403 DNA Pol III Epsilon Chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76470.1 DNA Pol III Epsilon Chain [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.7.7 |
| 6775, | | | | | | | | |
| 6776 | 3 | | | Cytophaga hutchinsonii | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | |
| 6777, | 29346773 | 53 | 2.00E-54 | | | | | |
| 6778 | | | | | | | | |
| 6781, | 48855683 | 53 | 3.00E-42 | | | | | |
| 6782 | | | | | | | | |

| | | | | | | | | | |
|-------|----------|----|----------|---|--|--|--|--|---------|
| 6783, | 15678598 | 47 | 5.00E-29 | Methanothermobacter thermautotrophicus str. Delta H | hypothetical protein MTH570 [Methanothermobacter thermautotrophicus str. Delta H] gi AAB85076.1 unknown [Methanothermobacter thermautotrophicus str. Delta H] pir E69175 hypothetical protein MTH570 - Methanothermobacterium thermotrophicum (strain Delta H) | | | | |
| 6785, | 53714487 | 56 | 3.00E-44 | Bacteroides fragilis YCH46 | SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD48945.1 SsrA- binding protein [Bacteroides fragilis YCH46] | | | | |
| 679, | 53712369 | 24 | 2.00E-15 | Bacteroides fragilis YCH46 | peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] dbj BAD47827.1 peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] | | | | |
| 6791, | | | | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] | | | | |
| 6792, | 53714651 | 40 | 3.00E-42 | Bacteroides fragilis YCH46 | two-component system response regulator [Bacteroides fragilis YCH46] | | | | |
| 6793, | 48831352 | 24 | 5.00E-23 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | | 2.7.3.- |
| 6797, | | | | Thermococcus kodakaraensis | predicted transcription regulator, DUF118 helix-turn-helix family [Thermococcus kodakaraensis] ref YP_184182.1 predicted transcription regulator, DUF118 helix-turn-helix family [Thermococcus kodakaraensis] | | | | |
| 6798 | 57160028 | 30 | 3.00E-09 | Bacteroides thetataotomicron VPI-5482 | ABC transporter, ATP-binding protein [Bacteroides thetaiotaomicron VPI- 5482] gi AAO77601.1 ABC transporter, ATP-binding protein [Bacteroides thetataotomicron VPI-5482] | | | | 1.8.- |
| 6799, | 29347904 | 66 | 3.00E-77 | Cytophaga hutchinsonii | COG1331: Highly conserved protein containing a thioredoxin domain [Cytophaga hutchinsonii] | | | | |
| 6801, | 48856612 | 44 | 1.00E-32 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gi EAL56874.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 6802 | 57168392 | 38 | 5.00E-40 | Wolinella succinogenes DSM 1740 | PUTATIVE METHYL TRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09463.1 PUTATIVE METHYL TRANSFERASE [Wolinella succinogenes] | | | | |
| 6803, | 34556748 | 32 | 7.00E-17 | Clostridium thermocellum ATCC 27405 | COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | | 2.7.3.- |
| 6804 | 48858932 | 42 | 9.00E-36 | Trichodesmium erythraeum IMS101 | COG2314: Predicted membrane protein [Trichodesmium erythraeum IMS101] | | | | |
| 6805, | 48894405 | 27 | 4.00E-08 | Porphyromonas gingivalis W83 | MutS2 family protein [Porphyromonas gingivalis W83] ref NP_904691.1 MutS2 family protein [Porphyromonas gingivalis W83] | | | | |
| 6806 | 34396524 | 36 | 2.00E-35 | Bacteroides fragilis YCH46 | hypothetical protein BF1779 [Bacteroides fragilis YCH46] dbj BAD48526.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 6807, | 53713068 | 29 | 1.00E-09 | Bacteroides fragilis YCH46 | | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|----------|
| 6817, 6818 | 48478030 | 36 | 4.00E-16 | Picrophilus torridus DSM 9790 | hypothetical conserved protein DUF52 [Picrophilus torridus DSM 9790] gb AA143543.1 hypothetical conserved protein DUF52 [Picrophilus torridus DSM 9790] | | | |
| 6821, 6822 | 15896812 | 43 | 1.00E-28 | acyl-carrier-protein Wolinella succinogenes DSM 1740 | 3-oxoacyl-acyl-carrier-protein synthase III [Clostridium acetobutylicum ATCC 824] gb AAK81501.1 3-oxoacyl-acyl-carrier-protein synthase III [Clostridium acetobutylicum ATCC 824] p B97339 3-oxoacyl-acyl-carrier-protein synthase III [imported] - Clostridium acetobutylicum sp Q97DA2 FABH_CLOAB 3-oxoacyl-acyl-carrier-protein synthase III (Beta-ketoacyl-ACP synthase III) (KAS III) | | | 2.3.1.41 |
| 6823, 6824 | 34557550 | 38 | 9.00E-20 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1180 [Wolinella succinogenes DSM 1740] emb CAE10265.1 hypothetical protein [Wolinella succinogenes] | | | |
| 6825, 6826 | 34557550 | 33 | 7.00E-26 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1180 [Wolinella succinogenes DSM 1740] emb CAE10265.1 hypothetical protein [Wolinella succinogenes] | | | |
| 6827, 6828 | 7592813 | 47 | 6.00E-64 | Actinobacillus actinomycetemcomitans | GDP-mannose pyrophosphorylase homolog [Actinobacillus actinomycetemcomitans] | | | 2.7.7.22 |
| 6829, 6830 | 48853833 | 49 | 3.00E-41 | Cytophaga hutchinsonii | COG0576: Molecular chaperone GrpE (heat shock protein) [Cytophaga hutchinsonii] | | | |
| 6831, 6832 | 45358644 | 54 | 4.00E-76 | Methanococcus maripaludis S2 | putative LPS biosynthesis protein WbpG [Methanococcus maripaludis S2] emb CAF30637.1 putative LPS biosynthesis protein WbpG [Methanococcus maripaludis S2] | | | |
| 6833, 6834 | 30249085 | 52 | 4.00E-57 | Nitrosomonas europaea ATCC 19718 | Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb CAD85004.1 Transposase IS4 family [Nitrosomonas europaea ATCC 19718] | | | |
| 6837, 6838 | 45547643 | 30 | 5.00E-27 | Rubrobacter xylanophilus DSM 9941 | COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Rubrobacter xylanophilus DSM 9941] | | | |
| 6847, 6848 | 48854546 | 35 | 1.00E-15 | Cytophaga hutchinsonii | COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii] | | | |
| 6849, 6850 | 53760393 | 40 | 4.00E-48 | Methylobacillus flagellatus KT | COG2821: Membrane-bound lytic murein transglycosylase [Methylobacillus flagellatus KT] | | | 3.2.1.- |
| 685, 686 | 48839466 | 94 | 2.00E-63 | Methanosarcina barkeri str. fusaro | COG1335: Amidases related to nicotinamidase [Methanosarcina barkeri str. fusaro] | | | |
| 6851, 6852 | 14994235 | 32 | 2.00E-31 | Scyllorhinus torazame | L-gulonolactone oxidase [Scyllorhinus torazame] sp Q90YK3 GGLO_SCYTO L-gulonolactone oxidase (LGO) (L-gulonolactone oxidase) (GLO) | | | 1.1.3.8 |
| 6855, 6856 | 57506273 | 61 | 8.00E-45 | Campylobacter upsaliensis RM3195 | Fic family protein [Campylobacter upsaliensis RM3195] gb EAL52255.1 Fic family protein [Campylobacter upsaliensis RM3195] | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|----|----------|----------|
| 6857, 6858 | 52006879 | 36 | 8.00E-45 | Thiobacillus denitrificans ATCC 25259 | COG2199: FOG: GGDEF domain [Thiobacillus denitrificans ATCC 25259] phosphopantothenoylcysteine decarboxylase/phosphopantothenate-- cysteine ligase [Campylobacter lari RM2100] gb EAL55505.1 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-- cysteine ligase [Campylobacter lari RM2100] | Clostridium acetobutylicum ATCC 824 section 66 of 356 of the complete genome | 89 | 7.00E-07 | 2.7.3.- |
| 6859, 6860 | 57240391 | 47 | 6.00E-19 | Campylobacter lari RM2100 | | | | | |
| 6861, 6862 | 52007207 | 37 | 1.00E-50 | Thiobacillus denitrificans ATCC 25259 | COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Thiobacillus denitrificans ATCC 25259] | | | | 3.1.21.3 |
| 6865, 6866 | 53712714 | 28 | 5.00E-20 | Bacteroides fragilis YCH46 | hypothetical protein BF1421 [Bacteroides fragilis YCH46] dbj BAD48172.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 6869, 6870 | 48895292 | 50 | 2.00E-35 | Trichodesmium erythraeum IMS101 | COG4123: Predicted O-methyltransferase [Trichodesmium erythraeum IMS101] | | | | 2.1.1.- |
| 687, 688 | 29349986 | 34 | 4.00E-21 | Bacteroides thetaitaomicron VPI-5482 | transposase [Bacteroides thetaitaomicron VPI-5482] ref NP_812545.1 transposase [Bacteroides thetaitaomicron VPI-5482] ref NP_811586.1 transposase [Bacteroides thetaitaomicron VPI-5482] ref NP_811340.1 transposase [Bacteroides thetaitaomicron VPI-5482] ref NP_811312.1 transposase [Bacteroides thetaitaomicron VPI-5482] ref NP_810805.1 integrase [Bacteroides thetaitaomicron VPI-5482] ref NP_809831.1 integrase [Bacteroides thetaitaomicron VPI-5482] ref NP_809271.1 transposase [Bacteroides thetaitaomicron VPI-5482] gb AAO79683.1 transposase [Bacteroides thetaitaomicron VPI-5482] gb AAO78739.1 transposase [Bacteroides thetaitaomicron VPI-5482] gb AAO77780.1 transposase [Bacteroides thetaitaomicron VPI-5482] gb AAO77534.1 transposase [Bacteroides thetaitaomicron VPI-5482] gb AAO77506.1 transposase [Bacteroides thetaitaomicron VPI-5482] gb AAO76999.1 integrase [Bacteroides thetaitaomicron VPI-5482] gb AAO76025.1 integrase [Bacteroides thetaitaomicron VPI-5482] gb AAO75465.1 transposase [Bacteroides thetaitaomicron VPI-5482] | | | | |
| 6871, 6872 | 46446869 | 37 | 4.00E-38 | Parachlamydia sp. UWE25 | putative cysteinyl tRNA synthetase [Parachlamydia sp. UWE25] emb CAF23959.1 putative cysteinyl tRNA synthetase [Parachlamydia sp. UWE25] | | | | 6.1.1.16 |
| 6873, 6874 | 45657880 | 54 | 2.00E-60 | Leptospira interrogans serovar Copenhagani str. Fiocruz L1-130 | cysteinyl-tRNA synthetase [Leptospira Interrogans serovar Copenhagani str. Fiocruz L1-130] gb AAS70603.1 cysteinyl-tRNA synthetase [Leptospira interrogans serovar Copenhagani str. Fiocruz L1-130] | | | | 6.1.1.16 |

| | | | | | | | | |
|---------------|----------|----|----------|---------------------------------------|--|--|-------------|----------|
| 6875, 6876 | 34557269 | 53 | 2.00E-75 | Wolinella succinogenes DSM 1740 | ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolinella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolinella succinogenes] | | | 3.6.1.- |
| 6877, 6878 | 34557269 | 64 | 2.00E-65 | Wolinella succinogenes DSM 1740 | ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolinella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolinella succinogenes] | | | 3.6.1.- |
| 6881, 6882 | 48855504 | 58 | 8.00E-46 | Cytophaga hutchinsonii | COG0045: Succinyl-CoA synthetase, beta subunit [Cytophaga hutchinsonii] | | | 6.2.1.5 |
| 6883, 6884 | 34558415 | 47 | 1.00E-50 | Wolinella succinogenes DSM 1740 | PUTATIVE HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE1130.1 PUTATIVE HYDROLASE [Wolinella succinogenes] | | | 3.1.3.18 |
| 6885, 6886 | 34557246 | 43 | 2.00E-35 | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | | | |
| 6887, 6888 | 34557873 | 48 | 3.00E-48 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1545 [Wolinella succinogenes DSM 1740] emb CAE10588.1 conserved hypothetical protein [Wolinella succinogenes] orf [Wolinella succinogenes] pir S50154 hypothetical protein 2 - Wolinella | | | |
| 6889, 6890 | 558266 | 62 | 1.00E-67 | Wolinella succinogenes | succinogenes | | | |
| 689, 690 | 48855088 | 60 | 2.00E-73 | Cytophaga hutchinsonii | COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Cytophaga hutchinsonii] | | | 1.6.6.4 |
| 6891, 6892 | 34557291 | 46 | 5.00E-22 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 6895, 6896 | 558266 | 55 | 2.00E-43 | Wolinella succinogenes | orf [Wolinella succinogenes] pir S50154 hypothetical protein 2 - Wolinella succinogenes | | | |
| 6897, 6898 | 558266 | 61 | 3.00E-71 | Wolinella succinogenes | orf [Wolinella succinogenes] pir S50154 hypothetical protein 2 - Wolinella succinogenes | | | |
| 69, 70 | 48783402 | 23 | 7.00E-08 | Burkholderia fungorum LB400 | COG0396: ABC-type transport system involved in Fe-S cluster assembly, ATPase component [Burkholderia fungorum LB400] | | | |
| 6903, 6904 | 57241681 | 71 | 2.00E-88 | Campylobacter lari RM2100 | DNA gyrase, B subunit [Campylobacter lari RM2100] gb EAL54351.1 DNA gyrase, B subunit [Campylobacter lari RM2100] | | 85 2.00E-28 | 5.99.1.3 |
| 6905, 6906 | 34556843 | 39 | 6.00E-35 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0414 [Wolinella succinogenes DSM 1740] emb CAE09558.1 conserved hypothetical protein [Wolinella succinogenes] | | | 2.7.3.- |

| | | | | | | | | | | |
|---------------|----------|----|----------|------------------|---|---|--|--|--|---------|
| 6907, 6908 | 34558149 | 31 | 1.00E-17 | 1740 | Wolinella succinogenes DSM | SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes DSM 1740] emb[CAE10864.1] | | | | |
| 6909, 6910 | 57167731 | 62 | 1.00E-29 | RM2228 | Campylobacter coli RM2228 | SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes] conserved hypothetical protein TIGR00044 [Campylobacter coli RM2228] gbl[EAL57517.1] conserved hypothetical protein TIGR00044 [Campylobacter coli RM2228] | | | | |
| 6911, 6912 | 34556508 | 48 | 4.00E-27 | 1740 | Wolinella succinogenes DSM | PUTATIVE UDP-GLUCOSE 6-DEHYDROGENASE [Wolinella succinogenes DSM 1740] emb[CAE09223.1] PUTATIVE UDP-GLUCOSE 6- DEHYDROGENASE [Wolinella succinogenes] | | | | 1.1.1.- |
| 6913, 6914 | 23111511 | 37 | 1.00E-14 | hafnense DCB-2 | Desulfotobacterium hafnense DCB-2 | COG0494: NTP pyrophosphohydrolases including oxidative damage repair enzymes [Desulfotobacterium hafnense DCB-2] | | | | 3.6.1.- |
| 6915, 6916 | 4972799 | 63 | 3.00E-29 | fennelliae | Helicobacter fennelliae | DNA-directed RNA polymerase beta and beta' subunits [Helicobacter fennelliae] | | | | 2.7.7.6 |
| 6917, 6918 | 34556481 | 29 | 4.00E-44 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb[CAE09196.1] conserved hypothetical protein [Wolinella succinogenes] | | | | 2.7.3.- |
| 6923, 6924 | 45523345 | 39 | 1.00E-12 | watsonii WH 8501 | Crocospaera watsonii WH 8501 | COG1253: Hemolysins and related proteins containing CBS domains [Crocospaera watsonii WH 8501] | | | | |
| 6925, 6926 | 34557967 | 45 | 8.00E-25 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS1651 [Wolinella succinogenes DSM 1740] emb[CAE10682.1] conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 6927, 6928 | 34558795 | 25 | 3.00E-11 | 6C6 | Alvinella pompejana epibiont 6C6 | TonB-dependent receptor [Alvinella pompejana epibiont 6C6] | | | | |
| 6929, 6930 | 45523887 | 46 | 1.00E-66 | watsonii WH 8501 | Crocospaera watsonii WH 8501 | COG5433: Transposase [Crocospaera watsonii WH 8501] | | | | |
| 693, 694 | 46187901 | 29 | 6.00E-13 | syningae B728a | Pseudomonas syningae pv. syningae B728a | COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a] ref[P_00205512.1] COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a] | | | | |
| 6931, 6932 | 48845760 | 34 | 2.00E-09 | 15 | Geobacter metallireducens GS | COG2234: Predicted aminopeptidases [Geobacter metallireducens GS-15] | | | | |
| 6945, 6946 | 53692806 | 34 | 1.00E-16 | somnus 129PT | Haemophilus somnus 129PT | hypothetical protein Hsom02000321 [Haemophilus somnus 129PT] | | | | |
| 6947, 6948 | 21228303 | 22 | 6.00E-12 | mazei Go1 | Methanosarcina mazei Go1 | hypothetical protein MM2201 [Methanosarcina mazei Go1] gb[AAM31897.1] hypothetical protein [Methanosarcina mazei Go1] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|--|---------|
| 6949, 6950 | 53691562 | 41 | 2.00E-55 | Desulfovibrio desulfuricans G20 | COG3437: Response regulator containing a CheY-like receiver domain and an HD-GYP domain [Desulfovibrio desulfuricans G20] | | | | |
| 695, 696 | 21674062 | 52 | 1.00E-73 | Chlorobium tepidum TLS | preprotein translocase SecA subunit [Chlorobium tepidum TLS] gb AAAM72469.1 preprotein translocase SecA subunit [Chlorobium tepidum TLS] | | | | |
| 6951, 6952 | 53711371 | 40 | 8.00E-26 | Bacteroides fragilis YCH46 | putative zinc ABC transporter zinc-binding protein [Bacteroides fragilis YCH46] db BAD46829.1 putative zinc ABC transporter zinc-binding protein [Bacteroides fragilis YCH46] | | | | |
| 6953, 6954 | 57168109 | 37 | 1.00E-21 | Campylobacter coli RM2228 | signal-transducing protein, histidine kinase, putative [Campylobacter coli RM2228] gb EAL57152.1 signal-transducing protein, histidine kinase, putative [Campylobacter coli RM2228] | | | | 2.7.3.- |
| 6955, 6956 | 16330194 | 51 | 5.00E-07 | Synechocystis sp. PCC 6803 | carboxynorspermidine decarboxylase [Synechocystis sp. PCC 6803] db BAA17602.1 carboxynorspermidine decarboxylase [Synechocystis sp. PCC 6803] pir S77268 carboxynorspermidine decarboxylase - Synechocystis sp. (strain PCC 6803) | | | | 4.1.1.- |
| 6957, 6958 | 57237871 | 30 | 5.00E-13 | Campylobacter jejuni RM1221 | hypothetical protein CJE1127 [Campylobacter jejuni RM1221] gb AAW35454.1 hypothetical protein CJE1127 [Campylobacter jejuni RM1221] | | | | |
| 6959, 6960 | 48630999 | 31 | 2.00E-17 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] DNA POLYMERASE III SUBUNITS GAMMA AND TAU [Wolnella succinogenes DSM 1740] emb CAE11094.1 DNA POLYMERASE III SUBUNITS GAMMA AND TAU [Wolnella succinogenes] | | | | 2.7.3.- |
| 6961, 6962 | 34558379 | 34 | 2.00E-08 | Photobacterium profundum SS9 | hypothetical protein PBPRB0486 [Photobacterium profundum SS9] emb CAG22359.1 hypothetical protein [Photobacterium profundum] | | | | |
| 6967, 6968 | 54302166 | 33 | 2.00E-32 | Campylobacter jejuni subsp. jejuni NCTC 11168 | hypothetical protein Cj0458c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281645.1 hypothetical protein Cj0458c [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81390 hypothetical protein Cj0458c [imported] - Campylobacter jejuni (strain NCTC 11168) | | | | 1.8.- |
| 697, 698 | 48854227 | 50 | 1.00E-11 | Cytophaga hutchinsonii | COG2908: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | | |
| 6971, 6972 | 57240857 | 61 | 1.00E-62 | Campylobacter lari RM2100 | tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter lari RM2100] gb EAL55250.1 tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter lari RM2100] | | | | 1.8.- |
| 6973, 6974 | 37520502 | 24 | 2.00E-10 | Gloeobacter violaceus PCC 7421 | potassium channel protein [Gloeobacter violaceus PCC 7421] db BAC88874.1 potassium channel protein [Gloeobacter violaceus PCC 7421] | | | | |
| 6975, 6976 | 48863979 | 32 | 2.00E-36 | Microbulbifer degradans 2-40 | COG1033: Predicted exporters of the RND superfamily [Microbulbifer degradans 2-40] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|--|---------------|
| 6977, 6978 | 34556927 | 60 | 3.00E-97 | Wolinella succinogenes DSM 1740 | PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09642.1 PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes] | | | | |
| 6979, 6980 | 23015878 | 54 | 5.00E-78 | Magnetospirillum magnetotacticum MS-1 | COG2703: Hemerythrin [Magnetospirillum magnetotacticum MS-1] | | | | |
| 6981, 6982 | 52007207 | 47 | 7.00E-68 | Thiobacillus denitrificans ATCC 25259 | COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Thiobacillus denitrificans ATCC 25259] | | | | 3.1.21.3 |
| 6983, 6984 | 48839711 | 46 | 9.00E-25 | Methanosarcina barkeri str. fusaro | COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro] | | | | 3.1.21.3 |
| 6985, 6986 | 16272498 | 44 | 3.00E-16 | Haemophilus Influenzae Rd KW20 | hypothetical protein HI0554 [Haemophilus Influenzae Rd KW20] gb AAC22217.1 H. Influenzae predicted coding region HI0554 [Haemophilus influenzae Rd KW20] pir [E64009 hypothetical protein HI0554 - Haemophilus influenzae (strain Rd KW20) sp P44014 Y554_HAEIN Hypothetical protein HI0554] | | | | |
| 6987, 6988 | 48860427 | 49 | 3.00E-63 | Clostridium thermocellum ATCC 27405 | COG1052: Lactate dehydrogenase and related dehydrogenases [Clostridium thermocellum ATCC 27405] | | | | 1.1.1.95 |
| 6989, 6990 | 34558097 | 46 | 7.00E-51 | Wolinella succinogenes DSM 1740 | MULTIDRUG-EFFLUX TRANSPORTER [Wolinella succinogenes DSM 1740] emb CAE10812.1 MULTIDRUG-EFFLUX TRANSPORTER [Wolinella succinogenes] | | | | |
| 699, 700 | 48854228 | 54 | 1.00E-42 | Cytophaga hutchinsonii | COG1819: Glycosyl transferases, related to UDP-glucuronosyltransferase [Cytophaga hutchinsonii] | | | | |
| 6991, 6992 | 53712708 | 35 | 3.00E-25 | Bacteroides fragilis YCH46 | hypothetical protein BF1415 [Bacteroides fragilis YCH46] db BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 6995, 6996 | 48864065 | 45 | 1.00E-30 | Microbulbifer degradans 2-40 | COG0328: Ribonuclease HI [Microbulbifer degradans 2-40] | | | | |
| 6997, 6998 | 48864065 | 43 | 4.00E-12 | Microbulbifer degradans 2-40 | COG0328: Ribonuclease HI [Microbulbifer degradans 2-40] | | | | |
| 6999, 7000 | 49237161 | 53 | 7.00E-38 | Moorella thermoacetica ATCC 39073 | COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Moorella thermoacetica ATCC 39073] | | | | 1.2.1.2 |
| 7003, 7004 | 23130700 | 32 | 2.00E-25 | Nostoc punctiforme PCC 73102 | COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Nostoc punctiforme PCC 73102] | | | | 1.1.1.10 0 |
| 7005, 7006 | 15612820 | 58 | 2.00E-58 | Bacillus halodurans C-125 | urease accessory protein [Bacillus halodurans C-125] db BAB03976.1 urease accessory protein [Bacillus halodurans C-125] pir [A83682 urease accessory protein ureG [imported] - Bacillus halodurans (strain C-125)] | | | | |

| | | | | | | | | |
|---------------|-----------|----|----------|--|---|--|--|----------|
| 7009, 7010 | 42522153 | 26 | 8.00E-07 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd0554 [Bdellovibrio bacteriovorus HD100] emb CAE78526.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100] | | | |
| 7011, 7012 | 32262806 | 40 | 3.00E-53 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860786.1 hypothetical protein HH1255 [Helicobacter hepaticus ATCC 51449] | | | |
| 7015, 7016 | 34105120 | 22 | 1.00E-09 | Chromobacterium violaceum ATCC 12472 | probable type II secretion system protein [Chromobacterium violaceum ATCC 12472] ref NP_903484.1 probable type II secretion system protein [Chromobacterium violaceum ATCC 12472] | | | |
| 7017, 7018 | 20807566 | 33 | 8.00E-31 | Thermoanaerobacter tengcongensis MB4 | Diguanylate cyclase/phosphodiesterase domain 1 (GGDEF) [Thermoanaerobacter tengcongensis MB4] gb AAM24341.1 Diguanylate cyclase/phosphodiesterase domain 1 (GGDEF) [Thermoanaerobacter tengcongensis MB4] | | | 2.7.3.- |
| 7019, 7020 | 51245892 | 25 | 1.00E-06 | Desulfotalea psychrophila LSV54 | related to integrase [Desulfotalea psychrophila LSV54] emb CAG36769.1 related to integrase [Desulfotalea psychrophila LSV54] | | | |
| 7021, 7022 | 48864587 | 46 | 4.00E-21 | Microbulbifer degradans 2-40 | COG0684: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Microbulbifer degradans 2-40] | | | |
| 7023, 7024 | 48864587 | 31 | 2.00E-18 | Microbulbifer degradans 2-40 | COG0684: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Microbulbifer degradans 2-40] | | | |
| 7027, 7028 | 34558792 | 34 | 5.00E-26 | Alvinella pompejana epibiont 6C6 | conserved hypothetical protein [Alvinella pompejana epibiont 6C6] | | | |
| 7035, 7036 | 48862944 | 37 | 3.00E-58 | Microbulbifer degradans 2-40 | COG2274: ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain [Microbulbifer degradans 2-40] | | | 3.4.21.- |
| 7039, 7040 | 23024040 | 38 | 8.00E-48 | Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293 | COG0442: Polyl-IRNA synthetase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293] | | | 6.1.1.15 |
| 7041, 7042 | AAW9001 8 | 25 | 5.00E-12 | | Desc:Expressed antigen for cluster 43. Org:Helicobacter pylori | | | 3.2.1.- |
| 7045, 7046 | 4049717 | 24 | 2.00E-07 | Melanoplus sanguinipes entomopoxvirus | ORF MSV156 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] pir T28317 ORF MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus ref NP_048227.1 ORF MSV156 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] | | | |

| | | | | | | | | |
|---------------|----------|----|-----------|---|--|----------|--|--|
| 7049, 7050 | 34396413 | 69 | 3.00E-66 | Porphyromonas gingivalis W83 | conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_904581.1 hypothetical protein PG0257 [Porphyromonas gingivalis W83] | | | |
| 705, 706 | 48856969 | 33 | 6.00E-22 | Cytophaga hutchinsonii | COG1792: Cell shape-determining protein [Cytophaga hutchinsonii] | | | |
| 7051, 7052 | 15606924 | 45 | 2.00E-20 | Aquifex aeolicus VF5 | dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] gb AAC07699.1 dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] pir G70463 dolichol-phosphate mannosyltransferase - Aquifex aeolicus | 2.4.1.83 | | |
| 7053, 7054 | 53685350 | 25 | 5.00E-22 | Desulfotobacterium hafniense DCB-2 | COG0535: Predicted Fe-S oxidoreductases [Desulfotobacterium hafniense DCB-2] | | | |
| 7055, 7056 | 13488172 | 27 | 2.00E-12 | Mesorhizobium loti MAFF303099 | hypothetical protein ml9374 [Mesorhizobium loti MAFF303099] dbj BAB54981.1 ml9374 [Mesorhizobium loti MAFF303099] | | | |
| 7057, 7058 | 57505523 | 35 | 1.00E-18 | Campylobacter upsaliensis RM3195 | conserved hypothetical protein [Campylobacter upsaliensis RM3195] gb EAL52857.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195] | | | |
| 7059, 7060 | 34557616 | 35 | 2.00E-40 | Wolinella succinogenes DSM 1740 | HELICASE [Wolinella succinogenes DSM 1740] emb CAE10331.1 HELICASE [Wolinella succinogenes] | | | |
| 7061, 7062 | 23126372 | 37 | 2.00E-13 | Nostoc punctiforme PCC 73102 | COG1943: Transposase and inactivated derivatives [Nostoc punctiforme PCC 73102] | | | |
| 7063, 7064 | 32262499 | 49 | 3.00E-13 | Helicobacter hepaticus ATCC 51449 | hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449] ref NP_860480.1 hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449] | | | |
| 7069, 7070 | 57505360 | 73 | 1.00E-122 | Campylobacter upsaliensis RM3195 | ribonucleoside-diphosphate reductase, alpha subunit [Campylobacter upsaliensis RM3195] gb EAL53281.1 ribonucleoside-diphosphate reductase, alpha subunit [Campylobacter upsaliensis RM3195] | 1.17.4.1 | | |
| 707, 708 | 34397903 | 51 | 2.00E-47 | Porphyromonas gingivalis W83 | excinuclease ABC, C subunit [Porphyromonas gingivalis W83] ref NP_906065.1 excinuclease ABC, C subunit [Porphyromonas gingivalis W83] | 2.7.7.7 | | |
| 7071, 7072 | 57241418 | 33 | 9.00E-17 | Campylobacter lari RM2100 | Protein of unknown function (DUF452) superfamily [Campylobacter lari RM2100] gb EAL54530.1 Protein of unknown function (DUF452) superfamily [Campylobacter lari RM2100] | | | |
| 7073, 7074 | 21672890 | 36 | 5.00E-18 | Chlorobium tepidum TLS | biotin synthesis protein, putative [Chlorobium tepidum TLS] gb AAM71297.1 biotin synthesis protein, putative [Chlorobium tepidum TLS] | | | |
| 7075, 7076 | 21672890 | 29 | 4.00E-24 | Chlorobium tepidum TLS | biotin synthesis protein, putative [Chlorobium tepidum TLS] gb AAM71297.1 biotin synthesis protein, putative [Chlorobium tepidum TLS] | | | |

| | | | | | | | | |
|--------|----------|----|----------|--------------------------|--|--|--|----------|
| 7077, | 52144430 | 26 | 1.00E-23 | Bacillus cereus ZK | hypothetical protein BCZK0794 [Bacillus cereus ZK] gb AAU19449.1] | | | |
| 7078 | | | | Bacillus cereus ZK | conserved hypothetical protein [Bacillus cereus ZK] | | | |
| 7079, | | | | Campylobacter coli | chemotaxis regulatory protein Cj1118c [Campylobacter coli RM2228] | | | |
| 7080 | 57168004 | 38 | 7.00E-14 | RM2228 | gb EAL57047.1] chemotaxis regulatory protein Cj1118c [Campylobacter coli RM2228] | | | 2.7.3.- |
| 7081, | | | | Wolinella | PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] | | | |
| 7082 | 34557717 | 74 | 3.00E-50 | succinogenes DSM 1740 | emb CAE10432.1] PUTATIVE TRANSPOSASE [Wolinella succinogenes] | | | |
| 7083, | | | | Cytophaga | COG1512: Beta-propeller domains of methanol dehydrogenase type | | | |
| 7084 | 48854336 | 37 | 6.00E-20 | hutchinsonii | [Cytophaga hutchinsonii] | | | |
| 7085, | | | | Geobacter | | | | |
| 7086 | 39998549 | 26 | 3.00E-13 | sulfurreducens PCA | glycosyl transferase, group 2 family protein [Geobacter sulfurreducens PCA] | | | |
| 7087, | | | | Wolinella | DNA POLYMERASE III EPSILON SUBUNIT DNAQ [Wolinella succinogenes DSM 1740] emb CAE09379.1] DNA POLYMERASE III EPSILON SUBUNIT DNAQ [Wolinella succinogenes] | | | 2.7.7.7 |
| 7088 | 34556664 | 46 | 1.00E-42 | succinogenes DSM 1740 | probable conjugal transfer protein TrbE [Desulfotalea psychrophila LSV54] | | | |
| 7089, | | | | Desulfotalea | emb CAG37878.1] probable conjugal transfer protein TrbE [Desulfotalea psychrophila LSV54] | | | |
| 7090 | 51246985 | 44 | 7.00E-53 | psychrophila LSV54 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 7093, | 48831001 | 26 | 2.00E-26 | Magnetococcus sp. MC-1 | hypothetical protein [Klebsiella pneumoniae] | | | |
| 7095, | 7328117 | 26 | 5.00E-12 | Klebsiella pneumoniae | | | | |
| 7096 | | | | Wolinella | DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] | | | 2.7.7.- |
| 7099, | 34558196 | 33 | 2.00E-28 | succinogenes DSM 1740 | emb CAE10911.1] DNA PRIMASE PROTEIN [Wolinella succinogenes] | | | |
| 7100 | | | | Bacteroides | putative ABC transporter permease [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 71, 72 | 29346875 | 28 | 2.00E-16 | thetaitaomicron VPI-5482 | gb AAO76572.1] putative ABC transporter permease [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 7101, | | | | Campylobacter | tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] | | | 4.2.1.70 |
| 7102 | 57237984 | 53 | 2.00E-47 | jejun RM1221 | gb AAW35567.1] tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] | | | |
| 7103, | | | | Wolinella | ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolinella succinogenes DSM 1740] emb CAE09984.1] ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolinella succinogenes] | | | 3.6.1.- |
| 7104 | 34557269 | 60 | 4.00E-93 | succinogenes DSM 1740 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] | | | |
| 7105, | | | | Helicobacter | ref NP_859903.1] hypothetical protein HH0372 [Helicobacter hepaticus ATCC 51449] | | | 2.6.1.17 |
| 7106 | 32261920 | 57 | 5.00E-49 | hepaticus ATCC 51449 | COG0859: ADP-heptose-LPS heptosyltransferase [Cytophaga hutchinsonii] | | | |
| 7107, | 48853786 | 50 | 5.00E-78 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|----------|
| 7109, 7110 | 32469872 | 29 | 2.00E-14 | Campylobacter jejuni | hypothetical protein [Campylobacter jejuni] gb AAN46942.1 unknown | | | |
| 7111, 7112 | 54029077 | 62 | 6.00E-41 | Polaromonas sp. JS666 | COG1089: GDP-D-mannose dehydratase [Polaromonas sp. JS666] | | | 4.2.1.47 |
| 7113, 7114 | 57241068 | 39 | 3.00E-15 | Campylobacter lari RM2100 | Archaea bacterial proteins of unknown function family [Campylobacter lari RM2100] gb EAL54764.1 Archaea bacterial proteins of unknown function family [Campylobacter lari RM2100] | | | |
| 7115, 7116 | AAW5565 | 5 | 60 | 1.00E-60 | Desci-H. pylori ORF 06gp71906_25504187_f3_112 cytoplasmic protein. | | | 1.8.-.- |
| 7117, 7118 | 21674237 | 43 | 2.00E-19 | Chlorobium tepidum TLS | Org.Helicobacter pylori | | | |
| 7119, 7120 | 52853852 | 37 | 2.00E-36 | Psychrobacter sp. 273-4 | glycosyl transferase [Chlorobium tepidum TLS] gb AAM72644.1 glycosyl transferase [Chlorobium tepidum TLS] | | | |
| 7121, 7122 | 32477471 | 28 | 5.00E-17 | Rhodopirellula baltica SH 1 | COG0442: Prolyl-tRNA synthetase [Psychrobacter sp. 273-4] | | | |
| 7123, 7124 | 34397620 | 63 | 3.00E-76 | Porphyrromonas gingivalis W83 | peroxiredoxin [Rhodopirellula baltica SH 1] emb CAD77542.1 peroxiredoxin [Pirellula sp.] | | | |
| 7127, 7128 | 34556661 | 42 | 2.00E-27 | Wolinella succinogenes DSM 1740 | ABC transporter, ATP-binding protein [Porphyrromonas gingivalis W83] ref NP_905783.1 ABC transporter, ATP-binding protein [Porphyrromonas gingivalis W83] | | | 1.8.-.- |
| 7129, 7130 | 48856007 | 35 | 8.00E-11 | Cytophaga hutchinsonii | PUTATIVE FRUCTOSE-1,6-BISPHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE09376.1 PUTATIVE FRUCTOSE-1,6-BISPHOSPHATASE [Wolinella succinogenes] | | | 3.1.3.11 |
| 7131, 7132 | 39995395 | 31 | 4.00E-07 | Geobacter sulfurreducens PCA | COG0308: Aminopeptidase N [Cytophaga hutchinsonii] | | | |
| 7133, 7134 | 51894433 | 46 | 5.00E-73 | Symbiobacterium thermophilum IAM 14863 | PBS lyase HEAT-like repeat protein [Geobacter sulfurreducens PCA] gb AAR33619.1 PBS lyase HEAT-like repeat protein [Geobacter sulfurreducens PCA] | | | |
| 7137, 7138 | 15678496 | 34 | 6.00E-22 | Methanothermobacter thermautotrophicus str. Delta H | sigma-54-dependent transcriptional regulator [Symbiobacterium thermophilum IAM 14863] dbj BAD42280.1 sigma-54-dependent transcriptional regulator [Symbiobacterium thermophilum IAM 14863] | | | |
| 7139, 7140 | 54302013 | 43 | 3.00E-29 | Photobacterium profundum SS9 | sensory transduction histidine kinase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB84974.1 sensory transduction histidine kinase [Methanothermobacter thermautotrophicus str. Delta H] pir C69161 sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Delta H) | | | 2.7.3.- |
| 7141, 7142 | 56707454 | 41 | 6.00E-26 | Francisella tularensis subsp. tularensis Schu 4 | hypothetical protein PBPRB0333 [Photobacterium profundum SS9] emb CAG22206.1 hypothetical protein [Photobacterium profundum] | | | |

| | | | | | | | | | |
|---------------|----------|----|-----------|---|--|---|----|----------|--|
| 7143, 7144 | 56707453 | 36 | 1.00E-07 | Francisella tularensis subsp. tularensis Schu 4 | hypothetical protein FTT0300 [Francisella tularensis subsp. tularensis Schu 4] gb AAV29688.1 NT02FT0892 [synthetic construct] emb CAG44933.1 hypothetical protein [Francisella tularensis subsp. tularensis] | | | | |
| 7145, 7146 | 48855541 | 72 | 3.00E-50 | Cytophaga hutchinsonii | COG1875: Predicted ATPase related to phosphate starvation-inducible protein PhoH [Cytophaga hutchinsonii] | Parachlamydia- related symbiont UWE25, complete genome | 85 | 7.00E-08 | |
| 7147, 7148 | 29346304 | 56 | 1.00E-107 | Bacteroides thetaiotaomicron VPI-5482 | DNA ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76001.1 DNA ligase [Bacteroides thetaiotaomicron VPI-5482] | | | 6.5.1.2 | |
| 7149, 7150 | 29346304 | 61 | 1.00E-77 | Bacteroides thetaiotaomicron VPI-5482 | DNA ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76001.1 DNA ligase [Bacteroides thetaiotaomicron VPI-5482] | | | 6.5.1.2 | |
| 7151, 7152 | 52421238 | 53 | 2.00E-25 | Bacteroides fragilis YCH46 | hypothetical protein BFP0024 [Bacteroides fragilis YCH46] db BAD51351.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 7153, 7154 | 20091731 | 71 | 1.00E-96 | Methanosarcina acetivorans C2A | 2-oxoisovalerate ferredoxin oxidoreductase, beta subunit [Methanosarcina acetivorans C2A] gb AAM06286.1 2-oxoisovalerate ferredoxin oxidoreductase, beta subunit [Methanosarcina acetivorans str. C2A] | | | 1.2.7.- | |
| 7155, 7156 | 24372513 | 28 | 6.00E-16 | Shewanella oneidensis MR-1 | acetyltransferase, GNAT family [Shewanella oneidensis MR-1] gb AAN54000.1 acetyltransferase, GNAT family [Shewanella oneidensis MR- 1] | | | | |
| 7157, 7158 | 15791002 | 37 | 1.00E-11 | Halobacterium salinarum NRC-1 | hypothetical protein VNG2170H [Halobacterium salinarum NRC-1] gb AAG20306.1 Vng2170h [Halobacterium sp. NRC-1] pir F84367 hypothetical protein Vng2170h [imported] - Halobacterium sp. NRC-1 | | | | |
| 7161, 7162 | 34557666 | 30 | 1.00E-39 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1305 [Wolinella succinogenes DSM 1740] emb CAE10381.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 7163, 7164 | 21241124 | 40 | 1.00E-26 | Xanthomonas axonopodis pv. citri str. 306 | hypothetical protein XAC0350 [Xanthomonas axonopodis pv. citri str. 306] gb AAM35242.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 7165, 7166 | 29346750 | 54 | 2.00E-67 | Bacteroides thetaiotaomicron VPI-5482 | putative lipopolysaccharide biosynthesis glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76447.1 putative lipopolysaccharide biosynthesis glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.4.1.- | |
| 7169, 7170 | 34558443 | 25 | 3.00E-07 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2166 [Wolinella succinogenes DSM 1740] emb CAE11158.1 hypothetical protein [Wolinella succinogenes] | | | | |

| | | | | | | | | | |
|-------|----------|----|-----------|--|--|--|--|--|----------|
| 7171, | 34558443 | 36 | 2.00E-13 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2166 [Wolinella succinogenes DSM 1740] emb[CAE11158.1] hypothetical protein [Wolinella succinogenes] | | | | |
| 7172 | | | | | | | | | 2.4.1.18 |
| 7173, | 48855019 | 56 | 2.00E-66 | Cytophaga hutchinsonii | COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii] | | | | 2 |
| 7174 | | | | | | | | | |
| 7175, | | | | | | | | | |
| 7176 | 24373599 | 34 | 4.00E-09 | Shewanella oneidensis MR-1 | hypothetical protein SO2039 [Shewanella oneidensis MR-1] conserved domain protein [Shewanella oneidensis MR-1] | | | | |
| 7177, | | | | | | | | | |
| 7178 | 54307149 | 52 | 6.00E-89 | Bacteroides uniformis | hypothetical protein NB1_09 [Bacteroides uniformis] gb AAF74441.1 unknown [Bacteroides uniformis] | | | | |
| | | | | | | | | | |
| 7179, | | | | | | | | | |
| 7180 | 57241290 | 60 | 3.00E-31 | Campylobacter lari RM2100 | Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100] gb EAL54986.1 Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100] | | | | |
| 7185, | | | | | | | | | |
| 7186 | 23474222 | 58 | 8.00E-53 | Desulfovibrio desulfuricans G20 | COG2998: ABC-type tungstate transport system, permease component [Desulfovibrio desulfuricans G20] | | | | |
| | | | | | | | | | |
| 7187, | | | | | | | | | |
| 7188 | 34558490 | 65 | 1.00E-103 | Wolinella succinogenes DSM 1740 | GLUTAMYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb[CAE11205.1] GLUTAMYL-TRNA SYNTHETASE [Wolinella succinogenes] sp Q7M7L9 SYE_WOLSU Glutamyl-tRNA synthetase (Glutamate-tRNA ligase) (GluRS) | | | | |
| 7189, | | | | | | | | | |
| 7190 | 48855372 | 32 | 3.00E-13 | Cytophaga hutchinsonii | COG2931: RTX toxins and related Ca2+-binding proteins [Cytophaga hutchinsonii] | | | | |
| 719, | | | | | | | | | |
| 720 | 48862211 | 47 | 5.00E-33 | Microbulbifer degradans 2-40 | COG2989: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] | | | | |
| | | | | | | | | | |
| 7191, | | | | | | | | | |
| 7192 | 48859660 | 38 | 2.00E-47 | Clostridium thermocellum ATCC 27405 | COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Clostridium thermocellum ATCC 27405] | | | | 3.4.21.- |
| | | | | | | | | | |
| 7193, | | | | | | | | | |
| 7194 | 19704426 | 29 | 1.00E-23 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Sigma factor sigB regulation protein rsbU [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95287.1 Sigma factor sigB regulation protein rsbU [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | 3.1.3.16 |
| 7197, | | | | | | | | | |
| 7198 | 48831001 | 40 | 2.00E-41 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | | 2.7.3.- |
| | | | | | | | | | |
| 7199, | | | | | | | | | |
| 7200 | 34557246 | 64 | 1.00E-35 | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb[CAE09961.1] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | | | | 2.7.3.- |
| | | | | | | | | | |
| 7203, | | | | | | | | | |
| 7204 | 34556562 | 58 | 6.00E-53 | Wolinella succinogenes DSM 1740 | PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes DSM 1740] emb[CAE09277.1] PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|--|----------|
| 7209, 7210 | 51246604 | 66 | 6.00E-66 | Desulfotalea psychrophila LSV54 | probable arginyl-tRNA synthetase [Desulfotalea psychrophila LSV54] emb CAG37481.1 probable arginyl-tRNA synthetase [Desulfotalea psychrophila LSV54] | | | | 6.1.1.19 |
| 721, 722 | 53758638 | 37 | 2.00E-32 | Methylococcus capsulatus str. Bath | conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_113480.1 hypothetical protein MCA1003 [Methylococcus capsulatus str. Bath] | | | | |
| 7211, 7212 | 57237610 | 57 | 2.00E-27 | Campylobacter jejuni RM1221 | histidyl-tRNA synthetase [Campylobacter jejuni RM1221] gb AAW35193.1 histidyl-tRNA synthetase [Campylobacter jejuni RM1221] emb CAB73030.1 | | | | |
| 7213, 7214 | 53714483 | 40 | 3.00E-18 | Bacteroides fragilis YCH46 | histidyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281926.1 histidyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81347 histidine-tRNA ligase (EC 6.1.1.21) C 0765c [Imported] - Campylobacter jejuni (strain NCTC 11168) sp Q9PPF4 SYH_CAM JE Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS) | | | | 6.1.1.21 |
| 7215, 7216 | 29345593 | 36 | 3.00E-41 | Bacteroides thetaiotaomicron VPI-5482 | transglycosylase [Bacteroides fragilis YCH46] db BAD49941.1 transglycosylase [Bacteroides fragilis YCH46] | | | | |
| 7217, 7218 | 48891870 | 50 | 1.00E-56 | Trichodesmium erythraeum IMS101 | transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75290.1 transglycosylase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 7219, 7220 | 49477542 | 29 | 7.00E-25 | Bacillus thuringiensis serovar konkukian str. 97-27 | COG0566: rRNA methylases [Trichodesmium erythraeum IMS101] UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAAT59744.1 UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacillus thuringiensis serovar konkukian str. 97-27] | | | | 2.1.1.- |
| 7221, 7222 | 34558309 | 50 | 5.00E-36 | Wolinella succinogenes DSM 1740 | ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11024.1 ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes] | | | | 6.3.2.15 |
| 7223, 7224 | 57240653 | 27 | 2.00E-17 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55046.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | 1.8.- |
| 7229, 7230 | 2313711 | 28 | 1.00E-07 | Helicobacter pylori 26695 | H. pylori predicted coding region HP0586 [Helicobacter pylori 26695] pir B64593 hypothetical protein HP0586 - Helicobacter pylori (strain 26695) ref NP_207381.1 hypothetical protein HP0586 [Helicobacter pylori 26695] | | | | |
| 723, 724 | 48855418 | 65 | 2.00E-84 | Cytophaga hutchinsonii | COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii] | | | | |

| | | | | | | |
|---------------|----------|----|----------|--|--|----------|
| 7231, 7232 | 20094914 | 60 | 8.00E-14 | Methanopyrus kandleri AV19 | DNA-directed RNA polymerase, subunit N [Methanopyrus kandleri AV19] gb AA02691.1 DNA-directed RNA polymerase, subunit N [Methanopyrus kandleri AV19] sp Q8TVB4 RPON_METKA DNA-directed RNA polymerase subunit N | 2.7.7.6 |
| 7233, 7234 | 34763018 | 32 | 5.00E-11 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | DNA TOPOLOGY MODULATION PROTEIN FLAR-RELATED PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24413.1 DNA TOPOLOGY MODULATION PROTEIN FLAR-RELATED PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | |
| 7235, 7236 | 9655841 | 46 | 2.00E-37 | Vibrio cholerae O1 biovar eltor str. N16961 | sensory box sensor histidine kinase/response regulator [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230993.1 sensory box sensor histidine kinase/response regulator [Vibrio cholerae O1 biovar eltor str. N16961] pir H48221.1 sensory box sensor histidine kinase/response regulator VC1349 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | 2.7.3.- |
| 7237, 7238 | 48833325 | 27 | 9.00E-26 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221] | 2.7.3.- |
| 7239, 7240 | 57238620 | 48 | 2.00E-26 | Campylobacter jejuni RM1221 | gb AAW36203.1 ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221] | 2.7.7.60 |
| 7241, 7242 | 48856860 | 49 | 2.00E-29 | Cytophaga hutchinsonii | COG0781: Transcription termination factor [Cytophaga hutchinsonii] probable methionyl-tRNA synthetase [Desulfotalea psychrophila LSV54] emb CAG35515.1 probable methionyl-tRNA synthetase [Desulfotalea psychrophila LSV54] | 6.1.1.10 |
| 7243, 7244 | 51244638 | 61 | 9.00E-70 | Desulfotalea psychrophila LSV54 | hypothetical protein BF3086 [Bacteroides fragilis YCH46] db BAD49831.1 hypothetical protein [Bacteroides fragilis YCH46] | |
| 7245, 7246 | 53714373 | 29 | 2.00E-21 | Bacteroides fragilis YCH46 | Small-conductance mechanosensitive channel [Idiomarina loihiensis L2TR] gb AAV82847.1 Small-conductance mechanosensitive channel [Idiomarina loihiensis L2TR] | |
| 7249, 7250 | 56461115 | 48 | 2.00E-71 | Idiomarina loihiensis L2TR | hypothetical protein BT0882 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75989.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482] | |
| 7251, 7252 | 30721677 | 26 | 7.00E-07 | Plasmodium falciparum | phosphoprotein 300 [Plasmodium falciparum] | |
| 7253, 7254 | 47227859 | 29 | 1.00E-06 | Tetraodon nigroviridis | unnamed protein product [Tetraodon nigroviridis] | |
| 7255, 7256 | 34556947 | 41 | 4.00E-19 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0526 [Wolinella succinogenes DSM 1740] emb CAE09662.1 hypothetical protein [Wolinella succinogenes] | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|---------|
| 7257, 7258 | 34557269 | 58 | 1.00E-74 | Wollinella succinogenes DSM 1740 | ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes DSM 1740] emb[CAE0984.1] ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes] | | | 3.6.1.- |
| 7259, 7260 | 34557268 | 62 | 2.00E-57 | Wollinella succinogenes DSM 1740 | TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wollinella succinogenes DSM 1740] emb[CAE0983.1] TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wollinella succinogenes] | | | |
| 7261, 7262 | 34556595 | 38 | 1.00E-35 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0147 [Wollinella succinogenes DSM 1740] emb[CAE09310.1] conserved hypothetical protein [Wollinella succinogenes] | | | |
| 7263, 7264 | 34558202 | 40 | 6.00E-21 | Wollinella succinogenes DSM 1740 | LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wollinella succinogenes DSM 1740] emb[CAE10917.1] LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wollinella succinogenes] | | | 2.3.1.- |
| 7267, 7268 | 52006955 | 25 | 4.00E-07 | Thiobacillus denitrificans ATCC 25259 | COG3660: Predicted nucleoside-diphosphate-sugar epimerase [Thiobacillus denitrificans ATCC 25259] | | | |
| 7271, 7272 | 27365538 | 23 | 4.00E-14 | Vibrio vulnificus CMCP6 | hypothetical protein VV12211 [Vibrio vulnificus CMCP6] gb AAO10593.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6] | | | |
| 7273, 7274 | 34558170 | 46 | 1.00E-50 | Wollinella succinogenes DSM 1740 | RIBONUCLEASE [Wollinella succinogenes DSM 1740] emb[CAE10885.1 RIBONUCLEASE [Wollinella succinogenes] | | | 3.1.-.- |
| 7275, 7276 | 57167878 | 32 | 5.00E-17 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL57664.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | |
| 7277, 7278 | 21242142 | 47 | 2.00E-27 | Xanthomonas axonopodis pv. citri str. 306 | ABC transporter ATP-binding protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM36260.1 ABC transporter ATP-binding protein [Xanthomonas axonopodis pv. citri str. 306] | | | |
| 7283, 7284 | 20808914 | 22 | 2.00E-12 | Thermoanaerobact er tengcongensis MB4 | Transcription-repair coupling factor - superfamily II helicase [Thermoanaerobacter tengcongensis MB4] gb AAM25689.1 Transcription- repair coupling factor - superfamily II helicase [Thermoanaerobacter tengcongensis MB4] | | | |
| 7285, 7286 | 34557966 | 56 | 1.00E-63 | Wollinella succinogenes DSM 1740 | ATP-DEPENDENT HELICASE [Wollinella succinogenes DSM 1740] emb[CAE10681.1] ATP-DEPENDENT HELICASE [Wollinella succinogenes] | | | 3.6.1.- |
| 7287, 7288 | 48853613 | 33 | 3.00E-40 | Cytophaga hutchinsonii | COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii] | | | |
| 7289, 7290 | 48833229 | 30 | 3.00E-30 | Magnetococcus sp. MC-1 | COG1226: Kef-type K+ transport systems, predicted NAD-binding component [Magnetococcus sp. MC-1] | | | |
| 729, 730 | 48854473 | 29 | 4.00E-10 | Cytophaga hutchinsonii | COG1648: Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain) [Cytophaga hutchinsonii] | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---------------------------------------|--|---|----|----------|----------|
| 7293, 7294 | 53713067 | 28 | 6.00E-19 | Bacteroides fragilis YCH46 | hypothetical protein BF1778 [Bacteroides fragilis YCH46] dbj BAD48525.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 7295, 7296 | 14591697 | 46 | 6.00E-64 | Pyrococcus horikoshii OT3 | oligopeptide transport ATP-binding protein appF [Pyrococcus horikoshii OT3] dbj BAA31085.1 335aa long hypothetical oligopeptide transport ATP-binding protein appF [Pyrococcus horikoshii OT3] pir F71211 probable oligopeptide transport ATP-binding protein appF - Pyrococcus horikoshii | | | | 1.8.-.- |
| 7297, 7298 | 34557268 | 49 | 3.00E-57 | Wolinella succinogenes DSM 1740 | TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09983.1 TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wolinella succinogenes] | | | | |
| 7299, 7300 | 34558285 | 55 | 3.00E-56 | Wolinella succinogenes DSM 1740 | PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes] | Wolinella succinogenes, complete genome; segment 6/7 | 87 | 1.00E-10 | |
| 73, 74 | 15644379 | 38 | 1.00E-09 | Thermotoga maritima MSB8 | hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD36698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 conserved hypothetical protein - Thermotoga maritima (strain MSB8) | | | | |
| 7303, 7304 | 47568045 | 47 | 9.00E-21 | Bacillus cereus G9241 | glycogen synthase [Bacillus cereus G9241] gb EAL13693.1 glycogen synthase [Bacillus cereus G9241] | | | | 2.4.1.21 |
| 7307, 7308 | 57238299 | 50 | 1.00E-31 | Campylobacter jejuni RM1221 | hypothetical protein CJE0604 [Campylobacter jejuni RM1221] gb AAW35882.1 conserved hypothetical protein [Campylobacter jejuni RM1221] emb CAB75134.1 hypothetical protein Cj0496 [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281683.1 hypothetical protein Cj0496 [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81395 hypothetical protein Cj0496 [imported] - Campylobacter jejuni (strain NCTC 11168) | | | | |
| 7309, 7310 | 34558209 | 42 | 3.00E-48 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-SAM dependent methyltransferases [Wolinella succinogenes DSM 1740] emb CAE10924.1 conserved hypothetical protein-SAM dependent methyltransferases [Wolinella succinogenes] | | | | 2.1.1.52 |
| 731, 732 | 15613113 | 35 | 2.00E-37 | Bacillus halodurans C-125 | ABC transporter (ATP-binding protein) [Bacillus halodurans C-125] dbj BAB04269.1 ABC transporter (ATP-binding protein) [Bacillus halodurans C-125] pir F83718 ABC transporter (ATP-binding protein) BH0550 [imported] - Bacillus halodurans (strain C-125) | | | | 1.8.-.- |
| 7311, 7312 | 57240846 | 58 | 2.00E-45 | Campylobacter lari RM2100 | UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate ligase [Campylobacter lari RM2100] gb EAL55039.1 UDP-N-acetylmuramoylalanyl- D-glutamyl-2, 6-diaminopimelate ligase [Campylobacter lari RM2100] | | | | 6.3.2.13 |

| | | | | | | | |
|---------------|----------|----|---|----------|----|--|----------|
| 7313, 7314 | 34557905 | 50 | Wolinella succinogenes DSM 1740 | 2.00E-69 | 50 | PROLYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb[CAG10620.1] PROLYL-TRNA SYNTHETASE [Wolinella succinogenes] | 6.1.1.15 |
| 7317, 7318 | 48858096 | 33 | Clostridium thermocellum ATCC 27405 | 3.00E-37 | 33 | COG0572: Uridine kinase [Clostridium thermocellum ATCC 27405] | 2.7.1.48 |
| 7319, 7320 | 54308510 | 39 | Photobacterium profundum SS9 | 3.00E-50 | 39 | hypothetical protein PBPR1317 [Photobacterium profundum SS9] emb[CAG19728.1] hypothetical protein [Photobacterium profundum] | |
| 7321, 7322 | 54308510 | 53 | Photobacterium profundum SS9 | 5.00E-09 | 53 | hypothetical protein PBPR1317 [Photobacterium profundum SS9] emb[CAG19728.1] hypothetical protein [Photobacterium profundum] DNA topoisomerase I [Thermosynechococcus elongatus BP-1] dbj[BAC09433.1] DNA topoisomerase I [Thermosynechococcus elongatus BP-1] | 5.99.1.2 |
| 7323, 7324 | 22299424 | 34 | Thermosynechococcus elongatus BP-1 | 4.00E-17 | 34 | RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes DSM 1740] emb[CAG10661.1] RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes] | 3.1.4.17 |
| 7327, 7328 | 34557946 | 41 | Wolinella succinogenes DSM 1740 | 1.00E-42 | 41 | hypothetical protein CT0328 [Chlorobium tepidum TLS] gb AAM71574.1 conserved hypothetical protein [Chlorobium tepidum TLS] polysaccharide biosynthesis protein [Shewanella oneidensis MR-1] gb AAN55507.1 polysaccharide biosynthesis protein [Shewanella oneidensis MR-1] | 6.1.1.5 |
| 7329, 7330 | 21673167 | 40 | Chlorobium tepidum TLS | 4.00E-33 | 40 | Serine/threonine protein kinases [Leptospira interrogans serovar 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] COG0507: ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Desulfovibrio desulfuricans G20] | 3.1.3.16 |
| 733, 734 | 24374020 | 43 | Shewanella oneidensis MR-1 | 1.00E-43 | 43 | hypothetical protein [Deinococcus radiodurans] pir G75368 hypothetical protein - Deinococcus radiodurans (strain R1) ref NP_295399.1 hypothetical protein DR1676 [Deinococcus radiodurans R1] | 3.1.11.5 |
| 7331, 7332 | 24214122 | 35 | Leptospira Interrogans serovar Lai str. 56601 | 5.00E-37 | 35 | S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79078.1 S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Bacteroides thetaiotaomicron VPI-5482] | 5.--- |
| 7333, 7334 | 53691714 | 53 | Desulfovibrio desulfuricans G20 | 2.00E-51 | 53 | COG0778: Nitroreductase [Nostoc punctiforme PCC 73102] | |
| 7335, 7336 | 6459446 | 33 | Deinococcus radiodurans | 1.00E-18 | 33 | | |
| 7339, 7340 | 29349381 | 53 | Bacteroides thetaiotaomicron VPI-5482 | 7.00E-75 | 53 | | |
| 7343, 7344 | 23130537 | 36 | Nostoc punctiforme PCC 73102 | 7.00E-24 | 36 | | |

| | | | | | | | | |
|---------------------------------|----------------------------------|----------------|----------------------------------|--|---|---|----------------|---------------------------------|
| 7349, 7350, 735, 736 | 34558196 40062985 | 57 50 | 4.00E-71 3.00E-39 | Wolinella succinogenes DSM 1740 uncultured bacterium 443 | DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes] | Wolinella succinogenes, complete genome; segment 6/7 | 91 5.00E-07 | 2.7.7.- |
| 7353, 7354, 7355, 7356 | 40062985 54302734 41722784 | 50 31 55 | 3.00E-39 4.00E-30 1.00E-31 | uncultured bacterium 443 Photobacterium profundum SS9 Dechloromonas aromatica RCB | phytoene dehydrogenase [uncultured bacterium 443] hypothetical dinitrification protein NorD [Photobacterium profundum SS9] emb CAG22927.1 hypothetical dinitrification protein NorD [Photobacterium profundum] COG4548: Nitric oxide reductase activation protein [Dechloromonas aromatica RCB] | | | 1.3.3.4 1.7.99.7 1.7.99.7 |
| 7357, 7358 | 3455828 | 25 | 7.00E-08 | Alvinella pompejana epibiont 7G3 | KIAA1005 protein [Alvinella pompejana epibiont 7G3] conserved hypothetical protein-Predicted amidohydrolase [Wolinella succinogenes DSM 1740] emb CAE10901.1 conserved hypothetical protein-Predicted amidohydrolase [Wolinella succinogenes] | | | |
| 7359, 7360 | 34558186 | 52 | 3.00E-31 | Wolinella succinogenes DSM 1740 | HOMOSERINE O-ACETYLTRANSFERASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10903.1 HOMOSERINE O-ACETYLTRANSFERASE PROTEIN [Wolinella succinogenes] | | | 2.3.1.31 |
| 7365, 7366 | 53714371 | 30 | 2.00E-32 | Bacteroides fragilis YCH46 uncultured | putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] fragilis YCH46] | | | |
| 7369, 7370 | 52548475 | 36 | 1.00E-07 | archaeon GZfos14B8 | prophage LambdaSa1 transcriptase/maturase family protein [uncultured archaeon GZfos14B8] | | | |
| 7371, 7372, 7373, 7374 | 34556965 48832225 | 45 63 | 1.00E-29 4.00E-61 | Wolinella succinogenes DSM 1740 Magnetococcus sp. MC-1 | PEROXIDE STRESS REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09880.1 PEROXIDE STRESS REGULATOR [Wolinella succinogenes] COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1] | | | |
| 7375, 7376 | 48854031 | 54 | 2.00E-77 | Cytophaga hutchinsonii | COG0445: NAD/FAD-utilizing enzyme apparently involved in cell division [Cytophaga hutchinsonii] | Desc:Mycoplasma genitalium genome. Org:Mycoplasma genitalium | 83 3.00E-12 | |
| 7377, 7378 | 45657719 | 26 | 9.00E-08 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC11856 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70442.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |

| | | | | | | | | | |
|---------------|----------|----|-----------|--|--|--|--|--|---------------|
| 7381, 7382 | 48858283 | 53 | 6.00E-63 | Clostridium thermocellum ATCC 27405 | COG2304: Uncharacterized protein containing a von Willebrand factor type A (vWA) domain [Clostridium thermocellum ATCC 27405] | | | | |
| 7383, 7384 | 23099115 | 37 | 1.00E-46 | Oceanobacillus ihayensis HTE831 | sulfur deprivation response regulator [Oceanobacillus ihayensis HTE831] dbj BAC13616.1 sulfur deprivation response regulator [Oceanobacillus ihayensis HTE831] | | | | |
| 7385, 7386 | 53715139 | 33 | 3.00E-43 | Bacteroides fragilis YCH46 | putative acetyltransferase [Bacteroides fragilis YCH46] dbj BAD50597.1 | | | | 2.3.1.- |
| 7387, 7388 | 48786589 | 50 | 2.00E-58 | Burkholderia fungorum LB400 | putative acetyltransferase [Bacteroides fragilis YCH46] | | | | |
| 739, 740 | 48855418 | 62 | 1.00E-101 | Cytophaga hutchinsonii | COG2202: FOG: PAS/PAC domain [Burkholderia fungorum LB400] | | | | |
| 7391, 7392 | 57237984 | 42 | 1.00E-38 | Campylobacter jejuni RM1221 | COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii] tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] gb AAW35567.1 tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] | | | | 4.2.1.70 |
| 7393, 7394 | 34557273 | 37 | 2.00E-11 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0881 [Wolinella succinogenes DSM 1740] emb CAE09988.1 hypothetical protein [Wolinella succinogenes] | | | | 2.7.1.14 8 |
| 7395, 7396 | 48845647 | 43 | 1.00E-46 | Geobacter metallireducens GS 15 | hypothetical protein Gmet02001892 [Geobacter metallireducens GS-15] | | | | |
| 7399, 7400 | 39995205 | 60 | 2.00E-46 | Geobacter sulfurreducens PCA | DNA polymerase III, gamma and tau subunits [Geobacter sulfurreducens PCA] gb AAR33429.1 DNA polymerase III, gamma and tau subunits [Geobacter sulfurreducens PCA] | | | | 2.7.7.7 |
| 7401, 7402 | 34556460 | 51 | 2.00E-62 | Wolinella succinogenes DSM 1740 | DNA POLYMERASE III, BETA CHAIN [Wolinella succinogenes DSM 1740] emb CAE09175.1 DNA POLYMERASE III, BETA CHAIN [Wolinella succinogenes] | | | | 2.7.7.7 |
| 7403, 7404 | 23003425 | 53 | 1.00E-31 | Lactobacillus gasseri | COG1207: N-acetylglucosamine-1-phosphate uridylyltransferase (contains nucleotidyltransferase and l-patch acetyltransferase domains) [Lactobacillus gasseri] | | | | 2.7.7.23 |
| 7407, 7408 | 45508536 | 39 | 3.00E-20 | Anabaena variabilis ATCC 29413 | COG0535: Predicted Fe-S oxidoreductases [Anabaena variabilis ATCC 29413] gb AAA93025.1 NifX2 | | | | |
| 7409, 7410 | 23023289 | 34 | 1.00E-33 | Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293 | COG4928: Predicted P-loop ATPase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---------------------------------|--|--|----|----------|-------------------|
| 741, 742 | 53713222 | 34 | 4.00E-16 | Bacteroides fragilis YCH46 | polysialic acid transport protein [Bacteroides fragilis YCH46] dbj BAD48680.1 polysialic acid transport protein [Bacteroides fragilis YCH46] | | | | |
| 7413, 7414 | 17231532 | 28 | 3.00E-14 | Nostoc sp. PCC 7120 | hypothetical protein all4040 [Nostoc sp. PCC 7120] pir A12310 hypothetical protein all4040 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75739.1 all4040 [Nostoc sp. PCC 7120] | | | | |
| 7415, 7416 | 48856157 | 39 | 1.00E-46 | Cytophaga hutchinsonii | COG0046: Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Cytophaga hutchinsonii] | | | | |
| 7417, 7418 | 56475703 | 44 | 2.00E-26 | Azoarcus sp. Ebn1 | putative transposase [Azoarcus sp. Ebn1] emb CA106391.1 putative transposase [Azoarcus sp. Ebn1] | | | | |
| 7419, 7420 | 56477204 | 62 | 8.00E-90 | Azoarcus sp. Ebn1 | 2-oxoglutarate ferredoxin oxidoreductase beta subunit [Azoarcus sp. Ebn1] emb CA107892.1 2-oxoglutarate ferredoxin oxidoreductase beta subunit [Azoarcus sp. Ebn1] | | | | 1.2.7.3 |
| 7423, 7424 | 34556768 | 68 | 5.00E-95 | Wolinella succinogenes DSM 1740 | DIAMINOPIMELATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes DSM 1740] emb CAE09483.1 DIAMINOPIMELATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes] | | | 83 | 1.00E-08 4.1.1.20 |
| 7425, 7426 | 34556736 | 27 | 6.00E-13 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0300 [Wolinella succinogenes DSM 1740] emb CAE09451.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 7427, 7428 | 34557003 | 48 | 3.00E-59 | Wolinella succinogenes DSM 1740 | PUTATIVE RIBOFLAVIN KINASE /FMN ADENYLYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09718.1 PUTATIVE RIBOFLAVIN KINASE /FMN ADENYLYLTRANSFERASE [Wolinella succinogenes] | | | | 2.7.1.26 |
| 7429, 7430 | 56420170 | 64 | 8.00E-57 | Geobacillus kaustophilus HTA426 | hypothetical protein GK1635 [Geobacillus kaustophilus HTA426] dbj BAD75920.1 hypothetical conserved protein [Geobacillus kaustophilus HTA426] | | | | |
| 743, 744 | 48854498 | 59 | 3.00E-68 | Cytophaga hutchinsonii | hypothetical protein Chut02002697 [Cytophaga hutchinsonii] | | | | |
| 7431, 7432 | 34556550 | 22 | 9.00E-09 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0098 [Wolinella succinogenes DSM 1740] emb CAE09265.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 7433, 7434 | 57234107 | 32 | 8.00E-11 | Dehalococcoides ethenogenes 195 | hypothetical protein DET110 [Dehalococcoides ethenogenes 195] gb AAW39612.1 conserved hypothetical protein [Dehalococcoides ethenogenes 195] | | | | |
| 7435, 7436 | 34557509 | 64 | 4.00E-44 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wolinella succinogenes] | Wolinella succinogenes, complete genome; segment 4/7 | ## | 6.00E-09 | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|--|---|----|----------|--|
| 7437, 7438 | 48853602 | 50 | 1.00E-63 | Cytophaga hutchinsonii | COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii] | Oceanobacillus theysensis HTE831 genomic DNA, section 1/13 | 91 | 6.00E-07 | |
| 7439, 7440 | 48853602 | 57 | 9.00E-76 | Cytophaga hutchinsonii | COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii] | | | | |
| 7441, 7442 | 34558244 | 32 | 1.00E-21 | Wolinella succinogenes DSM 1740 | SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wolinella succinogenes DSM 1740] emb[CAB10959.1] SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wolinella succinogenes] | | | 2.7.3.- | |
| 7443, 7444 | 53712102 | 50 | 3.00E-61 | Bacteroides fragilis YCH46 | putative dNDP-4-keto-6-deoxy-glucose-2,3- dehydratase [Bacteroides fragilis YCH46] putative dNDP-4-keto-6-deoxy-glucose-2,3- dehydratase [Bacteroides fragilis YCH46] | | | | |
| 7445, 7446 | 17547595 | 28 | 1.00E-07 | Ralstonia solanacearum GMI1000 | PUTATIVE MEMBRANE-BOUND LYTIC MUREIN TRANSGLYCOSYLASE A TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GMI1000] emb[CAD16583.1] PUTATIVE MEMBRANE-BOUND LYTIC MUREIN TRANSGLYCOSYLASE A TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] | | | 3.2.1.- | |
| 7447, 7448 | 37525725 | 41 | 1.00E-57 | Phototribadus luminescens subsp. laumondii TTO1 | hypothetical protein plu1791 [Phototribadus luminescens subsp. laumondii TTO1] emb[CAB14084.1] unnamed protein product [Phototribadus luminescens subsp. laumondii TTO1] | | | | |
| 7449, 7450 | 20807293 | 42 | 7.00E-36 | Thermoanaerobact er tengcongensis MB4 | Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Thermoanaerobacter tengcongensis MB4] gb AAM24068.1] Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Thermoanaerobacter tengcongensis MB4] sp Q8RBK5 PURL_THETN Phosphoribosylformylglycinamide synthase II (FGAM synthase II) | | | 6.3.5.3 | |
| 745, 746 | 16329492 | 74 | 4.00E-90 | Synechocystis sp. PCC 6803 | ABC transporter [Synechocystis sp. PCC 6803] dbj BAA16900.1 ABC transporter [Synechocystis sp. PCC 6803] pir S74749 ABC-type transport protein sir0982 - Synechocystis sp. (strain PCC 6803) | | | 1.8.- | |
| 7451, 7452 | 29345967 | 58 | 4.00E-58 | Bacteroides thetaiotaomicron VPI-5482 | carbamyl phosphate synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75664.1] carbamyl phosphate synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | 6.3.5.5 | |
| 7453, 7454 | 24373965 | 54 | 1.00E-34 | Shewanella oneidensis MR-1 | ISSod5, transposase [Shewanella oneidensis MR-1] gb AAN55452.1] ISSod5, transposase [Shewanella oneidensis MR-1] | | | | |

| | | | | | | | | | |
|---------------|----------|----|-----------|--|---|---|----|----------|----------|
| 7455, 7456 | 34556892 | 66 | 3.00E-94 | Wolnella succinogenes DSM 1740 | DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wolnella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wolnella succinogenes] sp Q7MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [Includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)] | Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome | 82 | 9.00E-15 | 2.7.7.6 |
| 7461, 7462 | 57238474 | 44 | 7.00E-45 | Campylobacter jejuni RM1221 | deoxyuridine triphosphatase domain protein [Campylobacter jejuni RM1221] gb AAW36057.1 deoxyuridine triphosphatase domain protein | | | | |
| 7465, 7466 | 57168280 | 62 | 1.00E-103 | Campylobacter coli RM2228 | [Campylobacter jejuni RM1221] conserved hypothetical protein TIGR00423 [Campylobacter coli RM2228] gb EAL57323.1 conserved hypothetical protein TIGR00423 [Campylobacter coli RM2228] | | | | |
| 7469, 7470 | 17227449 | 33 | 2.00E-41 | Nostoc sp. PCC 7120 | hypothetical protein all8075 [Nostoc sp. PCC 7120] pir AD2560 hypothetical protein all8075 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120gamma dbj BAB77405.1 ORF_ID:all8075~probable helicase [Nostoc sp. PCC 7120] | | | | 3.1.21.3 |
| 747, 748 | 49484307 | 44 | 3.00E-18 | Staphylococcus aureus subsp. aureus MRSA252 | putative UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate-- D- alanine-D-alanine ligase [Staphylococcus aureus subsp. aureus MRSA252] emb CAG41150.1 putative UDP-N-acetylmuramoylalanine-D-glutamate-2, 6- diaminopimelate-- D-alanine-D-alanine ligase [Staphylococcus aureus subsp. aureus MRSA252] | | | | 6.3.2.15 |
| 7471, 7472 | 42520897 | 34 | 1.00E-08 | Wolbachia endosymbiont of Drosophila melanogaster | methyltransferase, putative [Wolbachia endosymbiont of Drosophila melanogaster] gb AAS14746.1 methyltransferase, putative [Wolbachia endosymbiont of Drosophila melanogaster] sp Q73G71 TRMB_WOLPM tRNA (guanine-N(7))-methyltransferase (tRNA(m7G46)-methyltransferase) | | | | 2.1.1.- |
| 7475, 7476 | 28852723 | 58 | 3.00E-59 | Pseudomonas syringae pv. tomato str. DC3000 | hydrolase, haloacid dehalogenase-like family [Pseudomonas syringae pv. tomato str. DC3000] ref NP_792100.1 hydrolase, haloacid dehalogenase- like family [Pseudomonas syringae pv. tomato str. DC3000] | | | | 3.1.3.3 |
| 7477, 7478 | 50083834 | 28 | 4.00E-15 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD0599 [Acinetobacter sp. ADP1] emb CAG67522.1 conserved hypothetical protein [Acinetobacter sp. ADP1] | | | | |
| 7479, 7480 | 50955568 | 30 | 3.00E-21 | Leifsonia xyl subsp. xyl str. CTCB07 | glycosyltransferase [Leifsonia xyl subsp. xyl str. CTCB07] gb AAT89751.1 glycosyltransferase [Leifsonia xyl subsp. xyl str. CTCB07] | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|----------|
| 7481, 7482 | 20807825 | 32 | 4.00E-24 | Thermoanaerobacter tengcongensis MB4 | DNA segregation ATPase FtsK/SpoIIIE and related proteins [Thermoanaerobacter tengcongensis MB4] gb AAM24600.1 DNA segregation ATPase FtsK/SpoIIIE and related proteins [Thermoanaerobacter tengcongensis MB4] sp Q8R5S4 FTSK THETN DNA translocase ftsK | | | |
| 7483, 7484 | 45658174 | 35 | 5.00E-14 | Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 | hypothetical protein LIC12326 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70897.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | |
| 7487, 7488 | 57241004 | 23 | 3.00E-10 | Campylobacter lari RM2100 | probable transmembrane protein Cj0390 [Campylobacter lari RM2100] gb EAL54700.1 probable transmembrane protein Cj0390 [Campylobacter lari RM2100] | | | |
| 7489, 7490 | 16328450 | 42 | 1.00E-47 | Synechocystis sp. PCC 6803 | regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] db BAA16858.1 regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] pir S74707 nitrogen fixation positive activator protein - Synechocystis sp. (strain PCC 6803) | | | 2.7.3.- |
| 749, 750 | 28377119 | 43 | 2.00E-28 | Lactobacillus plantarum WCFS1 | alpha-amylase [Lactobacillus plantarum WCFS1] emb CAD62849.1 alpha-amylase [Lactobacillus plantarum WCFS1] | | | 3.2.1.1 |
| 7493, 7494 | 30019367 | 55 | 1.00E-57 | Bacillus cereus ATCC 14579 | dTDP-glucose 4,6-dehydratase [Bacillus cereus ATCC 14579] gb AAP08199.1 dTDP-glucose 4,6-dehydratase [Bacillus cereus ATCC 14579] | | | 4.2.1.46 |
| 7495, 7496 | 48855000 | 61 | 4.00E-94 | Cytophaga hutchinsonii | COG2509: Uncharacterized FAD-dependent dehydrogenases [Cytophaga hutchinsonii] | | | |
| 7497, 7498 | 23129971 | 33 | 1.00E-07 | Nostoc punctiforme PCC 73102 | hypothetical protein Npun02001199 [Nostoc punctiforme PCC 73102] | | | |
| 7499, 7500 | 19881279 | 35 | 7.00E-14 | Campylobacter jejuni | RioB [Campylobacter jejuni] gb AAM00862.1 RioB [Campylobacter jejuni] gb AAM00829.1 RioB [Campylobacter jejuni] | | | |
| 75, 76 | 48853747 | 56 | 6.00E-27 | Cytophaga hutchinsonii | COG0441: Threonyl-tRNA synthetase [Cytophaga hutchinsonii] | | | 6.1.1.3 |
| 7507, 7508 | 42524004 | 32 | 1.00E-15 | Bdellovibrio bacteriovorus HD100 | cell wall surface anchor family protein [Bdellovibrio bacteriovorus HD100] emb CAE80377.1 cell wall surface anchor family protein [Bdellovibrio bacteriovorus HD100] | | | |
| 7509, 7510 | 53735875 | 38 | 3.00E-36 | Crocospaera watsonii WH 8501 | COG5421: Transposase [Crocospaera watsonii WH 8501] | | | |
| 7511, 7512 | 53715023 | 55 | 8.00E-42 | Bacteroides fragilis YCH46 | hypothetical protein BF3739 [Bacteroides fragilis YCH46] db BAD50481.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | |
|-------|----------|----|------------------------------------|---|--|--|-------------|----------|
| 7513, | 48855619 | 53 | Cytophaga hutchinsonii | COG1587: Uroporphyrinogen-III synthase [Cytophaga hutchinsonii] | | | | |
| 7514 | | | | ATP-dependent DNA helicase RecQ [Coxiella burnetii RSA 493] | | | | |
| 7515, | 29653815 | 36 | Coxiella burnetii RSA 493 | gb AAO90021.1 ATP-dependent DNA helicase RecQ [Coxiella burnetii RSA 493] | | | | 3.6.1.- |
| 7516 | | | | hypothetical protein PFL2170c [Plasmodium falciparum 3D7] | | | | |
| 7517, | 23508126 | 40 | Plasmodium falciparum 3D7 | gb AAN36518.1 hypothetical protein PFL2170c [Plasmodium falciparum 3D7] | | | | |
| 7518 | | | | putative methyltransferase-endonuclease [Halovirus HF2] ref NP_861654.1 | | | | |
| 7519, | 18000405 | 41 | Halovirus HF2 | putative methyltransferase-endonuclease [Halovirus HF1] gb AAO61365.1 | | | | |
| 7520 | | | | putative methyltransferase-endonuclease [Halovirus HF1] ref NP_542568.1 | | | | 2.1.1.72 |
| 7521, | | | | putative methyltransferase-endonuclease [Halovirus HF2] | | | | |
| 7522, | 2984552 | 50 | Aquifex aeolicus VF5 | putative protein [Aquifex aeolicus VF5] ref NP_046399.1 hypothetical protein aq_aa03 [Aquifex aeolicus VF5] sp O66399 YZ03_AQUAE Hypothetical protein AA03 | | | | |
| 7523, | 48839272 | 30 | Methanosarcina barkeri str. fusaro | COG1401: GTPase subunit of restriction endonuclease [Methanosarcina barkeri str. fusaro] | | | | 3.1.21.- |
| 7524 | | | | hypothetical protein WS2211 [Wollinella succinogenes DSM 1740] | | | | |
| 7525, | 34558485 | 44 | Wollinella succinogenes DSM 1740 | emb CAE11200.1 hypothetical protein [Wollinella succinogenes] | | | | 2.7.3.- |
| 7526 | | | | hypothetical protein aq_1630 [Aquifex aeolicus VF5] gb AAC07520.1 | | | | |
| 7527, | | | | hypothetical protein [Aquifex aeolicus VF5] pir F70440 conserved | | | | |
| 7528 | 15606737 | 36 | Aquifex aeolicus VF5 | hypothetical protein aq_1630 - Aquifex aeolicus | | | | |
| 7529, | | | | hypothetical protein WS1882 [Wollinella succinogenes DSM 1740] | | | | 2.7.1.37 |
| 7530 | 34558177 | 22 | Wollinella succinogenes DSM 1740 | emb CAE10892.1 hypothetical protein [Wollinella succinogenes] | | | | |
| 7531, | | | | hypothetical protein WS1305 [Wollinella succinogenes DSM 1740] | | | | |
| 7532 | 34557666 | 24 | Wollinella succinogenes DSM 1740 | emb CAE10381.1 hypothetical protein [Wollinella succinogenes] | | | | |
| 7533, | | | | hypothetical protein WS1243 [Wollinella succinogenes DSM 1740] | | | | |
| 7534 | 34557608 | 25 | Wollinella succinogenes DSM 1740 | emb CAE10323.1 conserved hypothetical protein [Wollinella succinogenes] | | | | |
| 7535, | | | | folypolyglutamate synthase (folC) [Campylobacter coli RM2228] | | | | |
| 7536 | 57167971 | 51 | Campylobacter coli RM2228 | gb EAL57014.1 folypolyglutamate synthase (folC) [Campylobacter coli RM2228] | | | | 6.3.2.17 |
| 7537, | | | | RNA POLYMERASE SIGMA FACTOR [Wollinella succinogenes DSM 1740] | | | | |
| 7538 | 34558185 | 76 | Wollinella succinogenes DSM 1740 | emb CAE10900.1 RNA POLYMERASE SIGMA FACTOR [Wollinella succinogenes] | | | 88 3.00E-24 | |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|---|-------------|----------|
| 7539, 7540 | 57167942 | 46 | 5.00E-46 | Campylobacter coli RM2228 | Isoleucyl-tRNA synthetase [Campylobacter coli RM2228] gb EAL56985.1 Isoleucyl-tRNA synthetase [Campylobacter coli RM2228] | | | 6.1.1.5 |
| 7543, 7544 | 34557246 | 42 | 1.00E-18 | Wollinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes] | | | |
| 7545, 7546 | 48858827 | 53 | 1.00E-25 | Cytophaga hutchinsonii | COG2315: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii] | | | |
| 7547, 7548 | 57237512 | 63 | 3.00E-64 | Campylobacter jejuni RM1221 | tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter jejuni RM1221] gb AAW35095.1 tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter jejuni RM1221] | | | 1.8.-- |
| 7549, 7550 | 34558082 | 51 | 1.00E-41 | Wollinella succinogenes DSM 1740 | LIPOPROTEIN [Wollinella succinogenes DSM 1740] emb CAE10797.1 LIPOPROTEIN [Wollinella succinogenes] | | | |
| 755, 756 | 20093112 | 77 | 6.00E-74 | Methanosarcina acetivorans C2A | hypothetical protein MA4324 [Methanosarcina acetivorans C2A] gb AAM07667.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] | Methanosarcina acetivorans str. C2A, section 213 of 534 of the complete genome | 84 1.00E-77 | 3.4.24.- |
| 7551, 7552 | 34556740 | 34 | 1.00E-42 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0304 [Wollinella succinogenes DSM 1740] emb CAE09455.1 conserved hypothetical protein [Wollinella succinogenes] conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir E83031 conserved hypothetical protein PA4927 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253614.1 hypothetical protein PA4927 [Pseudomonas aeruginosa PAO1] | | | |
| 7553, 7554 | 9951205 | 36 | 1.00E-23 | Pseudomonas aeruginosa PAO1 | Hemin receptor [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24234.1 Hemin receptor [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | |
| 7555, 7556 | 34763190 | 27 | 3.00E-19 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | | Desc:Borrelia burgdorferi polynucleotide sequence #1. Org:Borrelia burgdorferi | 93 2.00E-13 | |
| 7557, 7558 | 52673266 | 57 | 1.00E-99 | Bacillus amyloliquefaciens | UvrABC system protein B [Bacillus amyloliquefaciens] DNA topoisomerase I [Bacteroides fragilis YCH46] db BAD51157.1 DNA topoisomerase I [Bacteroides fragilis YCH46] | | | 5.99.1.2 |
| 7559, 7560 | 53715699 | 53 | 9.00E-64 | Bacteroides fragilis YCH46 | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|----|----------|---------|
| 7561, 7562 | 37528384 | 43 | 1.00E-47 | Photorhabdus luminescens subsp. laumondii TTO1 | hypothetical protein plu4565 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16937.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] | | | 2.-.-.- | |
| 7565, 7566 | 57285642 | 61 | 5.00E-69 | Staphylococcus aureus subsp. aureus COL | uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus COL] ref NP_645353.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus MW2] ref NP_373792.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus N315] dbj BAB56743.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus Mu50] dbj BAB94401.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus MW2] dbj BAB41770.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus N315] ref NP_371105.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus Mu50] pir G89826 uracil-DNA glycosylase ung [imported] - Staphylococcus aureus (strain N315) sp P67075 UNG_STAAM Uracil-DNA glycosylase (UDG) sp P67077 UNG_STAAM Uracil-DNA glycosylase (UDG) sp P67076 UNG_STAAM Uracil-DNA glycosylase (UDG) ref YP_185512.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus COL] | Blochmannia floridanus complete genome; segment 3/3 | 81 | 1.00E-07 | 3.2.2.- |
| 757, 758 | 23501128 | 58 | 1.00E-39 | Brucella suis 1330 | transcriptional regulator, MerR family [Brucella suis 1330] gb AAN29170.1 transcriptional regulator, MerR family [Brucella suis 1330] | | | 5.4.1.2 | |
| 7571, 7572 | 48855446 | 36 | 7.00E-10 | Cytophaga hutchinsonii | COG1173: ABC-type dipeptide/oligopeptide/nickel transport systems, permease components [Cytophaga hutchinsonii] | | | | |
| 7573, 7574 | 53712874 | 48 | 3.00E-63 | Bacteroides fragilis YCH46 | ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD48332.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] | | | 1.8.-.- | |
| 7583, 7584 | 34556902 | 40 | 1.00E-29 | NADP+ | FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATE DEHYDROGENASE [NADP+]) [Wolinella succinogenes DSM 1740] emb CAE09617.1 FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATE DEHYDROGENASE [NADP+]) [Wolinella succinogenes] response regulator [Thermotoga maritima MSB8] gb AAD35484.1 response regulator [Thermotoga maritima MSB8] pir H72382 response regulator - Thermotoga maritima (strain MSB8) | | | 1.6.5.3 | |
| 7585, 7586 | 15643165 | 36 | 9.00E-39 | Thermotoga maritima MSB8 | COG0479: Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit [Magnetococcus sp. MC-1] | | | 2.7.3.- | |
| 7587, 7588 | 48834056 | 35 | 5.00E-32 | Magnetococcus sp. MC-1 | methyl-accepting chemotaxis protein, putative [Campylobacter upsaliensis RM3195] gb EAL53448.1 methyl-accepting chemotaxis protein, putative [Campylobacter upsaliensis RM3195] | | | 1.3.99.1 | |
| 7589, 7590 | 57242735 | 40 | 2.00E-21 | Campylobacter upsaliensis RM3195 | | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|----------|
| 759, 760 | 29349012 | 41 | 2.00E-14 | Bacteroides thetaiotaomicron VPI-5482 | putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO78709.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 7591, 7592 | 48855125 | 48 | 1.00E-59 | Cytophaga hutchinsonii | COG2081: Predicted flavoproteins [Cytophaga hutchinsonii] | | | |
| 7593, 7594 | 22094882 | 31 | 3.00E-09 | Flavobacterium johnsoniae | GldH [Flavobacterium johnsoniae] | | | |
| 7595, 7596 | 21668035 | 31 | 5.00E-11 | Bacteroides fragilis | hypothetical transposase [Bacteroides fragilis] | | | |
| 7597, 7598 | 57159487 | 35 | 1.00E-42 | Thermococcus kodakaraensis | probable molybdenum cofactor biosynthesis protein A [Thermococcus kodakaraensis] ref YP_18384.1 probable molybdenum cofactor biosynthesis protein A [Thermococcus kodakaraensis] | | | |
| 7599, 7600 | 57240895 | 40 | 3.00E-51 | Campylobacter lari RM2100 | proline dehydrogenase [Campylobacter lari RM2100] gb EAL55288.1 proline dehydrogenase [Campylobacter lari RM2100] | | | 1.5.99.8 |
| 7601, 7602 | 34558306 | 44 | 7.00E-53 | Wolinella succinogenes DSM 1740 | PUTATIVE RIBOFLAVIN-SPECIFIC DEAMINASE EC 3.5.4. [Wolinella succinogenes DSM 1740] emb CAE11021.1 PUTATIVE RIBOFLAVIN- SPECIFIC DEAMINASE EC 3.5.4. [Wolinella succinogenes] | | | 3.5.4.26 |
| 7603, 7604 | 11498376 | 31 | 2.00E-21 | Archaeoglobus fulgidus DSM 4304 | signal-transducing histidine kinase [Archaeoglobus fulgidus DSM 4304] gb AAE90464.1 signal-transducing histidine kinase [Archaeoglobus fulgidus DSM 4304] pir B69346 signal-transducing histidine kinase homolog - Archaeoglobus fulgidus | | | 2.7.3.- |
| 7609, 7610 | 28379430 | 30 | 5.00E-10 | Lactobacillus plantarum WCFS1 | ABC transporter, ATP-binding and permease protein [Lactobacillus plantarum WCFS1] emb CAD65182.1 ABC transporter, ATP-binding and permease protein [Lactobacillus plantarum WCFS1] | | | |
| 761, 762 | 48729246 | 28 | 2.00E-15 | Pseudomonas fluorescens PFO-1 | COG0457: FOG: TPR repeat [Pseudomonas fluorescens Pfo-1] | | | |
| 7611, 7612 | 57168857 | 57 | 4.00E-58 | Campylobacter coli RM2228 | anaerobic glycerol-3-phosphate dehydrogenase, subunit C [glpC] [Campylobacter coli RM2228] gb EAL56379.1 anaerobic glycerol-3- phosphate dehydrogenase, subunit C [glpC] [Campylobacter coli RM2228] | | | |
| 7613, 7614 | 52840519 | 52 | 8.00E-48 | Legionella pneumophila subsp. pneumophila str. Philadelphia 1 | hypothetical protein [pg0264 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU2637.1 hypothetical protein [pg0264 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] | | | |
| 7615, 7616 | 16415962 | 38 | 2.00E-41 | Acinetobacter lwoffii | Alol restriction modification enzyme [Acinetobacter lwoffii] | | | 2.1.1.72 |
| 7617, 7618 | 53715164 | 30 | 1.00E-16 | Bacteroides fragilis YCH46 | hypothetical protein BF3880 [Bacteroides fragilis YCH46] dbj BAD50622.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|----------|--|
| 7619, 7620 | 34557635 | 43 | 3.00E-54 | Wollinella succinogenes DSM 1740 | RND PUMP PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10350.1 RND PUMP PROTEIN [Wollinella succinogenes] | | | | |
| 7623, 7624 | 34558169 | 33 | 1.00E-23 | Wollinella succinogenes DSM 1740 | conserved hypothetical protein-DNA polymerase III delta subunit [Wollinella succinogenes DSM 1740] emb CAE10884.1 conserved hypothetical protein-DNA polymerase III delta subunit [Wollinella succinogenes] | | | | |
| 7625, 7626 | 34557200 | 30 | 1.00E-37 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0802 [Wollinella succinogenes DSM 1740] emb CAE09915.1 conserved hypothetical protein [Wollinella succinogenes] | | | | |
| 7627, 7628 | 34557237 | 29 | 8.00E-08 | Wollinella succinogenes DSM 1740 | COMPONENTS OF SENSORY TRANSDUCTION SYSTEM [Wollinella succinogenes DSM 1740] emb CAE09952.1 COMPONENTS OF SENSORY TRANSDUCTION SYSTEM [Wollinella succinogenes] | | | | |
| 7629, 7630 | 34557202 | 63 | 2.00E-57 | Wollinella succinogenes DSM 1740 | ATP PHOSPHORIBOSYLTRANSFERASE [Wollinella succinogenes DSM 1740] emb CAE09917.1 ATP PHOSPHORIBOSYLTRANSFERASE [Wollinella succinogenes] sp Q7M9N0 HIS1_WOLSU ATP phosphoribosyltransferase (ATP-PRTase) (ATP-PRT) | | | 2.4.2.17 | |
| 763, 764 | 29349976 | 27 | 2.00E-24 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BT4568 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79673.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 7631, 7632 | 53711927 | 29 | 4.00E-16 | Bacteroides fragilis YCH46 | hypothetical protein BF0636 [Bacteroides fragilis YCH46] db BAD47385.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 7633, 7634 | 22036085 | 35 | 2.00E-15 | Vibrio parahaemolyticus | hypothetical ATP-binding protein [Vibrio parahaemolyticus] | | | | |
| 7635, 7636 | 53731251 | 41 | 7.00E-23 | Methanococcoides burtonii DSM 6242 | COG0642: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242] | | | 2.7.3.- | |
| 7637, 7638 | 57241137 | 48 | 5.00E-75 | Campylobacter lari RM2100 | oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter lari RM2100] gb EAL54833.1 oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter lari RM2100] | | | 1.-.-.- | |
| 7643, 7644 | 57168975 | 59 | 1.00E-31 | Campylobacter coli RM2228 | 3'(2''),5'-bisphosphate nucleotidase [Campylobacter coli RM2228] gb EAL56330.1 3'(2''),5'-bisphosphate nucleotidase [Campylobacter coli RM2228] | | | | |

| | | | | | | | | | | |
|---------------|----------|----|----------|---|--|---|----|----------|----------|--|
| 7645, 7646 | 54639980 | 69 | 1.00E-75 | Campylobacter jejuni | putative adenylylsulfate kinase [Campylobacter jejuni] | Campylobacter jejuni OH4384 peptide chain release factor 2 (prfB) gene, partial cds; alpha-2,3- sialyltransferase (cst-I), sulfate adenylyltransferase subunit CysD (cysD), sulfate adenylyltransferase subunit CysN (cysN), putative sodium/sulfate symporter (sodium sulfate symporter), putative adenylylsulfate kinase (cysC), hypothetical protein, putative glycosyltransferase, and hypothetical protein genes, complete cds; and cj1457c gene, partial cds | 84 | 4.00E-07 | 2.7.1.25 | |
| 7647, 7648 | 24373737 | 50 | 8.00E-72 | Shewanella oneidensis MR-1 | peptidase, M23/M37 family [Shewanella oneidensis MR-1] gb AAN55224.1 peptidase, M23/M37 family [Shewanella oneidensis MR-1] | | | | 3.5.1.- | |
| 7649, 7650 | 53711855 | 40 | 5.00E-21 | Bacteroides fragilis YCH46 | putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides fragilis YCH46] dbj BAD47313.1 putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides fragilis YCH46] | | | | 3.1.4.16 | |
| 765, 766 | 27382256 | 49 | 4.00E-31 | Bradyrhizobium japonicum USDA 110 | hypothetical protein bli7145 [Bradyrhizobium japonicum USDA 110] dbj BAC52410.1 bli7145 [Bradyrhizobium japonicum USDA 110] | | | | | |
| 7651, 7652 | 48892249 | 33 | 3.00E-30 | Trichodesmium erythraeum IMS101 | COG4886: Leucine-rich repeat (LRR) protein [Trichodesmium erythraeum erythraeum IMS101] | | | | | |

| | | | | | | | | |
|---------------|----------------------|----------|----------------------|--|--|----|----------|----------|
| 7653, 7654 | 23112865 | 45 | 2.00E-44 | Desulfotobacterium hafniense DCB-2 | COG4636: Uncharacterized protein conserved in cyanobacteria [Desulfotobacterium hafniense DCB-2] | | | |
| 7655, 7656 | 32262541 | 70 | 1.00E-100 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860522.1 hypothetical protein HH0591 [Helicobacter hepaticus ATCC 51449] | 80 | 2.00E-16 | |
| 7657, 7658 | AAB5256 4 | 45 | 1.00E-53 | | Desc:Helicobacter pylori bait polypeptide #82. Org:Helicobacter pylori | | | 3.4.-.- |
| 7661, 7662 | 52008034 | 28 | 5.00E-14 | Thiobacillus denitrificans ATCC 25259 | COG2202: FOG: PAS/PAC domain [Thiobacillus denitrificans ATCC 25259] hypothetical protein BCZK0794 [Bacillus cereus ZK] gb AAU19449.1 | | | 2.7.3.- |
| 7663, 7664 | 52144430 | 27 | 6.00E-30 | Bacillus cereus ZK | conserved hypothetical protein [Bacillus cereus ZK] | | | |
| 7665, 7666 | 52007674 | 33 | 3.00E-16 | Thiobacillus denitrificans ATCC 25259 | COG1959: Predicted transcriptional regulator [Thiobacillus denitrificans ATCC 25259] | | | |
| 7667, 7668 | 57159034 | 51 | 2.00E-57 | Thermococcus kodakaraensis | deblocking aminopeptidase [Thermococcus kodakaraensis] ref YP_183188.1 deblocking aminopeptidase [Thermococcus kodakaraensis] | | | 3.4.11.- |
| 7675, 7676 | 31747866 | 58 | 1.00E-68 | Fritschea bemisiae | unknown [Fritschea bemisiae] related to iron (III) ABC transporter, ATP-binding protein [Desulfotalea psychrophila LSv54] emb CAG37707.1 related to iron (III) ABC transporter, ATP-binding protein [Desulfotalea psychrophila LSv54] | | | |
| 7677, 7678 | 51246830 | 28 | 1.00E-10 | Desulfotalea psychrophila LSv54 | transcriptional regulatory protein KdpE, putative [Campylobacter coli RM2228] gb EAL56224.1 transcriptional regulatory protein KdpE, putative [Campylobacter coli RM2228] | | | 2.7.3.- |
| 7679, 7680 | 57169075 | 29 | 5.00E-19 | Campylobacter coli RM2228 | hypothetical protein HH0539 [Helicobacter hepaticus ATCC 51449] ref NP_860070.1 hypothetical protein HH0539 [Helicobacter hepaticus ATCC 51449] | | | |
| 7681, 7682 | 32262087 | 38 | 2.00E-10 | Helicobacter hepaticus ATCC 51449 | L-SERYL-TRNA(SEC) SELENIUM TRANSFERASE [Wolfinella succinogenes DSM 1740] emb CAE09951.1 L-SERYL-TRNA(SEC) SELENIUM TRANSFERASE [Wolfinella succinogenes] sp Q7M9L1 SELA_WOLSU L- seryl-tRNA(SEC) selenium transferase (Cysteinylyl-tRNA(Sec) selenium transferase) (Selenocysteine synthase) (Selenocysteinyl-tRNA(Sec) synthase) | | | 2.9.1.1 |
| 7683, 7684 | 34557236 34557385 | 60 40 | 6.00E-94 3.00E-39 | Wolfinella succinogenes DSM 1740 Wolfinella succinogenes DSM 1740 | SELENOPHOSPHATE SYNTHETASE [Wolfinella succinogenes DSM 1740] emb CAE10100.1 SELENOPHOSPHATE SYNTHETASE [Wolfinella succinogenes] | | | 2.7.9.3 |

| | | | | | | | | | | |
|---------------|----------|----|----------|--|---|---|----|----------|---------|---------------|
| 7689, 7690 | 34558184 | 29 | 1.00E-07 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1889 [Wolinella succinogenes DSM 1740] emb CAE10899.1 hypothetical protein [Wolinella succinogenes] flagellar basal-body P-ring formation protein FigA, putative [Shewanella oneidensis MR-1] gb AAAN56251.1 flagellar basal-body P-ring formation protein FigA, putative [Shewanella oneidensis MR-1] COG0451: Nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii] | | | | | |
| 7691, 7692 | 24374764 | 27 | 3.00E-23 | Shewanella oneidensis MR-1 | | | | | | |
| 7693, 7694 | 48853513 | 74 | 2.00E-52 | Cytophaga hutchinsonii | | | | | | 4.2.1.46 |
| 7695, 7696 | 34556844 | 27 | 1.00E-17 | Wolinella succinogenes DSM 1740 | SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE09559.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes] PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10413.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | | 2.7.3.- |
| 7697, 7698 | 34557698 | 31 | 5.00E-11 | Wolinella succinogenes DSM 1740 | | Campylobacter jejuni strain TGH 9011 contig147 Tgh114, Tgh020, Tgh021, Tgh022, Tgh160, Tgh011, Tgh42, Tgh043, Tgh004, Tgh001, Tgh002, and Tgh003s genes, complete cds | 79 | 4.00E-10 | 2.3.1.- | |
| 7699, 7700 | 13123737 | 67 | 5.00E-51 | Campylobacter jejuni | putative acetyltransferase [Campylobacter jejuni] | | | | | 1.14.17. 3 |
| 77, 78 | 20090869 | 47 | 3.00E-39 | Methanosarcina acetivorans C2A | hypothetical protein MA2021 [Methanosarcina acetivorans C2A] gb AAM05424.1 hypothetical protein [Methanosarcina acetivorans str. C2A] DNA topoisomerase I [Thermosynechococcus elongatus BP-1] db BAC09433.1 DNA topoisomerase I [Thermosynechococcus elongatus BP-1] | | | | | 5.99.1.2 |
| 7703, 7704 | 22289424 | 41 | 2.00E-50 | Thermosynechococ cus elongatus BP-1 | excinuclease ABC, B subunit [Geobacter sulfurreducens PCA] gb AAR36653.1 excinuclease ABC, B subunit [Geobacter sulfurreducens PCA] | | | | | |
| 7709, 7710 | 39998352 | 67 | 2.00E-55 | Geobacter sulfurreducens PCA | | | | | | |
| 771, 772 | 48855742 | 51 | 4.00E-77 | Cytophaga hutchinsonii | COG0514: Superfamily II DNA helicase [Cytophaga hutchinsonii] | | | | | 3.6.1.- |
| 7711, 7712 | 34557410 | 55 | 1.00E-16 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1024 [Wolinella succinogenes DSM 1740] emb CAE10125.1 conserved hypothetical protein [Wolinella succinogenes] | | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|--|----------|
| 7719, 7720 | 28378865 | 25 | 1.00E-09 | Lactobacillus plantarum WCFS1 | DNA mismatch repair protein MutS2 [Lactobacillus plantarum WCFS1] emb CAD64608.1 DNA mismatch repair protein MutS2 [Lactobacillus plantarum WCFS1] | | | | |
| 7721, 7722 | 57241750 | 26 | 3.00E-10 | Campylobacter lari RM2100 | conserved domain protein [Campylobacter lari RM2100] gb EAL54420.1 conserved domain protein [Campylobacter lari RM2100] | | | | |
| 7723, 7724 | 20089933 | 27 | 5.00E-23 | Methanosarcina acetivorans C2A | capsular polysaccharide biosynthesis protein [Methanosarcina acetivorans C2A] gb AAM04488.1 capsular polysaccharide biosynthesis protein [Methanosarcina acetivorans str. C2A] | | | | |
| 7725, 7726 | 16077744 | 43 | 7.00E-40 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU06760 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12496.1 yeeA [Bacillus subtilis subsp. subtilis str. 168] pir E69792 conserved hypothetical protein yeeA - Bacillus subtilis | | | | |
| 773, 774 | 29346376 | 35 | 7.00E-19 | Bacteroides thetaiotaomicron VPI-5482 | RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO76073.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 7731, 7732 | 56459864 | 43 | 5.00E-33 | Idiomarina lohiensis L2TR | Signaling protein with a MHYT sensor domain, PAS, GGDEF and EAL domains [Idiomarina lohiensis L2TR] gb AAV81596.1 Signaling protein with a MHYT sensor domain, PAS, GGDEF and EAL domains [Idiomarina lohiensis L2TR] | | | | |
| 7735, 7736 | 57240666 | 39 | 2.00E-35 | Campylobacter lari RM2100 | radical SAM domain protein [Campylobacter lari RM2100] gb EAL55059.1 radical SAM domain protein [Campylobacter lari RM2100] | | | | |
| 7737, 7738 | 57240666 | 40 | 5.00E-30 | Campylobacter lari RM2100 | radical SAM domain protein [Campylobacter lari RM2100] gb EAL55059.1 radical SAM domain protein [Campylobacter lari RM2100] | | | | |
| 7743, 7744 | 46142119 | 63 | 5.00E-73 | Methanococcus burtonii DSM 6242 | COG0439: Biotin carboxylase [Methanococcus burtonii DSM 6242] | | | | |
| 7745, 7746 | 48855088 | 38 | 3.00E-21 | Cytophaga hutchinsonii | COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Cytophaga hutchinsonii] | | | | 1.2.1.2 |
| 7747, 7748 | 37523321 | 30 | 9.00E-12 | Gloeobacter violaceus PCC 7421 | probable oxidoreductase [Gloeobacter violaceus PCC 7421] dbj BAC91693.1 gl 3752 [Gloeobacter violaceus PCC 7421] | | | | |
| 7749, 7750 | 21244626 | 50 | 8.00E-19 | Xanthomonas axonopodis pv. citri str. 306 | mitomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM38744.1 mitomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 775, 776 | 34396946 | 29 | 4.00E-20 | Porphyrionomas gingivalis W83 | type IIS restriction endonuclease, putative [Porphyrionomas gingivalis W83] ref NP_905111.1 type IIS restriction endonuclease, putative [Porphyrionomas gingivalis W83] | | | | 2.1.1.72 |

| | | | | | | | | | |
|-------|----------|----|----------|---|--|--|--|--|----------|
| 7751, | 28854153 | 39 | 2.00E-09 | Pseudomonas syringae pv. tomato str. DC3000 | multiple antibiotic resistance protein MarR, putative [Pseudomonas syringae pv. tomato str. DC3000] ref NP_793523.1 multiple antibiotic resistance protein MarR, putative [Pseudomonas syringae pv. tomato str. DC3000] | | | | |
| 7752, | 52144398 | 29 | 8.00E-25 | Bacillus cereus ZK | hypothetical protein BCZK0826 [Bacillus cereus ZK] gb AAU19417.1 conserved hypothetical protein [Bacillus cereus ZK] | | | | |
| 7753, | | | | | CMP-N-acetylneuraminic acid synthetase [Leptospira interrogans serovar Copenhagani str. Flocruz L1-130] ref NP_711786.1 Probable | | | | |
| 7754, | | | | | acetylneuraminic acid synthetase [Leptospira interrogans serovar Lai str. 56601] gb AAU48804.1 Probable acetylneuraminic acid synthetase [Leptospira interrogans serovar lai str. 56601] gb AAS70749.1 CMP-N- | | | | |
| 7755, | | | | | acetylneuraminic acid synthetase [Leptospira interrogans serovar Copenhagani str. Flocruz L1-130] | | | | 2.7.7.43 |
| 7756, | 45658026 | 38 | 2.00E-27 | Thermoanaerobacter tengcongensis MB4 | Lipoate-protein ligase A [Thermoanaerobacter tengcongensis MB4] gb AAM23593.1 Lipoate-protein ligase A [Thermoanaerobacter tengcongensis MB4] | | | | 6.--- |
| 7757, | 20806818 | 48 | 7.00E-58 | Microbulbifer degradans 2-40 | COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Microbulbifer degradans 2-40] | | | | |
| 7759, | 48864587 | 33 | 8.00E-28 | Methylococcus capsulatus str. Bath | oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath] ref YP_113360.1 oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath] | | | | |
| 7761, | 53758726 | 42 | 1.00E-60 | Wolinella succinogenes DSM 1740 | PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolinella succinogenes DSM 1740] emb CAE09198.1 PUTATIVE UDP- | | | | 5.1.3.- |
| 7762, | 34556483 | 54 | 3.00E-37 | Idiomarina loihiensis L2TR | GLUCURONIC ACID EPIMERASE [Wolinella succinogenes] UDP-N-acetyl-D-mannosaminuronate dehydrogenase [Idiomarina loihiensis L2TR] gb AAV81397.1 UDP-N-acetyl-D-mannosaminuronate dehydrogenase [Idiomarina loihiensis L2TR] | | | | 1.1.1.- |
| 7765, | 58459665 | 72 | 4.00E-64 | Shewanella oneidensis MR-1 | GAF domain protein [Shewanella oneidensis MR-1] gb AAN56950.1 GAF domain protein [Shewanella oneidensis MR-1] | | | | 2.7.3.- |
| 7767, | 24375463 | 46 | 1.00E-49 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | | 2.7.3.- |
| 7768, | 48831167 | 38 | 3.00E-20 | uncultured crenarchaeote | hypothetical protein [uncultured crenarchaeote] | | | | |
| 7769, | 42557771 | 50 | 5.00E-54 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | 2.7.3.- |
| 777, | | | | | COG1826: Sec-independent protein secretion pathway components [Cytophaga hutchinsonii] | | | | |
| 7771, | | | | | | | | | |
| 7772, | 34557782 | 47 | 2.00E-18 | Cytophaga hutchinsonii | | | | | |
| 7773, | | | | | | | | | |
| 7774, | 48854952 | 45 | 4.00E-11 | | | | | | |

| | | | | | | | | | |
|-------|----------|----|----------|---------------------------------|--|--|--|--|----------|
| 7777, | 21226672 | 39 | 3.00E-17 | Methanosarcina mazel Go1 | ABC transporter, ATP-binding protein [Methanosarcina mazel Go1] | | | | |
| 7778, | | | | Wolinella succinogenes DSM 1740 | hypothetical protein WS0265 [Wolinella succinogenes DSM 1740] | | | | |
| 7779, | 34556704 | 48 | 4.00E-34 | Photobacterium profundum SS9 | emb CAE09419.1 conserved hypothetical protein [Wolinella succinogenes] | | | | 3.6.1.13 |
| 7780, | | | | Photobacterium profundum SS9 | emb CAG22359.1 conserved hypothetical protein [Photobacterium profundum] | | | | |
| 7781, | 54302166 | 30 | 4.00E-21 | Ralstonia eutropha JMP134 | COG1073: Hydrolases of the alpha/beta superfamily [Ralstonia eutropha JMP134] | | | | |
| 7782, | 53762765 | 34 | 7.00E-40 | Clostridium perfringens str. 13 | two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] | | | | |
| 7783, | | | | Cytophaga hutchinsonii | hypothetical protein Chut02000101 [Cytophaga hutchinsonii] | | | | |
| 7784, | 18310494 | 35 | 2.00E-20 | Cytophaga hutchinsonii | COG0044: Dihydroorotase and related cyclic amidohydrolases [Cytophaga hutchinsonii] | | | | 3.5.2.3 |
| 7785, | 48856384 | 23 | 3.00E-13 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 7786, | 48856383 | 40 | 6.00E-35 | Campylobacter coli RM2228 | gb EAL56259.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 7787, | 57169024 | 31 | 4.00E-11 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 7788, | | | | Streptococcus pyogenes MGAS8232 | putative ABC transporter (ATP-binding protein) [Streptococcus pyogenes MGAS8232] | | | | 1.8.-.- |
| 7789, | 57169025 | 39 | 8.00E-49 | Dechloromonas aromatica RCB | COG1988: Predicted membrane-bound metal-dependent hydrolases [Dechloromonas aromatica RCB] | | | | |
| 7790, | 19745834 | 40 | 8.00E-30 | Nostoc punctiforme PCC 73102 | COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | | | | 2.7.3.- |
| 7791, | 41724574 | 45 | 2.00E-27 | Bacteroides fragilis YCH46 | O-methyltransferase [Bacteroides fragilis YCH46] | | | | 2.1.1.- |
| 7792, | 23129412 | 30 | 6.00E-23 | Geobacter metallireducens GS-15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | | |
| 7793, | 53715760 | 50 | 4.00E-56 | Cytophaga hutchinsonii | COG2319: FOG: WD40 repeat [Cytophaga hutchinsonii] | | | | |
| 7794, | | | | Campylobacter coli RM2228 | proline dehydrogenase [Campylobacter coli RM2228] | | | | |
| 7795, | 48845444 | 54 | 1.00E-59 | | proline dehydrogenase [Campylobacter coli RM2228] | | | | 1.5.99.8 |
| 7796, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7797, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7798, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7799, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7800, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7801, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7802, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7803, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7804, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7805, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7806, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7807, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7808, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7809, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7810, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7811, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7812, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7813, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7814, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7815, | 48845444 | 54 | 1.00E-59 | | | | | | |
| 7816, | 48845444 | 54 | 1.00E-59 | | | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|---|-------------|----------|
| 7817, 7818 | 53715668 | 47 | 3.00E-33 | Bacteroides fragilis YCH46 | putative amidophosphoribosyl-transferase [Bacteroides fragilis YCH46] dbj BAD51126.1 putative amidophosphoribosyl-transferase [Bacteroides fragilis YCH46] | | | |
| 7819, 7820 | 50122191 | 34 | 4.00E-47 | Erwinia carotovora subsp. atroseptica SCRI1043 | HlyD family secretion protein [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76167.1 HlyD family secretion protein [Erwinia carotovora subsp. atroseptica SCRI1043] | | | 3.1.11.- |
| 7821, 7822 | 20095135 | 98 | 6.00E-59 | Providencia rettgeri | TraC [Providencia rettgeri] | Providencia rettgeri conjugative genomic island R391, complete sequence | 97 ##### | |
| 7823, 7824 | 29349895 | 49 | 3.00E-71 | Bacteroides thetaiotaomicron VPI-5482 | putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79592.1 putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482] | | | 3.2.1.- |
| 7825, 7826 | 48853332 | 39 | 5.00E-21 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | |
| 7827, 7828 | 20090484 | 33 | 2.00E-08 | Methanosarcina acetivorans C2A | transposase [Methanosarcina acetivorans C2A] gb AAM05039.1 transposase [Methanosarcina acetivorans str. C2A] | | | |
| 7829, 7830 | 53684697 | 26 | 1.00E-08 | Desulfotobacterium hafnense DCB-2 | COG2984: ABC-type uncharacterized transport system, periplasmic component [Desulfotobacterium hafnense DCB-2] | | | |
| 7831, 7832 | 48858849 | 51 | 2.00E-77 | Cytophaga hutchinsonii | COG0525: Valyl-tRNA synthetase [Cytophaga hutchinsonii] | Bacteroides fragilis YCH46 DNA, complete genome | 88 4.00E-08 | 6.1.1.9 |
| 7835, 7836 | 34557654 | 42 | 5.00E-33 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1291 [Wolinella succinogenes DSM 1740] emb CAE10369.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 7837, 7838 | 34557182 | 48 | 3.00E-38 | Wolinella succinogenes DSM 1740 | PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09897.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] | | | |
| 7839, 7840 | 34397867 | 24 | 1.00E-21 | Porphyromonas gingivalis W83 | TPR domain protein [Porphyromonas gingivalis W83] ref NP_906029.1 TPR domain protein [Porphyromonas gingivalis W83] | | | |
| 7843, 7844 | 53711601 | 51 | 5.00E-78 | Bacteroides fragilis YCH46 | UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate ligase [Bacteroides fragilis YCH46] dbj BAD47059.1 UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate ligase [Bacteroides fragilis YCH46] | | | 6.3.2.13 |
| 7849, 7850 | 48846045 | 36 | 1.00E-22 | Geobacter metallireducens GS | COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |

| | | | | | | | |
|---------------|----------|----|----------|---|---|--|----------|
| 785, 786 | 48853824 | 50 | 4.00E-62 | Cytophaga hutchinsonii | COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii] | | |
| 7851, 7852 | 14521387 | 33 | 2.00E-34 | Pyrococcus abyssi GE5 | hypothetical protein PAB0790 [Pyrococcus abyssi GE5] emb CAB50093.1 Hypothetical protein [Pyrococcus abyssi] pir H75098 hypothetical protein PAB0790 - Pyrococcus abyssi (strain Orsay) | | 3.6.1.- |
| 7853, 7854 | 15643214 | 26 | 2.00E-13 | Thermotoga maritima MSB8 | hypothetical protein TM0448 [Thermotoga maritima MSB8] gb AAD35531.1 hypothetical protein TM0448 [Thermotoga maritima MSB8] pir A72375 hypothetical protein - Thermotoga maritima (strain MSB8) | | |
| 7855, 7856 | 34558194 | 65 | 8.00E-53 | Wolinella succinogenes DSM 1740 | RIBONUCLEASE HI [Wolinella succinogenes DSM 1740] emb CAE10909.1 RIBONUCLEASE HI [Wolinella succinogenes] | | 3.1.26.4 |
| 7857, 7858 | 54302166 | 27 | 5.00E-09 | Photobacterium profundum SS9 | hypothetical protein PBPRB0486 [Photobacterium profundum SS9] emb CAG22359.1 hypothetical protein [Photobacterium profundum] | | |
| 7859, 7860 | 14718642 | 30 | 3.00E-21 | Sus scrofa | estrogen sulfotransferase [Sus scrofa] ref NP_999157.1 estrogen sulfotransferase [Sus scrofa] | | 2.8.2.4 |
| 7861, 7862 | 32262892 | 24 | 1.00E-17 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860872.1 hypothetical protein HH1341 [Helicobacter hepaticus ATCC 51449] | | |
| 7867, 7868 | 34556675 | 30 | 2.00E-34 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0233 [Wolinella succinogenes DSM 1740] emb CAE09390.1 conserved hypothetical protein [Wolinella succinogenes] | | 5.2.1.8 |
| 7869, 7870 | 53713306 | 45 | 2.00E-49 | Bacteroides fragilis YCH46 | ATP-independent RNA helicase [Bacteroides fragilis YCH46] db BAD48764.1 ATP-independent RNA helicase [Bacteroides fragilis YCH46] | | 2.7.7.- |
| 787, 788 | 48853824 | 44 | 7.00E-64 | Cytophaga hutchinsonii | COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii] cytochrome c551 peroxidase [Campylobacter jejuni RM1221] gb AAW34515.1 cytochrome c551 peroxidase [Campylobacter jejuni RM1221] | | 1.11.1.5 |
| 7871, 7872 | 57236932 | 45 | 6.00E-22 | Campylobacter jejuni RM1221 | ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes DSM 1740] emb CAE10562.1 ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes] | | |
| 7875, 7876 | 34557847 | 29 | 4.00E-07 | Wolinella succinogenes DSM 1740 | putative glycosyltransferase [Serratia marcescens] | | 2.4.1.- |
| 7877, 7878 | 4753136 | 38 | 1.00E-32 | Serratia marcescens | putative glycosyltransferase [Serratia marcescens] | | 2.4.1.- |
| 7879, 7880 | 4753136 | 35 | 3.00E-37 | Serratia marcescens | putative glycosyltransferase [Serratia marcescens] | | 2.4.1.- |

| | | | | | | | | | |
|---------------------------------|----------------|----------|----|---------------------------------------|---|--|--|--|----------|
| 7883, 7884, 7885, 7886 | 34558247 58 | 1.00E-68 | 58 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907863.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907529.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907441.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907411.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907300.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907278.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907223.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907162.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907120.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_906960.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_906534.1 TRANSPOSASE [Wolinella succinogenes DSM 1740] emb CAE10763.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes] emb CAE10429.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes] emb CAE10341.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes] emb CAE10311.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes] em COG0688: Phosphatidylserine decarboxylase [Pseudomonas fluorescens PfO-1] | | | | 4.1.1.65 |
| 7887, 7888 | 34557306 68 | 1.00E-47 | 68 | Wolinella succinogenes DSM 1740 | NOSZ PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10021.1 NOSZ PROTEIN [Wolinella succinogenes] PUTATIVE D-ALANINE-D-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09580.1 PUTATIVE D-ALANINE-D-ALANINE LIGASE [Wolinella succinogenes] sp Q7MA71 DDL_WOLSU D-alanine-D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase) | | | | 6.3.2.4 |
| 7889, 790 | 34556865 54 | 5.00E-40 | 54 | Wolinella succinogenes DSM 1740 | Inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714220.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar Lai str. 56601] gb AAN51238.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar lai str. 56601] sp Q8EZ21 PYR_LEPIN Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase) gb AAS71768.1 inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] | | | | 3.6.1.1 |

| | | | | | | | | |
|---------------|----------|----|----------|--|--|----------|--|--|
| 7893, 7894 | 6968117 | 50 | 6.00E-47 | Campylobacter jejuni subsp. jejuni NCTC 11168 | putative ATP /GTP binding protein [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281833.1 putative ATP /GTP binding protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81414 probable ATP /GTP binding protein Cj0650 [imported] - Campylobacter jejuni (strain NCTC 11168) sp Q9PHL7 ENGB_CAMJE Probable GTP-binding protein engB | | | |
| 7897, 7898 | 53714509 | 26 | 3.00E-17 | Bacteroides fragilis YCH46 | hypothetical protein BF3222 [Bacteroides fragilis YCH46] db BAD49867.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 7899, 7900 | 56489415 | 25 | 2.00E-07 | Plasmodium berghiei | Pb-reticulocyte binding protein [Plasmodium berghiei] | | | |
| 79, 80 | 34398333 | 45 | 2.00E-50 | Porphyromonas gingivalis W83 | conserved domain protein [Porphyromonas gingivalis W83] ref NP_904501.1 hypothetical protein PG0160 [Porphyromonas gingivalis W83] | | | |
| 7901, 7902 | 55819425 | 26 | 1.00E-13 | Mimivirus | putative DNA repair protein [Mimivirus] gb AAV50819.1 putative DNA repair protein [Mimivirus] | | | |
| 7903, 7904 | 34557690 | 54 | 2.00E-21 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1330 [Wolinella succinogenes DSM 1740] emb CAE10405.1 hypothetical protein [Wolinella succinogenes] | | | |
| 7905, 7906 | 28899263 | 43 | 2.00E-33 | Vibrio parahaemolyticus RIMD 2210633 | iron(III) ABC transporter, ATP-binding protein [Vibrio parahaemolyticus RIMD 2210633] db JBA60752.1 iron(III) ABC transporter, ATP-binding protein [Vibrio parahaemolyticus] | 1.8.-.- | | |
| 7907, 7908 | 34557200 | 34 | 5.00E-17 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0802 [Wolinella succinogenes DSM 1740] emb CAE09915.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 7909, 7910 | 23025125 | 46 | 5.00E-21 | Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293 | COG4974: Site-specific recombinase XerD [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293] | | | |
| 7911, 7912 | 15896153 | 50 | 4.00E-26 | Clostridium acetobutylicum ATCC 824 | Spore photoproduct lyase, SPL related protein [Clostridium acetobutylicum ATCC 824] gb AAK80842.1 Spore photoproduct lyase, SPL related protein [Clostridium acetobutylicum ATCC 824] pir G97256 spore photoproduct lyase, SPL related protein [imported] - Clostridium acetobutylicum | 4.1.99.- | | |
| 7913, 7914 | 34557291 | 45 | 2.00E-58 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | 2.7.3.- | | |
| 7915, 7916 | 48831167 | 39 | 1.00E-36 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | 2.7.3.- | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|----------|
| 7917, 7918 | 34558004 | 56 | 4.00E-92 | Wolinella succinogenes DSM 1740 | RNA POLYMERASE ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10719.1 RNA POLYMERASE ALPHA SUBUNIT [Wolinella succinogenes] sp Q7M87 RPOA_WOLSU DNA-directed RNA polymerase alpha chain (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit) | | | 2.7.7.6 |
| 7923, 7924 | 45658174 | 32 | 2.00E-13 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC12326 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AA570897.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |
| 793, 794 | 48856683 | 32 | 4.00E-15 | Cytophaga hutchinsonii | COG4258: Predicted exporter [Cytophaga hutchinsonii] | | | |
| 7933, 7934 | 57234354 | 42 | 1.00E-34 | Dehalococcoides ethenogenes 195 | hydrogenase, group 4, EchE subunit, putative [Dehalococcoides ethenogenes 195] gb AAW38859.1 hydrogenase, group 4, EchE subunit, putative [Dehalococcoides ethenogenes 195] | | | 1.-.-.- |
| 7937, 7938 | 34557782 | 41 | 4.00E-37 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | 2.7.3.- |
| 7939, 7940 | 29654150 | 47 | 1.00E-58 | Coxiella burnetii RSA 493 | hypothetical protein CBU0822 [Coxiella burnetii RSA 493] gb AAO90356.1 conserved hypothetical protein [Coxiella burnetii RSA 493] | | | |
| 7943, 7944 | 53798300 | 61 | 2.00E-32 | Chloroflexus aurantiacus | COG3945: ABC-type uncharacterized transport systems, ATPase components [Chloroflexus aurantiacus] | | | 1.8.-.- |
| 7945, 7946 | 48854975 | 56 | 2.00E-79 | Cytophaga hutchinsonii | COG0247: Fe-S oxidoreductase [Cytophaga hutchinsonii] | | | 1.3.99.1 |
| 7949, 7950 | 34558149 | 37 | 7.00E-44 | Wolinella succinogenes DSM 1740 | SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes DSM 1740] emb CAE10864.1 | | | |
| 7951, 7952 | 51573026 | 26 | 4.00E-15 | Borrelia garinii PBI | SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes] conserved hypothetical protein [Borrelia garinii PBI] ref YP_072643.1 hypothetical protein BG0193 [Borrelia garinii PBI] | | | 2.7.3.- |
| 7953, 7954 | 17227393 | 60 | 6.00E-61 | Nostoc sp. PCC 7120 | hypothetical protein air8019 [Nostoc sp. PCC 7120] pir AD2553 hypothetical protein air8019 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120gamma dbj BAB77349.1 ORF_ID:air8019-transposase-unknown protein [Nostoc sp. PCC 7120] | | | |
| 7955, 7956 | 48854025 | 37 | 1.00E-16 | Cytophaga hutchinsonii | hypothetical protein Chut02003116 [Cytophaga hutchinsonii] | | | |
| 7957, 7958 | 29348766 | 45 | 1.00E-38 | Bacteroides thetaiotaomicron VPI-5482 | ribonuclease III [Bacteroides thetaiotaomicron VPI-5482] gb AAO78463.1 ribonuclease III [Bacteroides thetaiotaomicron VPI-5482] | | | 3.1.26.3 |

| | | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|----|----------|----------|
| 7959, 7960 | 41205694 | 30 | 1.00E-26 | Geobacillus stearothermophilus | putative rhamnosyltransferase [Geobacillus stearothermophilus] heme biosynthesis protein (nirJ-2) [Archaeoglobus fulgidus DSM 4304] gb AAB89245.1 heme biosynthesis protein (nirJ-2) [Archaeoglobus fulgidus DSM 4304] pir H69500 heme biosynthesis protein (nirJ-2) homolog - Archaeoglobus fulgidus | | | | 2.4.1.- | |
| 7963, 7964 | 11499591 | 28 | 9.00E-10 | Archaeoglobus fulgidus DSM 4304 | putative response regulator receiver protein [Azoarcus sp. EbN1] emb CAI07934.1 putative response regulator receiver protein [Azoarcus sp. EbN1] | | | | | |
| 7965, 7966 | 56477246 | 43 | 1.00E-26 | Azoarcus sp. EbN1 | | | | | | |
| 7967, 7968 | 34558196 | 32 | 7.00E-11 | Wolinella succinogenes DSM 1740 | DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes] | | | | | |
| 7969, 7970 | 15927758 | 28 | 1.00E-08 | Staphylococcus aureus subsp. aureus N315 | hypothetical protein SA1980 [Staphylococcus aureus subsp. aureus N315] dbj BAB58340.1 conserved hypothetical protein [Staphylococcus aureus subsp. aureus Mu50] pir E90013 conserved hypothetical protein SA1980 [Imported] - Staphylococcus aureus (strain N315) dbj BAB43270.1 conserved hypothetical protein [Staphylococcus aureus subsp. aureus N315] ref NP_372702.1 hypothetical protein SAV2178 [Staphylococcus aureus subsp. aureus Mu50] | | | | | |
| 7971, 7972 | 53730639 | 32 | 2.00E-16 | Dechloromonas aromatica RCB | hypothetical protein Daro03001950 [Dechloromonas aromatica RCB] | | | | | |
| 7973, 7974 | 56708496 | 61 | 4.00E-50 | Francisella tularensis subsp. tularensis Schu 4 | sugar transamine/perosamine synthetase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46088.1 sugar transamine/perosamine synthetase [Francisella tularensis subsp. tularensis] gb AAS60273.1 perosamine synthetase [Francisella tularensis subsp. tularensis] | | | | | |
| 7977, 7978 | 24374604 | 30 | 5.00E-26 | Shewanella oneidensis MR-1 | sensory box protein [Shewanella oneidensis MR-1] gb AAN56091.1 sensory box protein [Shewanella oneidensis MR-1] | | | | | |
| 7979, 7980 | 24374604 | 81 | 1.00E-49 | Shewanella oneidensis MR-1 | sensory box protein [Shewanella oneidensis MR-1] gb AAN56091.1 sensory box protein [Shewanella oneidensis MR-1] | | | 88 | 1.00E-21 | |
| 7981, 7982 | 15689217 | 50 | 9.00E-71 | Methanocaldococ- us jannaschii DSM 2661 | DNA topoisomerase VI, subunit B (top6B) [Methanocaldococcus jannaschii DSM 2661] gb AAB99032.1 DNA topoisomerase VI, subunit B (top6B) [Methanocaldococcus jannaschii DSM 2661] pir C64428 hypothetical protein MJ1028 - Methanocaldococcus jannaschii | | | | | 5.99.1.3 |

| | | | | | | | | | |
|---------------|----------|----|----------|-------------------------------------|--|--|--|--|----------|
| 7985, 7986 | 15612340 | 45 | 1.00E-48 | Helicobacter pylori J99 | PHOSPHATIDYL SERINE DECARBOXYLASE [Helicobacter pylori J99] sp Q9ZJN0 PSD_HELPJ Phosphatidylserine decarboxylase proenzyme [Contains: Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine decarboxylase beta chain] gb AAD06847.1 | | | | 4.1.1.65 |
| 7987, 7988 | 30248124 | 31 | 1.00E-18 | Nitrosomonas europaea ATCC 19718 | PHOSPHATIDYL SERINE DECARBOXYLASE [Helicobacter pylori J99] pir J71628 phosphatidylserine decarboxylase (EC 4.1.1.65) precursor - Helicobacter pylori (strain J99) | | | | |
| 7993, 7994 | 31195897 | 43 | 7.00E-29 | Anopheles gambiae | recQ; ATP-dependent DNA helicase [Nitrosomonas europaea ATCC 19718] emb CAD84004.1 recQ; ATP-dependent DNA helicase [Nitrosomonas europaea ATCC 19718] | | | | 3.6.1.- |
| 7995, 7996 | 48857810 | 48 | 9.00E-66 | Clostridium thermocellum | ENSANGP00000003278 [Anopheles gambiae] | | | | 3.4.13.9 |
| 7997, 7998 | 34557234 | 66 | 8.00E-77 | Wolinella succinogenes DSM 1740 | COG0249: Mismatch repair ATPase (MutS family) [Clostridium thermocellum ATCC 27405] | | | | |
| 7999, 8000 | 51246841 | 56 | 2.00E-32 | Desulfotalea psychrophila LSV54 | FDHD PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09949.1 FDHD PROTEIN [Wolinella succinogenes] related to molybdenum transport protein (ModE) [Desulfotalea psychrophila LSV54] emb CAG37718.1 related to molybdenum transport protein (ModE) [Desulfotalea psychrophila LSV54] | | | | |
| 8003, 8004 | 57241759 | 41 | 3.00E-31 | Campylobacter lari | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54429.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 8005, 8006 | 50085326 | 49 | 5.00E-25 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD2218 [Acinetobacter sp. ADP1] emb CAG69014.1 conserved hypothetical protein [Acinetobacter sp. ADP1] | | | | |
| 8007, 8008 | 15893643 | 34 | 7.00E-12 | Clostridium acetobutylicum ATCC 824 | Uncharacterized conserved membrane protein, SANA family [Clostridium acetobutylicum ATCC 824] gb AAK78332.1 Uncharacterized conserved membrane protein, SANA family [Clostridium acetobutylicum ATCC 824] pir J96943 uncharacterized conserved membrane protein, SANA family CAC0352 [imported] - Clostridium acetobutylicum | | | | |
| 801, 802 | 15894734 | 29 | 7.00E-22 | Clostridium acetobutylicum ATCC 824 | Two-component system regulator (CheY domain and HTH-like DNA-binding domain) [Clostridium acetobutylicum ATCC 824] gb AAK79423.1 Two-component system regulator (CheY domain and HTH-like DNA-binding domain) [Clostridium acetobutylicum ATCC 824] pir J97079 two-component system regulator (CheY domain and HTH-like DNA-binding domain) [imported] - Clostridium acetobutylicum | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|----|----------|----------|
| 8011, 8012 | 29345904 | 43 | 8.00E-42 | Bacteroides thetaiotaomicron VPI-5482 | protoporphyrin IX magnesium chelatase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75601.1 protoporphyrin IX magnesium chelatase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 8013, 8014 | 34557313 | 50 | 3.00E-50 | Wolinella succinogenes DSM 1740 | ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10028.1 ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes] | | | | 1.8.-.- |
| 8015, 8016 | 50914506 | 63 | 1.00E-64 | Streptococcus pyogenes MGAS10394 | Type II restriction-modification system methylation subunit [Streptococcus pyogenes MGAS10394] gb AAT87295.1 Type II restriction-modification system methylation subunit [Streptococcus pyogenes MGAS10394] gb AAT72355.1 methylase [Streptococcus pyogenes] gb AAR83196.1 type II modification methylase [Streptococcus pyogenes] | Bacteroides sp. 139 plasmid p139EF putative resolvase, putative C-5 cytosine-specific DNA methylase, putative HylD secretion protein, and putative ABC transporter protein genes, complete cds; and unknown gene | 83 | 7.00E-12 | 2.1.1.73 |
| 8017, 8018 | 57238060 | 56 | 8.00E-69 | Campylobacter jejuni RM1221 | glucose inhibited division protein A [Campylobacter jejuni RM1221] gb AAW35643.1 glucose inhibited division protein A [Campylobacter jejuni RM1221] | Desc:Haemophilus influenzae DNA for cellular proliferation protein #11. Org:Haemophilus influenzae | 89 | 6.00E-10 | |
| 8023, 8024 | 57234157 | 42 | 3.00E-51 | Dehalococcoides ethenogenes 195 | portal protein, HK97 family, putative [Dehalococcoides ethenogenes 195] gb AAW39662.1 portal protein, HK97 family, putative [Dehalococcoides ethenogenes 195] | | | | |
| 8025, 8026 | 15893941 | 46 | 7.00E-46 | Clostridium acetobutylicum ATCC 824 | Response regulator (CheY-like receiver domain and HTH DNA binding domain) [Clostridium acetobutylicum ATCC 824] gb AAK78630.1 Response regulator (CheY-like receiver domain and HTH DNA binding domain) [Clostridium acetobutylicum ATCC 824] pir C96980 response regulator (CheY-like receiver domain and HTH DNA binding domain) [imported] - Clostridium acetobutylicum | | | | 2.7.3.- |
| 8029, 8030 | 34557593 | 44 | 4.00E-43 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1227 [Wolinella succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wolinella succinogenes] sp P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridylyl synthase) [Uracil hydrolyase] | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|----------|
| 803, 804 | 48853695 | 59 | 6.00E-81 | Cytophaga hutchinsonii | hypothetical protein Chut02003551 [Cytophaga hutchinsonii] | | | |
| 8033, 8034 | 4838141 | 34 | 1.00E-23 | Bacteroides fragilis | BatD [Bacteroides fragilis] | | | |
| 8035, 8036 | 1488662 | 35 | 1.00E-10 | Bacillus subtilis | phosphatase-associated protein [Bacillus subtilis] sp P54421 LYTE_BACSU Probable endopeptidase lytE precursor (Gamma-D-glutamate-meso- diaminopimelate muropetidase lytE) (Phosphatase-associated protein papQ) (Cell wall-associated polypeptide CWBP33) | | | |
| 8037, 8038 | 57506273 | 59 | 6.00E-42 | Campylobacter upsaliensis RM3195 | Fic family protein [Campylobacter upsaliensis RM3195] gb EAL52255.1 Fic family protein [Campylobacter upsaliensis RM3195] | | | |
| 8039, 8040 | 34557297 | 53 | 3.00E-28 | Wolfinella succinogenes DSM 1740 | PUTATIVE TRANSPORTER [Wolfinella succinogenes DSM 1740] emb CAE10012.1 PUTATIVE TRANSPORTER [Wolfinella succinogenes] | | | 1.8.- |
| 8043, 8044 | 34556770 | 36 | 4.00E-18 | Wolfinella succinogenes DSM 1740 | Putative Dethiobiotin synthetase [Wolfinella succinogenes DSM 1740] emb CAE09485.1 Putative Dethiobiotin synthetase [Wolfinella succinogenes] | | | 6.3.3.3 |
| 8049, 8050 | 48856170 | 34 | 2.00E-09 | Cytophaga hutchinsonii | COG1452: Organic solvent tolerance protein OstA [Cytophaga hutchinsonii] | | | |
| 805, 806 | 21226435 | 60 | 6.00E-55 | Methanosarcina mazel Go1 | Methyl-accepting chemotaxis protein [Methanosarcina mazel Go1] | | | |
| 8051, 8052 | 48855476 | 52 | 7.00E-76 | Cytophaga hutchinsonii | COG0437: Fe-S-cluster-containing hydrogenase components 1 [Cytophaga hutchinsonii] | | | 1.2.7.- |
| 8053, 8054 | 16080273 | 37 | 7.00E-10 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU32200 [Bacillus subtilis subsp. subtilis str. 168] emb CAB15210.1 yutJ [Bacillus subtilis subsp. subtilis str. 168] pir D70024 NADH dehydrogenase homolog yutJ - Bacillus subtilis | | | 1.6.99.3 |
| 8059, 8060 | 53713209 | 45 | 1.00E-15 | Bacteroides fragilis YCH46 | hypothetical protein BF1919 [Bacteroides fragilis YCH46] dbj BAD48667.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 8061, 8062 | 46143358 | 48 | 2.00E-30 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | COG0242: N-formyl(methionyl)-tRNA deformylase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | 3.5.1.88 |
| 8065, 8066 | 34556591 | 46 | 4.00E-26 | Wolfinella succinogenes DSM 1740 | PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolfinella succinogenes DSM 1740] emb CAE09306.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolfinella succinogenes] | | | 4.2.1.70 |

| | | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|--|--|---------------|
| 8067, 8068 | 19699220 | 35 | 6.00E-34 | Arabidopsis thaliana | At1g49820/F10F5_1 [Arabidopsis thaliana] gb AAL09753.1 At1g49820/F10F5_1 [Arabidopsis thaliana] gb AAG51775.1 unknown protein; 11341-13243 [Arabidopsis thaliana] pir A96535 unknown protein, 11341-13243 [imported] - Arabidopsis thaliana ref NP_564555.1 5- methylthioribose kinase family [Arabidopsis thaliana] | | | | | 2.7.1.10 0 |
| 8069, 8070 | 48855291 | 41 | 1.00E-06 | Cytophaga hutchinsonii | COG2919: Septum formation Initiator [Cytophaga hutchinsonii] | | | | | |
| 8071, 8072 | 48864065 | 43 | 2.00E-22 | Microbulbifer degradans 2-40 | COG0328: Ribonuclease HI [Microbulbifer degradans 2-40] | | | | | |
| 8073, 8074 | 48864040 | 38 | 1.00E-35 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02000406 [Microbulbifer degradans 2-40] | | | | | |
| 8075, 8076 | 28854869 | 24 | 2.00E-17 | Pseudomonas syringae pv. tomato str. DC3000 | conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794236.1 hypothetical protein PSPTO4482 [Pseudomonas syringae pv. tomato str. DC3000] | | | | | |
| 8079, 8080 | 13661984 | 30 | 5.00E-13 | Rhizobium etli | LpeA [Rhizobium etli] | | | | | |
| 8081, 8082 | 48855832 | 43 | 6.00E-48 | Cytophaga hutchinsonii | hypothetical protein Chut02001044 [Cytophaga hutchinsonii] | | | | | |
| 8085, 8086 | 34557849 | 41 | 6.00E-61 | Wolinella succinogenes DSM 1740 | INTEGRAL MEMBRANE PROTEIN-Small-conductance mechanosensitive channel [Wolinella succinogenes DSM 1740] emb CAE10564.1 INTEGRAL MEMBRANE PROTEIN-Small-conductance mechanosensitive channel [Wolinella succinogenes] | | | | | |
| 8087, 8088 | 5091686 | 39 | 1.00E-40 | Pediococcus pentosaceus | unknown [Pediococcus pentosaceus] ref NP_037556.1 unknown [Pediococcus pentosaceus] | | | | | |
| 8091, 8092 | 16801535 | 37 | 4.00E-49 | Listeria innocua Clp11262 | hypothetical protein lin2473 [Listeria innocua Clp11262] emb CAC97700.1 lin2473 [Listeria innocua] pir AD1741 aspartate kinase homolog lin2473 [imported] - Listeria innocua (strain Clp11262) | | | | | 2.7.2.4 |
| 8093, 8094 | 56707343 | 41 | 5.00E-19 | Francisella tularensis subsp. tularensis Schu 4 | Acetyltransferase [Francisella tularensis subsp. tularensis Schu 4] emb CAG44810.1 Acetyltransferase [Francisella tularensis subsp. tularensis] | | | | | 2.3.1.12 8 |
| 8097, 8098 | 16330629 | 40 | 4.00E-11 | Synechocystis sp. PCC 6803 | hypothetical protein sil1411 [Synechocystis sp. PCC 6803] dbj BAA18037.1 sil1411 [Synechocystis sp. PCC 6803] pir S75476 hypothetical protein sil1411 - Synechocystis sp. (strain PCC 6803) | | | | | 2.7.7.- |
| 8099, 8100 | 57241805 | 47 | 6.00E-12 | Campylobacter lari RM2100 | glutamyl-tRNA(Gln) amidotransferase, C subunit [Campylobacter lari RM2100] gb EAL54223.1 glutamyl-tRNA(Gln) amidotransferase, C subunit [Campylobacter lari RM2100] | | | | | 6.3.5.- |

| | | | | | | | | |
|--------|----------|----|----------|---|--|--|----|----------|
| 81, 82 | 29346485 | 36 | 1.00E-29 | Bacteroides thetaiotaomicron VPI-5482 | putative two-component system sensor protein, but no histidine kinase domain [Bacteroides thetaiotaomicron VPI-5482] gblAAO76182.1 putative two-component system sensor protein, but no histidine kinase domain [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.3.- |
| 8101, | 48854159 | 36 | 7.00E-28 | Cytophaga hutchinsonii | COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii] | | | 3.1.1.24 |
| 8103, | AAB1996 | | | | | | | |
| 8104 | 1 | 36 | 3.00E-09 | | Desc:Staphylococcus aureus 509RR protein. Org:Staphylococcus aureus | | | |
| 8105, | | | | Wolinella succinogenes DSM | hypothetical protein WS0414 [Wolinella succinogenes DSM 1740] | | | |
| 8106 | 34556843 | 40 | 3.00E-41 | 1740 | emb CAE09558.1 conserved hypothetical protein [Wolinella succinogenes] | | | 2.7.3.- |
| 8107, | | | | Wolinella succinogenes DSM | PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR | | | |
| 8108 | 34557235 | 49 | 1.00E-72 | 1740 | [Wolinella succinogenes DSM 1740] emb CAE09950.1 PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes] | | | 3.6.1.48 |
| 8109, | | | | Campylobacter jejuni RM1221 | selenocysteine-specific elongation factor [Campylobacter jejuni RM1221] | | | |
| 8110 | 57238422 | 44 | 7.00E-42 | | gblAAW36005.1 selenocysteine-specific elongation factor [Campylobacter jejuni RM1221] | | | |
| 811, | ABU0070 | | | | Desc:S. pneumoniae type 4 strain protein from coding region #273. | | | 5.1.3.14 |
| 812 | 6 | 33 | 7.00E-33 | | Org:Streptococcus pneumoniae type 4 strain | | | |
| 8111, | | | | Campylobacter lari RM2100 | RNA methyltransferase, TrmH family, group 3 [Campylobacter lari RM2100] | | | 2.1.1.- |
| 8112 | 57241386 | 45 | 5.00E-48 | | gblAL54498.1 RNA methyltransferase, TrmH family, group 3 [Campylobacter lari RM2100] | | | |
| 8113, | | | | Bacteroides fragilis YCH46 | putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] | | | |
| 8114 | 53714371 | 24 | 4.00E-15 | | dbj BAD49829.1 putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] | | | |
| 8117, | | | | Campylobacter upsaliensis RM3195 | conserved hypothetical protein [Campylobacter upsaliensis RM3195] | | | |
| 8118 | 57242699 | 51 | 1.00E-38 | | gblEAL53412.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195] | | 80 | 9.00E-11 |
| 8121, | | | | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] | | | |
| 8122 | 32261677 | 52 | 2.00E-41 | | ref NP_859661.1 hypothetical protein HH0130 [Helicobacter hepaticus ATCC 51449] | | 92 | 1.00E-10 |
| 8123, | | | | Campylobacter upsaliensis RM3195 | response regulator, putative [Campylobacter upsaliensis RM3195] | | | |
| 8124 | 57242734 | 37 | 3.00E-34 | | gblEAL53447.1 response regulator, putative [Campylobacter upsaliensis RM3195] | | | 2.7.3.- |
| 8125, | | | | Geobacter metallireducens GS | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | |
| 8126 | 48846591 | 28 | 1.00E-16 | 15 | | | | 2.7.3.- |

| | | | | | | | | | |
|---------------|----------|----|----------|--------|---------------------------------|--|---|----|----------|
| 8127, 8128 | 32262467 | 41 | 3.00E-17 | 51449 | Helicobacter hepaticus ATCC | hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449] ref NP_860449.1 hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449] | | | |
| 813, 814 | 21227977 | 53 | 4.00E-28 | 1740 | Methanosarcina mazei Go1 | hypothetical protein MM1875 [Methanosarcina mazei Go1] gb AAM31571.1 conserved protein [Methanosarcina mazei Go1] | | | |
| 8131, 8132 | 34557564 | 34 | 1.00E-20 | 1740 | Wolinella succinogenes DSM | PUTATIVE MOLYBDOPTEIN BIOSYNTHESIS PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10279.1 PUTATIVE MOLYBDOPTEIN BIOSYNTHESIS PROTEIN [Wolinella succinogenes] | | | |
| 8133, 8134 | 57504783 | 47 | 2.00E-13 | RM2228 | Campylobacter coli RM2228 | probable molybdopterin biosynthesis protein Cj1519 [Campylobacter coli RM2228] gb EAL56045.1 probable molybdopterin biosynthesis protein Cj1519 [Campylobacter coli RM2228] | | | |
| 8135, 8136 | 56750401 | 30 | 2.00E-16 | 6301 | Synechococcus elongatus PCC | hypothetical protein syc0392_d [Synechococcus elongatus PCC 6301] db BAD78582.1 hypothetical protein [Synechococcus elongatus PCC 6301] | | | 2.7.3.- |
| 8137, 8138 | 45524550 | 35 | 6.00E-14 | 8501 | Crocospaera watsonii WH 8501 | hypothetical protein Cwat03005121 [Crocospaera watsonii WH 8501] | | | |
| 8139, 8140 | 57168616 | 61 | 5.00E-77 | RM2228 | Campylobacter coli RM2228 | MloA [Campylobacter coli RM2228] gb EAL56577.1 MloA [Campylobacter coli RM2228] | Campylobacter jejuni strain RM2240 HsdR (hsdR) gene, hsdR- 1 allele, complete cds; RloD (rloD) gene, complete cds; HsdS (hsdS) gene, hsdS-3 allele, complete cds; MloA (mloA) gene, complete cds; and HsdM (hsdM) gene, hsdM-1 allele, complete cds | 85 | 2.00E-16 |

| | | | | | | | | | | | |
|---------------|--------------|----|-----------|--|---|--|----|----------|---------|--|----------|
| 8143, 8144 | 57168973 | 72 | 1.00E-100 | Campylobacter coli RM2228 | sulfate adenylyltransferase, subunit 1/adenylylsulfate kinase [Campylobacter coli RM2228] gb EAL56328.1 sulfate adenylyltransferase, subunit 1/adenylylsulfate kinase [Campylobacter coli RM2228] | Campylobacter jejuni OH4384 peptide chain release factor 2 (prfB) gene, partial cds; alpha-2,3- sialyltransferase (cst-I), sulfate adenylyltransferase subunit CysD (cysD), sulfate adenylyltransferase subunit CysN (cysN), putative sodium/sulfate symporter (sodium sulfate symporter), putative adenylylsulfate kinase (cysC), hypothetical protein, putative glycosyltransferase, and hypothetical protein genes, complete cds; and cj1457c gene, partial cds | 82 | 5.00E-32 | 2.7.7.4 | | |
| 8149, 8150 | 56421524 | 29 | 9.00E-19 | Geobacillus kaustophilus HTA426 | transposase [Geobacillus kaustophilus HTA426] dbj BAD77274.1 transposase [Geobacillus kaustophilus HTA426] | | | | | | |
| 815, 816 | 18312740 | 28 | 1.00E-28 | Pyrobaculum aerophilum str. IM2 | aminopeptidase [Pyrobaculum aerophilum str. IM2] gb AAL63589.1 aminopeptidase [Pyrobaculum aerophilum str. IM2] | | | | | | 3.4.11.- |
| 8151, 8152 | ABP7901 3 | 54 | 1.00E-80 | | Desc:N. gonorrhoeae amino acid sequence SEQ ID 4556. Org:Neisseria gonorrhoeae | | | | | | 3.1.21.3 |
| 8153, 8154 | 16078046 | 47 | 3.00E-49 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU09810 [Bacillus subtilis subsp. subtilis str. 168] emb CAA74443.1 hypothetical protein [Bacillus subtilis] emb CAB12820.1 yhaZ [Bacillus subtilis subsp. subtilis str. 168] pir D69820 hypothetical protein yhaZ - Bacillus subtilis | | | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|--|----------|
| 8159, 8160 | 34556772 | 58 | 1.00E-77 | Wolinetta succinogenes DSM 1740 | ENDOPEPTIDASE CLP ATP-BINDING CHAIN A [Wolinetta succinogenes DSM 1740] embjCAE09487.1] ENDOPEPTIDASE CLP ATP-BINDING CHAIN A [Wolinetta succinogenes] | | | | |
| 8161, 8162 | 11282475 | 39 | 1.00E-43 | imported | hypothetical protein wblA [imported] - Vibrio cholerae dbj[BAA33632.1] probable beta-D-galactoside 2-alpha-L-fucosyl transferase [Vibrio cholerae] proline iminopeptidase, putative [Bacillus cereus ATCC 10987] gbjAAS40103.1] proline iminopeptidase, putative [Bacillus cereus ATCC 10987] | | | | 2.4.1.69 |
| 8163, 8164 | 42780248 | 32 | 2.00E-27 | Bacillus cereus ATCC 10987 | COG2065: Pyrimidine operon attenuation protein/uracil phosphoribosyltransferase [Cytophaga hutchinsonii] beta-galactosidase [Bacteroides thetaiotaomicron VPI-5482] gbjAAO76733.1] beta-galactosidase [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.4.11.5 |
| 8165, 8166 | 48855920 | 36 | 1.00E-28 | Cytophaga hutchinsonii | COG2172: Anti-sigma regulatory factor (Ser/Thr protein kinase) [Cytophaga hutchinsonii] | | | | 2.4.2.8 |
| 8167, 8168 | 29347036 | 35 | 3.00E-31 | Bacteroides thetaitaomicron VPI-5482 | 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228] gbjEAL57510.1] 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228] | | | | 3.2.1.23 |
| 8169, 8170 | 48854029 | 31 | 5.00E-08 | Cytophaga hutchinsonii | hypothetical protein WS1210 [Wolinetta succinogenes DSM 1740] embjCAE10292.1] conserved hypothetical protein [Wolinetta succinogenes] | | | | |
| 8171, 8172 | 57167724 | 43 | 4.00E-31 | Campylobacter coli RM2228 | Methyltransferase [Bacillus cereus ATCC 14579] gbjAAP11449.1] Methyltransferase [Bacillus cereus ATCC 14579] | | | | |
| 8177, 8178 | 34557577 | 36 | 5.00E-33 | Wolinetta succinogenes DSM 1740 | arginine repressor, transcriptional regulator of arginine metabolism [Bacteroides thetaiotaomicron VPI-5482] gbjAAO78867.1] arginine repressor, transcriptional regulator of arginine metabolism [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 8179, 8180 | 30022617 | 62 | 8.00E-30 | Bacillus cereus ATCC 14579 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinetta succinogenes DSM 1740] embjCAE09961.1] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinetta succinogenes] | | | | 2.7.3.- |
| 8181, 8182 | 29349170 | 45 | 3.00E-17 | Bacteroides thetaitaomicron VPI-5482 | PUTATIVE TWO-COMPONENT SENSOR [Wolinetta succinogenes DSM 1740] embjCAE10497.1] PUTATIVE TWO-COMPONENT SENSOR [Wolinetta succinogenes] | | | | 2.7.3.- |
| 8183, 8184 | 34557246 | 37 | 6.00E-53 | Wolinetta succinogenes DSM 1740 | COG1741: Pirin-related protein [Burkholderia fungorum LB400] Desc:Helicobacter pylori cellular proliferation protein #241. Org:Helicobacter pylori | | | | |
| 8185, 8186 | 34557782 | 45 | 3.00E-34 | Wolinetta succinogenes DSM 1740 | COG1544: Ribosome-associated protein Y (PSrp-1) [Moorella thermoacetica ATCC 39073] | | | | 4.6.1.4 |
| 8189, 820 | 48783002 | 49 | 9.00E-41 | Burkholderia fungorum LB400 | | | | | |
| 8191, 8192 | AAU35928 | 62 | 6.00E-46 | | | | | | |
| 8193, 8194 | 49236237 | 51 | 1.00E-27 | Moorella thermoacetica ATCC 39073 | | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--------|---------------------------------|--|--|--|----------|
| 8195, 8196 | 48846331 | 35 | 5.00E-37 | 15 | Geobacter metallireducens GS | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 8197, 8198 | 54308791 | 45 | 4.00E-41 | | Photobacterium profundum SS9 | hypothetical ATP-dependent helicase [Photobacterium profundum SS9] embjCAG20009.1 hypothetical ATP-dependent helicase [Photobacterium profundum] | | | 3.6.1.- |
| 8199, 8200 | 32261920 | 55 | 2.00E-47 | 51449 | Helicobacter hepaticus ATCC | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859903.1 hypothetical protein HH0372 [Helicobacter hepaticus ATCC 51449] | | | 2.6.1.17 |
| 8201, 8202 | 34558481 | 33 | 2.00E-44 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] embjCAE09196.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 8203, 8204 | 17233315 | 39 | 4.00E-08 | 7120 | Nostoc sp. PCC | hypothetical protein air7299 [Nostoc sp. PCC 7120] dbj BAB78383.1 air7299 [Nostoc sp. PCC 7120] pir JAC2515 hypothetical protein air7299 [Imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha | | | |
| 8205, 8206 | 34556510 | 38 | 3.00E-40 | 1740 | Wolinella succinogenes DSM | PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] embjCAE09225.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] | | | |
| 8207, 8208 | 48855393 | 32 | 8.00E-27 | | Cytophaga hutchinsonii | COG0665: Glycine/D-amino acid oxidases (deaminating) [Cytophaga hutchinsonii] | | | |
| 821, 822 | 24371725 | 44 | 1.00E-22 | | Shewanella oneidensis MR-1 | hypothetical protein SO0125 [Shewanella oneidensis MR-1] gb AAAN53212.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | |
| 8211, 8212 | 23129348 | 51 | 6.00E-69 | 73102 | Nostoc punctiforme PCC 73102 | COG4804: Uncharacterized conserved protein [Nostoc punctiforme PCC 73102] | | | |
| 8213, 8214 | 34557912 | 41 | 8.00E-36 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS1588 [Wolinella succinogenes DSM 1740] embjCAE10627.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 8215, 8216 | 57241469 | 34 | 3.00E-14 | RM2100 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54581.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | |
| 8219, 8220 | 15605716 | 59 | 3.00E-33 | VF5 | Aquifex aeolicus VF5 | cytochrome c peroxidase [Aquifex aeolicus VF5] gb AAC06485.1 cytochrome c peroxidase [Aquifex aeolicus VF5] pir B70313 cytochrome-c peroxidase (EC 1.11.1.5) - Aquifex aeolicus | | | 1.11.1.5 |

| | | | | | | |
|---------------|----------|----|----------|--|--|--------------------------|
| 8221, 8222 | 21672563 | 46 | 2.00E-23 | Buchnera aphidicola str. Sg (Schizaphis graminum) | hypothetical ABC transporter ATP-binding protein [Buchnera aphidicola str. Sg (Schizaphis graminum)] gb AAM67841.1 hypothetical ABC transporter ATP-binding protein [Buchnera aphidicola str. Sg (Schizaphis graminum)] sp Q44613 LOLD_BUCAP Lipoprotein releasing system ATP-binding protein [Buchnera aphidicola] pir I40068 probable ABC-type transport protein - Buchnera aphidicola prf 2107191B ORF C | 1.8.-.- |
| 8223, 8224 | 53728282 | 33 | 5.00E-11 | Haemophilus sommus 2336 | COG1396: Predicted transcriptional regulators [Haemophilus somnus 2336] ref ZP_00123339.1 COG1396: Predicted transcriptional regulators [Haemophilus somnus 129PT] | |
| 8225, 8226 | 19705186 | 33 | 8.00E-11 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | Esterase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93980.1 Esterase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | 3.-.- |
| 8227, 8228 | 57236803 | 50 | 7.00E-19 | Flavobacterium johnsoniae | SecDF [Flavobacterium johnsoniae] peptidase (M20/M25/M40 family) [Xylella fastidiosa Temecula1] gb AAO29682.1 peptidase (M20/M25/M40 family) [Xylella fastidiosa Temecula1] | 3.17.2 1 |
| 823, 824 | 28199719 | 33 | 2.00E-25 | Xylella fastidiosa Temecula1 | DNA mismatch repair ATPase MutS [Mimivirus] gb AAV50628.1 DNA mismatch repair ATPase MutS [Mimivirus] | |
| 8235, 8236 | 55819234 | 22 | 2.00E-09 | Mimivirus | COG0726: Predicted xylanase/chitin deacetylase [Geobacter metallireducens GS-15] | 3.5.1.- 3.4.17.2 1 |
| 8237, 8238 | 48847340 | 47 | 4.00E-37 | Geobacter metallireducens GS-15 | COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii] | |
| 8241, 8242 | 48854772 | 41 | 1.00E-52 | Cytophaga hutchinsonii | COG1775: Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB [Magnetospirillum magnetotacticum MS-1] | |
| 8243, 8244 | 46202765 | 44 | 3.00E-19 | Magnetospirillum magnetotacticum MS-1 | short-chain alcohol dehydrogenase family [Synechocystis sp. PCC 6803] dbj BAA17390.1 short-chain alcohol dehydrogenase family [Synechocystis sp. PCC 6803] pir IS77543 short-chain alcohol dehydrogenase-related protein, 72K - Synechocystis sp. (strain PCC 6803) | 1.-.- |
| 8249, 8250 | 16329982 | 43 | 2.00E-34 | Synechocystis sp. PCC 6803 | hydrogenase expression/information protein HypA [Shewanella oneidensis MR-1] gb AAN55136.1 hydrogenase expression/information protein HypA [Shewanella oneidensis MR-1] | |
| 8251, 8252 | 24373649 | 57 | 4.00E-31 | Shewanella oneidensis MR-1 | thymidylate kinase [Picrophilus torridus DSM 9790] gb AAT44007.1 thymidylate kinase [Picrophilus torridus DSM 9790] | |
| 8255, 8256 | 48478494 | 30 | 3.00E-13 | Picrophilus torridus DSM 9790 | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|---------------|
| 8257, 8258 | 53712165 | 40 | 1.00E-47 | Bacteroides fragilis YCH46 | Trk system K+ uptake protein TrkA [Bacteroides fragilis YCH46] dbj BAD47623.1 Trk system K+ uptake protein TrkA [Bacteroides fragilis YCH46] | | | |
| 8259, 8260 | 53711484 | 30 | 6.00E-12 | Bacteroides fragilis YCH46 | hypothetical protein BF0193 [Bacteroides fragilis YCH46] dbj BAD46942.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 8261, 8262 | 52007843 | 48 | 6.00E-32 | Thiobacillus denitrificans ATCC 25259 | COG0607: Rhodanese-related sulfurtransferase [Thiobacillus denitrificans ATCC 25259] | | | |
| 8263, 8264 | 42523774 | 35 | 2.00E-38 | Bdellovibrio bacteriovorus HD100 | HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] emb CAE80147.1 HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] | | | |
| 8265, 8266 | 48861439 | 33 | 1.00E-22 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02003392 [Microbulbifer degradans 2-40] hypothetical protein DP0517 [Desulfotalea psychrophila LSV54] | | | |
| 8269, 8270 | 51244369 | 21 | 6.00E-17 | Desulfotalea psychrophila LSV54 | emb CAG35246.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] | | | |
| 827, 828 | AAE3396 | 35 | 2.00E-10 | | Desc:Acetobacter turbidans alpha-amino ester hydrolase protein #5. Org:Acetobacter turbidans | | | |
| 8271, 8272 | 48856045 | 21 | 8.00E-09 | Cytophaga hutchinsonii | hypothetical protein Chut02001277 [Cytophaga hutchinsonii] hypothetical carboxypeptidase G2 [Photobacterium profundum SS9] | | | |
| 8273, 8274 | 54302390 | 52 | 3.00E-53 | Photobacterium profundum SS9 | emb CAG22583.1 hypothetical carboxypeptidase G2 [Photobacterium profundum] | | | 3.4.17.1 1 |
| 8277, 8278 | 13471403 | 40 | 2.00E-12 | Mesorhizobium loti MAFF303099 | NADH-ubiquinone dehydrogenase chain E 1 [Mesorhizobium loti MAFF303099] dbj BAB48755.1 NADH-ubiquinone dehydrogenase chain E 1 [Mesorhizobium loti MAFF303099] | | | 1.6.5.3 |
| 8279, 8280 | 15895797 | 44 | 8.00E-39 | Clostridium acetobutylicum ATCC 824 | HD_GYP hydrolase domain fused to HD hydrolase domain [Clostridium acetobutylicum ATCC 824] gb AAK80486.1 HD_GYP hydrolase domain fused to HD hydrolase domain [Clostridium acetobutylicum ATCC 824] pir C97212 HD_GYP hydrolase domain fused to HD hydrolase domain [imported] - Clostridium acetobutylicum | | | |
| 8281, 8282 | 9655294 | 32 | 1.00E-12 | Vibrio cholerae O1 biovar eltor str. N16961 | conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230490.1 hypothetical protein VC0842 [Vibrio cholerae O1 biovar eltor str. N16961] gb AAK20799.1 unknown [Vibrio cholerae] gb AAK20769.1 unknown [Vibrio cholerae] pir G82273 conserved hypothetical protein VC0842 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | |
| 8283, 8284 | 57505955 | 52 | 2.00E-38 | Campylobacter upsaliensis RM3195 | conjugative transposon protein TraG, putative [Campylobacter upsaliensis RM3195] gb EAL52545.1 conjugative transposon protein TraG, putative [Campylobacter upsaliensis RM3195] | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|--|--|----|-------------------|
| 8285, 8286 | 57505955 | 36 | 8.00E-32 | Campylobacter upsaliensis RM3195 | conjugative transposon protein TraG, putative [Campylobacter upsaliensis RM3195] gb EAL52545.1 conjugative transposon protein TraG, putative [Campylobacter upsaliensis RM3195] | | | |
| 8287, 8288 | 34557851 | 31 | 2.00E-34 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1518 [Wolinella succinogenes DSM 1740] emb CAE10566.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 8289, 8290 | 50120714 | 64 | 5.00E-42 | Erwinia carotovora subsp. atroseptica SCRI1043 | rhodanese-like protein [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG74886.1 rhodanese-like protein [Erwinia carotovora subsp. atroseptica SCRI1043] | | | |
| 829, 830 | 48895464 | 31 | 1.00E-26 | Trichodesmium erythraeum IMS101 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Trichodesmium erythraeum IMS101] | | | 2.4.1.83 |
| 8291, 8292 | 57236963 | 47 | 4.00E-29 | Campylobacter jejuni RM1221 | GTP-binding protein [Campylobacter jejuni RM1221] gb AAW34546.1 GTP- binding protein [Campylobacter jejuni RM1221] | | | |
| 8293, 8294 | 54309817 | 70 | 1.00E-32 | Photobacterium profundum SS9 | putative UDP-glucose dehydrogenase [Photobacterium profundum SS9] emb CAG21035.1 putative UDP-glucose dehydrogenase [Photobacterium profundum] | Escherichia coli kpsS, kfoG, kfoF, kfoE, kfoD, kfoS, kfoC, kfoB, kfoA, kpsT genes for KpsS hypothetical protein, predicted glycosyltransferase, UDP-glucose dehydrogenase, KfoE hypothetical protein, KfoD hypothetical protein, IS hypothetical protein, chondroitin polymerase, KfoB hypothetical protein, UDP-glucose 4- epimerase, ABC transporter, partial and complete cds | 84 | 2.00E-07/1.1.1.22 |

| | | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|--|----------|
| 8295, 8296 | 34556483 | 67 | 7.00E-49 | Wolinella succinogenes DSM 1740 | PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolinella succinogenes DSM 1740] emb CAE09198.1 PUTATIVE UDP- GLUCURONIC ACID EPIMERASE [Wolinella succinogenes] | | | | 5.1.3.- |
| 8297, 8298 | 53715387 | 58 | 1.00E-92 | Bacteroides fragilis YCH46 | ABC transporter ATP-binding protein [Bacteroides fragilis dbj BAD50845.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] | | | | 1.8.-.- |
| 8299, 8300 | 53715387 | 43 | 4.00E-19 | Bacteroides fragilis YCH46 | ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD50845.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] | | | | |
| 83. 84 | 32474477 | 27 | 5.00E-08 | Rhodopirellula baltica SH 1 | hypothetical protein-transmembrane prediction [Rhodopirellula baltica SH 1] emb CAD75017.1 hypothetical protein-transmembrane prediction [Pirellula sp.] | | | | |
| 8305, 8306 | 26988521 | 60 | 3.00E-71 | Pseudomonas putida KT2440 | acyneuraminase cytidyltransferase, putative [Pseudomonas putida KT2440] gb AAN67410.1 acylneuraminase cytidyltransferase, putative [Pseudomonas putida KT2440] | | | | 2.7.7.43 |
| 8307, 8308 | 18310494 | 29 | 4.00E-25 | Clostridium perfringens str. 13 | two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] dbj BAB81218.1 two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] | | | | |
| 8309, 8310 | 48854548 | 35 | 8.00E-46 | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | | |
| 831, 832 | 55380037 | 28 | 1.00E-06 | Haloarcula marismortui ATCC 43049 | probable translation initiation factor 2 alpha subunit [Haloarcula marismortui ATCC 43049] gb AAV48181.1 probable translation initiation factor 2 alpha subunit [Haloarcula marismortui ATCC 43049] | | | | |
| 8311, 8312 | 45528473 | 37 | 3.00E-37 | Crocospaera watsonii WH 8501 | COG0457: FOG: TPR repeat [Crocospaera watsonii WH 8501] | | | | 5.2.1.8 |
| 8313, 8314 | 29349210 | 41 | 6.00E-32 | Bacteroides thetaiotaomicron VPI-5482 | peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Bacteroides thetaiotaomicron VPI-5482] gb AAO78907.1 peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Bacteroides thetaiotaomicron VPI-5482] | | | | 5.2.1.8 |
| 8315, 8316 | 34557362 | 37 | 3.00E-15 | Wolinella succinogenes DSM 1740 | TWO-COMPONENT HYBRID PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10077.1 TWO-COMPONENT HYBRID PROTEIN [Wolinella succinogenes] | | | | 2.7.3.- |
| 8317, 8318 | 34556704 | 49 | 3.00E-36 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0265 [Wolinella succinogenes DSM 1740] emb CAE09419.1 conserved hypothetical protein [Wolinella succinogenes] | | | | 3.6.1.13 |
| 8319, 8320 | 48832341 | 31 | 6.00E-17 | Magnetococcus sp. MC-1 | COG0842: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | | |
| 8321, 8322 | 34557444 | 49 | 6.00E-44 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1061 [Wolinella succinogenes DSM 1740] emb CAE10159.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |

| | | | | | | | | |
|---------------|----------|----|-----------|---|--|--|--|----------|
| 8323, 8324 | 57241252 | 45 | 1.00E-34 | Campylobacter lari RM2100 | signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54948.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100] | | | 2.7.3.- |
| 8327, 8328 | 34557494 | 41 | 1.00E-53 | Wolinella succinogenes DSM 1740 | PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes DSM 1740] emb CAE10209.1 PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes] | | | 6.3.4.6 |
| 8329, 8330 | 21673303 | 43 | 3.00E-55 | Chlorobium tepidum TLS | hypothetical protein CT0467 [Chlorobium tepidum TLS] gb AAM71710.1 conserved hypothetical protein [Chlorobium tepidum TLS] | | | |
| 833, 834 | 48856395 | 58 | 5.00E-51 | Cytophaga hutchinsonii | COG0327: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 8331, 8332 | 57505714 | 42 | 2.00E-29 | Campylobacter upsallensis RM3195 | AVG-specific adenine glycosylase [Campylobacter upsallensis RM3195] gb EAL52775.1 AVG-specific adenine glycosylase [Campylobacter upsallensis RM3195] | | | 3.2.2.- |
| 8335, 8336 | 34557297 | 55 | 2.00E-30 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSPORTER [Wolinella succinogenes DSM 1740] emb CAE10012.1 PUTATIVE TRANSPORTER [Wolinella succinogenes] | | | 1.8.- |
| 8337, 8338 | 57240764 | 44 | 3.00E-32 | Campylobacter lari RM2100 | proline dipeptidase TC0863 [Campylobacter lari RM2100] gb EAL55157.1 proline dipeptidase TC0863 [Campylobacter lari RM2100] | | | 3.4.11.9 |
| 8339, 8340 | 34556556 | 31 | 2.00E-21 | Wolinella succinogenes DSM 1740 | POSSIBLE PHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE0927.1 POSSIBLE PHOSPHATASE [Wolinella succinogenes] | | | 3.6.1.11 |
| 8341, 8342 | 53691630 | 50 | 3.00E-74 | Desulfovibrio desulfuricans G20 | COG1109: Phosphomannomutase [Desulfovibrio desulfuricans G20] | | | 5.4.2.8 |
| 8343, 8344 | 53736033 | 47 | 4.00E-72 | Crocospaera watsonii WH 8501 | COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Crocospaera watsonii WH 8501] | | | 1.8.- |
| 8347, 8348 | 57237455 | 43 | 5.00E-30 | Campylobacter jejuni RM1221 | ferric uptake regulation protein [Campylobacter jejuni RM1221] gb AAW35038.1 ferric uptake regulation protein [Campylobacter jejuni RM1221] | | | |
| 8349, 8350 | 48863156 | 35 | 7.00E-15 | Microbulbifer degradans 2-40 | COG4067: Uncharacterized protein conserved in archaea [Microbulbifer degradans 2-40] | | | |
| 8355, 8356 | 29349761 | 65 | 1.00E-106 | Bacteroides thetaiotaomicron VPI-5482 | valyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79458.1 valyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI- 5482] | | | 6.1.1.9 |
| 8357, 8358 | 48844990 | 62 | 1.00E-104 | Geobacter metallireducens GS-15 | COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Geobacter metallireducens GS-15] | | | 6.2.1.1 |
| 8359, 8360 | 23007833 | 34 | 1.00E-06 | Magnetospirillum magnetotacticum MS-1 | COG1409: Predicted phosphohydrolases [Magnetospirillum magnetotacticum MS-1] | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|---------------|
| 8363, 8364 | 48855923 | 32 | 1.00E-24 | Cytophaga hutchinsonii | COG2812: DNA polymerase III, gamma/tau subunits [Cytophaga hutchinsonii] | | | 2.7.7.7 |
| 8367, 8368 | 39933606 | 26 | 6.00E-15 | Rhodopseudomonas palustris CGA009 | putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) [Rhodopseudomonas palustris CGA009] emb[CAE25973.1] putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) [Rhodopseudomonas palustris CGA009] | | | |
| 8369, 8370 | 34556462 | 72 | 2.00E-46 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0003 [Wolinella succinogenes DSM 1740] emb[CAE09177.1] conserved hypothetical protein [Wolinella succinogenes] | | | |
| 837, 838 | 48856607 | 46 | 2.00E-48 | Cytophaga hutchinsonii | COG1321: Mn-dependent transcriptional regulator [Cytophaga hutchinsonii] oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter lari RM2100] gb[EA54833.1] oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter lari RM2100] | | | 1.--- |
| 8373, 8374 | 57241137 | 45 | 5.00E-48 | Campylobacter lari RM2100 | hypothetical protein WS1876 [Wolinella succinogenes DSM 1740] emb[CAE10886.1] conserved hypothetical protein [Wolinella succinogenes] | | | |
| 8375, 8376 | 34558171 | 32 | 7.00E-21 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb[CAE09196.1] conserved hypothetical protein [Wolinella succinogenes] | | | |
| 8377, 8378 | 34556481 | 30 | 5.00E-36 | Wolinella succinogenes DSM 1740 | orf, hypothetical protein [Escherichia coli O157:H7] ref NP_286822.1 hypothetical protein Z1297 [Escherichia coli O157:H7 EDL933] ref NP_309058.1 hypothetical protein ECs1031 [Escherichia coli O157:H7] pir E85621 hypothetical protein Z1297 [imported] - Escherichia coli (strain O157:H7, substrain EDL933) dbj BA34454.1 hypothetical protein [Escherichia coli O157:H7] pir G90757 hypothetical protein ECs1031 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) ABC transporter, ATP-binding protein/permease protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AA595497.1 ABC transporter, ATP-binding protein/permease protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | 3.4.21.- |
| 8381, 8382 | 12514126 | 40 | 2.00E-51 | Escherichia coli O157:H7 | oligopeptidase [Gloeobacter violaceus PCC 7421] dbj BAC88070.1 oligopeptidase [Gloeobacter violaceus PCC 7421] | | | 3.4.21.8 3 |
| 8385, 8386 | 46579430 | 43 | 2.00E-39 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | hypothetical protein BL02075 [Bacillus licheniformis ATCC 14580] gb AAU40965.1] conserved hypothetical protein [Bacillus licheniformis DSM 133] | | | |
| 8387, 8388 | 37519698 | 58 | 1.00E-84 | Gloeobacter violaceus PCC 7421 | general glycosylation pathway protein [Campylobacter jejuni RM1221] gb AAW35584.1] general glycosylation pathway protein [Campylobacter jejuni RM1221] | | | |
| 8389, 8390 | 52785829 | 39 | 1.00E-44 | Bacillus licheniformis ATCC 14580 | | | | |
| 8389, 8390 | 57238001 | 36 | 2.00E-25 | Campylobacter jejuni RM1221 | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|--|---------------|
| 839, 840 | 15679035 | 30 | 6.00E-23 | Methanothermobacter thermautotrophicus str. Delta H | hypothetical protein MTH1017 [Methanothermobacter str. Delta H] gb AAB85513.1 conserved protein [Methanothermobacter thermautotrophicus str. Delta H] pir F69002 conserved hypothetical protein MTH1017 - Methanothermobacterium thermoautotrophicum (strain Delta H) sp O27096 GCH3_METTH_GTP cyclohydrolase III | | | | |
| 8391, 8392 | 53712294 | 53 | 3.00E-66 | Bacteroides fragilis YCH46 | putative glycogen synthase [Bacteroides fragilis YCH46] dbj BAD47752.1 putative glycogen synthase [Bacteroides fragilis YCH46] | | | | 2.4.1.21 |
| 8395, 8396 | 28555201 | 44 | 1.00E-21 | Pseudomonas syringae pv. tomato str. DC3000 | sensory box histidine kinase [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794567.1 sensory box histidine kinase [Pseudomonas syringae pv. tomato str. DC3000] | | | | 2.7.3.- |
| 8399, 8400 | 16330855 | 49 | 6.00E-10 | Synechocystis sp. PCC 6803 | cytochrome b6/f complex iron-sulfur subunit [Synechocystis sp. PCC 6803] dbj BAA18263.1 cytochrome b6/f complex iron-sulfur subunit [Synechocystis sp. PCC 6803] pir S75804 plastocyanin-plastocyanin reductase (EC 1.10.99.1) Rieske iron-sulfur protein patC - Synechocystis sp. (strain PCC 6803) | | | | 1.10.99. 1 |
| 8405, 8406 | 57241290 | 56 | 2.00E-23 | Campylobacter lari RM2100 | Uncharacterized BCR, YoeG family COG1559 [Campylobacter lari RM2100] gb EAL54986.1 Uncharacterized BCR, YoeG family COG1559 [Campylobacter lari RM2100] | | | | 4.-.-.- |
| 8407, 8408 | 32034341 | 33 | 1.00E-15 | Actinobacillus pleuropneumoniae serovar 1 str. 4074 | COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Actinobacillus pleuropneumoniae serovar 1 str. 4074] | | | | |
| 8409, 8410 | 28275200 | 55 | 2.00E-37 | Shewanella oneidensis MR-1 | hypothetical cheY-homologous receiver domain protein [Shewanella oneidensis MR-1] | | | | 2.7.3.- |
| 8411, 8412 | 57240902 | 42 | 1.00E-32 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55295.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 8413, 8414 | 34557024 | 56 | 6.00E-84 | Wolinella succinogenes DSM 1740 | PROTEASE [Wolinella succinogenes DSM 1740] emb CAE09739.1 PROTEASE [Wolinella succinogenes] | | | | 3.4.21.- |
| 8415, 8416 | 16077746 | 47 | 8.00E-55 | Bacillus subtilis subsp. subtilis str. 168 | hypothetical protein BSU06780 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12498.1 yeeC [Bacillus subtilis subsp. subtilis str. 168] gb AAB66476.1 YeeC [Bacillus subtilis] pir G69792 hypothetical protein yeeC - Bacillus subtilis | | | | |
| 8417, 8418 | 41689105 | 60 | 8.00E-35 | Psychrobacter sp. 273-4 | COG0178: Excinuclease ATPase subunit [Psychrobacter sp. 273-4] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|---|----|----------|--|
| 8419, 8420 | 42528141 | 51 | 4.00E-62 | Treponema denticola ATCC 35405 | Fic family protein [Treponema denticola ATCC 35405] gb AAS13158.1 Fic family protein [Treponema denticola ATCC 35405] | Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 146 of 197 of the complete genome | 90 | 1.00E-10 | |
| 8421, 8422 | 56416014 | 78 | 3.00E-72 | Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150 | putative pseudouridine synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV79777.1 putative pseudouridine synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] | | | 4.2.1.70 | |
| 8427, 8428 | 23472302 | 24 | 9.00E-18 | Pseudomonas syringae pv. syringae B728a | COG0385: Predicted Na ⁺ -dependent transporter [Pseudomonas syringae pv. syringae B728a] | | | | |
| 8429, 8430 | 58422018 | 63 | 6.00E-71 | Geobacillus kaustophilus HTA426 | hypothetical protein GK3483 [Geobacillus kaustophilus HTA426] dbj BAD77768.1 hypothetical conserved protein [Geobacillus kaustophilus HTA426] | Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 183 of 197 of the complete genome | ## | 2.00E-09 | |
| 8431, 8432 | 2984552 | 50 | 5.00E-32 | Aquifex aerophilus VF5 | putative protein [Aquifex aerophilus VF5] ref NP_046399.1 hypothetical protein aq_aa03 [Aquifex aerophilus VF5] sp O66399 YZ03_AQUAE Hypothetical protein AA03 | | | | |
| 8433, 8434 | 39998400 | 40 | 5.00E-48 | Geobacter sulfurreducens PCA | hypothetical protein GSU3311 [Geobacter sulfurreducens PCA] gb AAR3670.1 hypothetical protein GSU3311 [Geobacter sulfurreducens PCA] | | | | |
| 8435, 8436 | 46119952 | 24 | 5.00E-16 | Crocospaera watsonii WH 8501 | COG2319: FOG: WD40 repeat [Crocospaera watsonii WH 8501] cytochrome c family protein, putative [Geobacter sulfurreducens PCA] | | | 2.7.1.37 | |
| 8437, 8438 | 39998517 | 33 | 1.00E-13 | Geobacter sulfurreducens PCA | gb AAR36818.1 cytochrome c family protein, putative [Geobacter sulfurreducens PCA] | | | | |
| 8439, 8440 | 29348769 | 51 | 2.00E-26 | Bacteroides thetaiotaomicron VPI-5482 | phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76466.1 phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.1.2.2 | |
| 8441, 8442 | 51245405 | 36 | 2.00E-27 | Desulfotalea psychrophila LSV54 | hypothetical protein DP1553 [Desulfotalea psychrophila LSV54] emb CAG36282.1 unknown protein [Desulfotalea psychrophila LSV54] | | | | |
| 8443, 8444 | 48113481 | 31 | 5.00E-27 | Exiguobacterium sp. 255-15 | COG1459: Type II secretory pathway, component PulF [Exiguobacterium sp. 255-15] | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|----------|
| 8445, 8446 | 34557014 | 41 | 4.00E-57 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0597 [Wollinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wollinella succinogenes] | | | |
| 8447, 8448 | 28974235 | 37 | 2.00E-33 | Campylobacter fetus | putative putative two-component sensor Cf0035 [Campylobacter fetus] hypothetical protein PHG054 [Cupriavidus necator] gb AAP85807.1 | | | 2.7.3.- |
| 8449, 8450 | 38637719 | 23 | 2.00E-08 | Cupriavidus necator | hypothetical protein PHG054 [Ralstonia eutropha] PUTATIVE OXIDOREDUCTASE PROTEIN [Sinorhizobium meliloti 1021] emb CAC47182.1 PUTATIVE OXIDOREDUCTASE PROTEIN [Sinorhizobium meliloti] | | | 1.1.1.- |
| 845, 846 | 15966356 | 31 | 5.00E-45 | Sinorhizobium meliloti 1021 | putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76689.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 8451, 8452 | 29346992 | 42 | 6.00E-41 | Bacteroides thetaitaomicron VPI-5482 | SENSORY BOX/GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wollinella succinogenes] | | | 2.7.3.- |
| 8453, 8454 | 34557573 | 35 | 5.00E-35 | Wollinella succinogenes DSM 1740 | folypolyglutamate synthase (folC) [Helicobacter pylori 26695] ref NP_208336.1 folypolyglutamate synthase (folC) [Helicobacter pylori 26695] pir A64713 folypolyglutamate synthase - Helicobacter pylori (strain 26695) | | | 6.3.2.17 |
| 8455, 8456 | 2314726 | 38 | 3.00E-44 | Helicobacter pylori 26695 | hypothetical protein WS0023 [Wollinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wollinella succinogenes] | | | 2.7.3.- |
| 8457, 8458 | 34556481 | 48 | 7.00E-48 | Wollinella succinogenes DSM 1740 | putative transposase [Aeromonas salmonicida subsp. salmonicida] ref NP_710165.1 putative transposase [Aeromonas salmonicida subsp. salmonicida] | | | |
| 8459, 8460 | 23897238 | 50 | 4.00E-67 | Aeromonas salmonicida subsp. salmonicida | hypothetical protein BT3559 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78665.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482] | | | |
| 8461, 8462 | 29348968 | 42 | 2.00E-15 | Bacteroides thetaitaomicron VPI-5482 | oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath] ref YP_113360.1 oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath] | | | |
| 8467, 8468 | 53758726 | 37 | 7.00E-33 | Methylococcus capsulatus str. Bath | hypothetical protein PP4291 [Pseudomonas putida KT2440] gb AAN6987.1.1 conserved hypothetical protein [Pseudomonas putida KT2440] | | | |
| 8469, 8470 | 26990982 | 27 | 3.00E-08 | Pseudomonas putida KT2440 | COG3832: Uncharacterized conserved protein [Cytophaga hutchinsonii] COG4772: Outer membrane receptor for Fe3+-dicitrate [Cytophaga hutchinsonii] | | | |
| 847, 848 | 48854395 | 52 | 4.00E-37 | Cytophaga hutchinsonii | | | | |
| 8473, 8474 | 48855757 | 44 | 7.00E-39 | Cytophaga hutchinsonii | | | | |

| | | | | | | | | | | |
|---------------|----------|----|-----------|---------------------|--|--|---|----|----------|----------|
| 8475, 8476 | 17938356 | 66 | 1.00E-104 | C58 | Agrobacterium tumefaciens str. C58 | ABC transporter, nucleotide binding/ATPase protein [Agrobacterium tumefaciens str. C58] gb AAL45461.1 ABC transporter, nucleotide binding/ATPase protein [Agrobacterium tumefaciens str. C58] pir AG3130 hypothetical protein Atu4667 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) | Pasteurella multocida subsp. multocida str. Pm70 section 201 of 204 of the complete genome | 87 | 4.00E-08 | 1.8-- |
| 8477, 8478 | 29346178 | 41 | 9.00E-27 | VPI-5482 | Bacteroides thetaiotaomicron | putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482] gb AAO75875.1 putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482] | | | | 4.--- |
| 8479, 8480 | 18310884 | 28 | 8.00E-10 | perfringens str. 13 | Clostridium | hypothetical protein CPE1902 [Clostridium perfringens str. 13] dbj BAB81608.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | | |
| 8481, 8482 | 24374626 | 50 | 3.00E-45 | MR-1 | Shewanella oneidensis MR-1 | hypothetical protein SO3107 [Shewanella oneidensis MR-1] gb AAN56113.1 conserved hypothetical protein [Shewanella oneidensis MR-1] | | | | |
| 8483, 8484 | 48864371 | 22 | 3.00E-08 | degradans 2-40 | Microbulbifer | COG0541: Signal recognition particle GTPase [Microbulbifer degradans 2- 40] | | | | |
| 8487, 8488 | 53715793 | 50 | 3.00E-40 | YCH46 | Bacteroides fragilis | FKBP-type peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] dbj BAD51251.1 FKBP-type peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] | | | | 5.2.1.8 |
| 8489, 8490 | 54030565 | 46 | 6.00E-30 | JS666 | Polaromonas sp. | COG2030: Acyl dehydratase [Polaromonas sp. JS666] | | | | |
| 849, 850 | 54030565 | 46 | 6.00E-30 | JS666 | | Desc: Human carbamyl phosphate synthase protein. Org: Homo sapiens | | | | 3.5.2.3 |
| 8493, 8494 | 5739402 | 48 | 3.00E-34 | Johnstoniae | Flavobacterium | TruB [Flavobacterium johnsoniae] sp Q9RB36 TRUB_CYTJO tRNA pseudouridine synthase B (tRNA pseudouridine 55 synthase) (Psi55 synthase) [Pseudouridylyl synthase] (Uracil hydrolyase) | | | | 4.2.1.70 |
| 85, 86 | 48854525 | 67 | 1.00E-102 | hutchinsonii | Cytophaga | COG0143: Methionyl-tRNA synthetase [Cytophaga hutchinsonii] | | | | 6.1.1.10 |
| 8501, 8502 | 34557661 | 50 | 1.00E-34 | 1740 | Wolinella succinogenes DSM | hypothetical protein WS1299 [Wolinella succinogenes DSM 1740] emb CAE10376.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 8507, 8508 | 29348887 | 36 | 9.00E-19 | VPI-5482 | Bacteroides thetaiotaomicron | integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78584.1 integrase [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 8509, 8510 | 29346738 | 36 | 6.00E-17 | VPI-5482 | Bacteroides thetaiotaomicron | hypothetical protein BT1328 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76435.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482] | | | | |

| | | | | | | | | |
|---------------|--------------|----|----------|--|--|---|----|---------------|
| 851, 852 | 42523143 | 39 | 1.00E-19 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bd1641 [Bdellovibrio bacteriovorus HD100] emb CAE79516.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100] | | | |
| 8513, 8514 | AAW9831 1 | 35 | 1.00E-28 | | Desc:H. pylori GHPO 881 protein. Org:Helicobacter pylori | | | |
| 8515, 8516 | 29350071 | 39 | 1.00E-47 | Bacteroides thetaiotaomicron VPI-5482 | two-component system sensor histidine kinase/response [Bacteroides thetaiotaomicron VPI-5482] gb AAO79768.1 two-component system sensor histidine kinase/response [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.3.- |
| 8517, 8518 | 23129857 | 48 | 5.00E-23 | Nostoc punctiforme PCC 73102 | COG3920: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | | | 2.7.3.- |
| 8519, 8520 | 48862078 | 42 | 3.00E-30 | Microbulbifer degradans 2-40 | COG2162: Arylamine N-acetyltransferase [Microbulbifer degradans 2-40] | | | 2.3.1.11 8 |
| 8521, 8522 | 34557352 | 27 | 3.00E-07 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0964 [Wolinella succinogenes DSM 1740] emb CAE10067.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 8523, 8524 | 48854031 | 54 | 4.00E-86 | Cytophaga hutchinsonii | COG0445: NAD/FAD-utilizing enzyme apparently involved in cell division [Cytophaga hutchinsonii] | Desc:Mycoplasma genitalium genome. Org:Mycoplasma genitalium | 86 | 4.00E-11 |
| 8525, 8526 | 39935542 | 32 | 4.00E-32 | Rhodopseudomonas palustris CGA009 | putative diguanylate cyclase (GGDEF) [Rhodopseudomonas palustris CGA009] emb CAE27917.1 putative diguanylate cyclase (GGDEF) [Rhodopseudomonas palustris CGA009] | | | 2.7.3.- |
| 8527, 8528 | 28898100 | 33 | 5.00E-17 | Vibrio parahaemolyticus RIMD 2210633 | hypothetical protein VP1326 [Vibrio parahaemolyticus RIMD 2210633] db BAC59589.1 hypothetical protein [Vibrio parahaemolyticus] | | | |
| 8529, 8530 | 21674737 | 40 | 2.00E-40 | Chlorobium tepidum TLS | transposase [Chlorobium tepidum TLS] ref NP_661348.1 transposase [Chlorobium tepidum TLS] gb AAM73144.1 transposase [Chlorobium tepidum TLS] gb AAM71690.1 transposase [Chlorobium tepidum TLS] | | | |
| 853, 854 | 51892061 | 38 | 4.00E-34 | Symbiobacterium thermophilum IAM 14863 | two-component response regulator [Symbiobacterium thermophilum IAM 14863] db BAD39908.1 two-component response regulator [Symbiobacterium thermophilum IAM 14863] | | | 3.1.1.61 |
| 8531, 8532 | 34557782 | 38 | 4.00E-33 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | 2.7.3.- |
| 8533, 8534 | 42524534 | 43 | 3.00E-29 | Bdellovibrio bacteriovorus HD100 | long-chain fatty-acid-CoA ligase [Bdellovibrio bacteriovorus HD100] emb CAE80907.1 long-chain fatty-acid-CoA ligase [Bdellovibrio bacteriovorus HD100] | | | 6.2.1.3 |

| | | | | | | | | |
|---------------|----------|----|-----------|---|---|--|--|---------|
| 8539, 8540 | 48834107 | 38 | 1.00E-40 | Magnetococcus sp. MC-1 | COG2301: Citrate lyase beta subunit [Magnetococcus sp. MC-1] | | | 4.1.3.6 |
| 8541, 8542 | 48855753 | 51 | 5.00E-73 | Cytophaga hutchinsonii | COG0058: Glucan phosphorylase [Cytophaga hutchinsonii] | | | 2.4.1.1 |
| 8543, 8544 | 45358014 | 35 | 5.00E-11 | Methanococcus maripaludis S2 | hypothetical protein MMP0451 [Methanococcus maripaludis S2] emb CAF30007.1 conserved hypothetical protein [Methanococcus maripaludis S2] | | | |
| 8549, 8550 | 32262172 | 28 | 9.00E-07 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860155.1 hypothetical protein HH0624 [Helicobacter hepaticus ATCC 51449] | | | |
| 855, 856 | 15834252 | 31 | 6.00E-09 | Escherichia coli O157:H7 | putative DNA modification protein [Escherichia coli O157:H7] dbj BAB38421.1 putative DNA modification protein [Escherichia coli O157:H7] pir F91253 probable DNA modification protein [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952) | | | |
| 8551, 8552 | 34557782 | 40 | 6.00E-11 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | |
| 8553, 8554 | 48833745 | 28 | 7.00E-34 | Magnetococcus sp. MC-1 | COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1] | | | |
| 8555, 8556 | 34558488 | 67 | 1.00E-107 | Wolinella succinogenes DSM 1740 | PUTATIVE ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11203.1 PUTATIVE ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes] | | | 1.8.-.- |
| 8557, 8558 | 54310629 | 44 | 6.00E-26 | Photobacterium profundum SS9 | hypothetical protein PBPRA3591 [Photobacterium profundum SS9] emb CAG21847.1 Conserved hypothetical protein [Photobacterium profundum] | | | |
| 8559, 8560 | 57240652 | 55 | 3.00E-53 | Campylobacter lari RM2100 | ABC transporter, ATP-binding protein (H1087) [Campylobacter lari RM2100] gb EAL55045.1 ABC transporter, ATP-binding protein (H1087) [Campylobacter lari RM2100] | | | 1.8.-.- |
| 8561, 8562 | 32262256 | 48 | 4.00E-51 | Helicobacter hepaticus ATCC 51449 | guanylate kinase [Helicobacter hepaticus ATCC 51449] ref NP_860238.1 guanylate kinase [Helicobacter hepaticus ATCC 51449] sp Q7VIA1 KGUA_HELHP Guanylate kinase (GMP kinase) | | | 2.7.4.8 |
| 8563, 8564 | 21328619 | 40 | 1.00E-14 | uncultured proteobacterium | photopigment and puc expression activator, putative [uncultured proteobacterium] | | | |
| 8565, 8566 | 29346910 | 58 | 4.00E-84 | Bacteroides thetaiotaomicron VPI-5482 | Ribonuclease G [Bacteroides thetaiotaomicron VPI-5482] gb AAO76607.1 Ribonuclease G [Bacteroides thetaiotaomicron VPI-5482] | | | 3.1.4.- |
| 8567, 8568 | 53711964 | 38 | 3.00E-30 | Bacteroides fragilis YCH46 | aminopeptidase N [Bacteroides fragilis YCH46] dbj BAD47422.1 aminopeptidase N [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|--|----------|
| 8569, 8570 | 24214122 | 44 | 1.00E-26 | Leptospira Interrogans serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] | | | | |
| 857, 858 | 47565585 | 40 | 2.00E-42 | Bacillus cereus G9241 | beta-lactamase [Bacillus cereus G9241] gb EAL15902.1 beta-lactamase [Bacillus cereus G9241] | | | | 3.5.2.6 |
| 8575, 8576 | 57169066 | 28 | 2.00E-10 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56215.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 8579, 8580 | 50120871 | 32 | 1.00E-41 | Erwinia carotovora subsp. atroseptica SCRI1043 | aconitate hydratase 1 [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG74844.1 aconitate hydratase 1 [Erwinia carotovora subsp. atroseptica SCRI1043] | | | | 4.2.1.3 |
| 8581, 8582 | 34556958 | 25 | 8.00E-10 | Wolonia succinogenes DSM 1740 | HYPOTHETICAL PROTEIN ; WS0538 [Wolonia succinogenes DSM 1740] emb CAE09673.1 HYPOTHETICAL PROTEIN ; WS0538 [Wolonia succinogenes] | | | | |
| 8583, 8584 | 53713067 | 30 | 1.00E-15 | Bacteroides fragilis YCH46 | hypothetical protein BF1778 [Bacteroides fragilis YCH46] db BAD48525.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 8585, 8586 | 57240997 | 37 | 1.00E-17 | Campylobacter lari RM2100 | probable periplasmic protein Cj0943 [Campylobacter lari RM2100] gb EAL54693.1 probable periplasmic protein Cj0943 [Campylobacter lari RM2100] | | | | |
| 8587, 8588 | 29347851 | 36 | 5.00E-29 | Bacteroides thetaiotaomicron VPI-5482 | putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77548.1 putative 5'-nucleotidase/2',3'- cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.1.4.16 |
| 8589, 8590 | 34558210 | 30 | 6.00E-33 | Wolonia succinogenes DSM 1740 | METHYL ACCEPTING CHEMOTAXIS PROTEIN [Wolonia succinogenes DSM 1740] emb CAE10925.1 METHYL ACCEPTING CHEMOTAXIS PROTEIN [Wolonia succinogenes] | | | | 2.7.3.- |
| 8591, 8592 | 51587625 | 36 | 1.00E-26 | Pseudomonas putida | 3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas putida] | | | | 2.5.1.19 |
| 8593, 8594 | 1944167 | 31 | 1.00E-06 | Actinobacillus actinomycetemcom itans | unnamed protein product [Actinobacillus actinomycetemcomitans] | | | | |
| 8595, 8596 | 15607008 | 33 | 6.00E-18 | Aquifex aeolicus VF5 | hypothetical protein aq_2027 [Aquifex aeolicus VF5] gb AAC07788.1 hypothetical protein [Aquifex aeolicus VF5] pir A70474 conserved hypothetical protein aq_2027 - Aquifex aeolicus sp O67821 YK27_AQUAE Hypothetical protein AQ_2027 | | | | |
| 8597, 8598 | 48845271 | 39 | 2.00E-49 | Geobacter metallireducens GS 15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | | 2.7.3.- |

| | | | | | | | | |
|------------|----------|----|----------|---|--|--|--|----------|
| 8601, 8602 | 48763336 | 27 | 1.00E-37 | Rhodospirillum rubrum | COG2905: Predicted signal-transduction protein containing cAMP-binding and CBS domains [Rhodospirillum rubrum] | | | |
| 8603, 8604 | 34557014 | 44 | 3.00E-38 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0597 [Wollinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wollinella succinogenes] | | | |
| 8605, 8606 | 53756218 | 34 | 7.00E-10 | Methylococcus capsulatus str. Bath | killer suppression protein HigA, putative [Methylococcus capsulatus str. Bath] ref YP_112810.1 killer suppression protein HigA, putative [Methylococcus capsulatus str. Bath] | | | |
| 8607, 8608 | 14518367 | 36 | 4.00E-46 | Microscilla sp. PRE1 | hypothetical protein MS162 [Microscilla sp. PRE1] MS162, hypothetical protein [Microscilla sp. PRE1] | | | |
| 8609, 8610 | 57169043 | 54 | 2.00E-66 | Campylobacter coli RM2228 | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Campylobacter coli RM2228] gb EAL56278.1 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Campylobacter coli RM2228] | | | 2.1.1.61 |
| 861, 862 | 56707657 | 53 | 5.00E-29 | Francisella tularensis subsp. tularensis Schu 4 | hypothetical protein FTT0522 [Francisella tularensis subsp. tularensis Schu 4] emb CAG45155.1 conserved hypothetical protein [Francisella tularensis subsp. tularensis] | | | 2.1.1.72 |
| 8611, 8612 | 34558300 | 58 | 4.00E-52 | 3-HYDROXYMYRISTOYL | UDP-3-O-[3-HYDROXYMYRISTOYL] N-ACETYLGLUCOSAMINE DEACETYLASE [Wollinella succinogenes DSM 1740] emb CAE11015.1 UDP-3-O-[3-HYDROXYMYRISTOYL] N-ACETYLGLUCOSAMINE DEACETYLASE [Wollinella succinogenes] | | | 3.5.1.- |
| 8613, 8614 | 57168696 | 49 | 3.00E-19 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56657.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | |
| 8615, 8616 | 34557246 | 66 | 3.00E-36 | Wollinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes] | | | 2.7.3.- |
| 8617, 8618 | 48856320 | 27 | 2.00E-13 | Cytophaga hutchinsonii | COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii] | | | |
| 8619, 8620 | 34558835 | 63 | 3.00E-88 | Alvinella pompejana epibiont 7G3 | hydroxymethylbutenyl pyrophosphate reductase [Alvinella pompejana epibiont 7G3] | | | |
| 8621, 8622 | 48856760 | 44 | 1.00E-25 | Cytophaga hutchinsonii | COG2062: Phosphohistidine phosphatase SixA [Cytophaga hutchinsonii] | | | |
| 8625, 8626 | 34557550 | 36 | 9.00E-21 | Wollinella succinogenes DSM 1740 | hypothetical protein WS1180 [Wollinella succinogenes DSM 1740] emb CAE10265.1 hypothetical protein [Wollinella succinogenes] | | | |
| 8627, 8628 | 23475621 | 34 | 3.00E-15 | Desulfovibrio desulfuricans G20 | COG0071: Molecular chaperone (small heat shock protein) [Desulfovibrio desulfuricans G20] | | | |

| | | | | | | | | | |
|---|--|--|---|---|---|---|----------------|----------------------------------|---------------------|
| 8629, 8630, 863, 864, 8631, 8632, 8635, 8636, 8637, 8638, 8639, 8640, 8643, 8644, 8645, 8646, 8647, 8648 | 15895537 57339644 38348674 34556481 57238619 34557261 29348816 34557656 57241264 | 77 49 37 40 56 47 75 59 25 | 1.00E-120 1.00E-49 8.00E-32 6.00E-58 1.00E-22 3.00E-42 3.00E-91 1.00E-91 6.00E-12 | Clostridium acetobutylicum ATCC 824 synthetic construct Microcystis aeruginosa Wolinella succinogenes DSM 1740 Campylobacter jejuni RM1221 Wolinella succinogenes DSM 1740 Bacteroides thetaiotaomicron VPI-5482 Wolinella succinogenes DSM 1740 Campylobacter lari RM2100 | Aspartyl-tRNA synthetase [Clostridium acetobutylicum ATCC 824] gb AAK80226.1 Aspartyl-tRNA synthetase [Clostridium acetobutylicum ATCC 824] pir G97179 aspartyl-tRNA synthetase [imported] - Clostridium acetobutylicum sp Q97GU6 SYD_CLOAB Aspartyl-tRNA synthetase (Aspartate-tRNA ligase) (AspRS) hypothetical protein FTT0520 [synthetic construct] putative transposase [Microcystis aeruginosa] hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes] ATP/GTP-binding protein [Campylobacter jejuni RM1221] gb AAW36202.1 ATP/GTP-binding protein [Campylobacter jejuni RM1221] GLUCOSE INHIBITED DIVISION PROTEIN B [Wolinella succinogenes DSM 1740] emb CAE09976.1 GLUCOSE INHIBITED DIVISION PROTEIN B [Wolinella succinogenes] sp Q7M8J8 GIDB_WOLSU Methyltransferase gldB (Glucose inhibited division protein B) ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78513.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] CLPY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10371.1 CLPY PROTEIN [Wolinella succinogenes] conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54960.1 conserved hypothetical protein [Campylobacter lari RM2100] | Clostridium tetani E88, section 8 of 10 of the complete genome Ceratium horridum extrachromosomal minicircle putative ABC transporter membrane protein Ycf24 (ycf24) gene, partial cds; and putative ATP- dependent transporter Ycf16 (ycf16) gene, complete cds Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 81 88 84 | 3.00E-61 1.00E-07 2.00E-13 | 6.1.1.12 1.8.-.- |
|---|--|--|---|---|---|---|----------------|----------------------------------|---------------------|

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|---------|
| 8649, 8650 | 34557188 | 46 | 4.00E-79 | Wolnella succinogenes DSM 1740 | TRANSCRIPTIONAL REGULATORY PROTEIN HYPF [Wolnella succinogenes DSM 1740] emb CAE09903.1 TRANSCRIPTIONAL REGULATORY PROTEIN HYPF [Wolnella succinogenes] | | | |
| 8651, 8652 | 37527394 | 62 | 2.00E-50 | Photorhabdus luminescens subsp. laumondii TTO1 | hypothetical protein plu3521 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15894.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] | | | |
| 8653, 8654 | 37527394 | 50 | 8.00E-80 | Photorhabdus luminescens subsp. laumondii TTO1 | hypothetical protein plu3521 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15894.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301665.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301374.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300257.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300170.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298468.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298384.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] | | | |
| 8655, 8656 | 48847450 | 39 | 3.00E-15 | Geobacter metallireducens GS-15 | ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ66097.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65681.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65455.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65413.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_905778.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_905198.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904782.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904556.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904514.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAD38020.1 transposase [Porphyromonas gingivalis] hypothetical protein lin2473 [Listeria innocua Clip11262] emb CAC97700.1 lin2473 [Listeria innocua] pir AD1741 aspartate kinase homolog lin2473 [imported] - Listeria innocua (strain Clip11262) | | | |
| 8657, 8658 | 34397615 | 30 | 8.00E-20 | Porphyromonas gingivalis W83 | TWO-COMPONENT REGULATOR [Wolnella succinogenes DSM 1740] emb CAE09457.1 TWO-COMPONENT REGULATOR [Wolnella succinogenes] | | | 2.7.2.4 |
| 8659, 8660 | 16801535 | 35 | 3.00E-22 | Listeria innocua Clip11262 | | | | |
| 8661, 8662 | 34556742 | 36 | 6.00E-16 | Wolnella succinogenes DSM 1740 | | | | |

| | | | | | | | | | |
|---------------|----------------|----|-----------|---|--|--|--|--|----------|
| 8663, 8664 | AAB9666 2 | 41 | 3.00E-25 | | | Desc: Putative high-affinity branched amino acid transport system ATPase #7. Org: Pyrococcus abyssi | | | 1.8.-.- |
| 8665, 8666 | 32262912 55 | | 1.00E-44 | Helicobacter hepaticus ATCC 51449 | | lipopolysaccharide core biosynthesis protein [Helicobacter hepaticus ATCC 51449] ref NP_860892.1 lipopolysaccharide core biosynthesis protein [Helicobacter hepaticus ATCC 51449] | | | 2.7.7.3 |
| 8667, 8668 | 15643586 22 | | 1.00E-09 | Thermotoga maritima MSB8 | | transcriptional regulator, TetR family [Thermotoga maritima MSB8] gb AAD35905.1 transcriptional regulator, TetR family [Thermotoga maritima MSB8] pir B72330 transcription regulator, TetR family - Thermotoga maritima (strain MSB8) | | | |
| 8669, 8670 | 34557966 56 | | 1.00E-63 | Wollinella succinogenes DSM 1740 | | ATP-DEPENDENT HELICASE [Wollinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wollinella succinogenes] | | | 3.6.1.- |
| 8673, 8674 | 29349715 57 | | 5.00E-72 | Bacteroides thetaiotaomicron VPI-5482 | | putative glycogen synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79412.1 putative glycogen synthase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.4.1.21 |
| 8675, 8676 | 39995299 52 | | 1.00E-86 | Geobacter sulfurreducens PCA | | ATP-dependent RNA helicase DbpA [Geobacter sulfurreducens PCA] gb AAR33523.1 ATP-dependent RNA helicase DbpA [Geobacter sulfurreducens PCA] | | | 2.7.7.- |
| 8677, 8678 | 50083983 24 | | 6.00E-10 | Acinetobacter sp. ADP1 | | hypothetical protein; putative membrane protein [Acinetobacter sp. ADP1] emb CAG67671.1 hypothetical protein; putative membrane protein [Acinetobacter sp. ADP1] | | | |
| 8679, 8680 | 29348209 46 | | 8.00E-60 | Bacteroides thetaiotaomicron VPI-5482 | | putative amidophosphoribosyl-transferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77906.1 putative amidophosphoribosyl-transferase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 8681, 8682 | 45656836 46 | | 3.00E-62 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | | ABC transporter, ATP-binding protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69559.1 ABC transporter, ATP-binding protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | 1.8.-.- |
| 8685, 8686 | 34557269 60 | | 1.00E-107 | Wollinella succinogenes DSM 1740 | | ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes] | | | 3.6.1.- |
| 8687, 8688 | 57241387 27 | | 1.00E-12 | Campylobacter lari RM2100 | | probable membrane protein Cj0152c [Campylobacter lari RM2100] gb EAL54499.1 probable membrane protein Cj0152c [Campylobacter lari RM2100] | | | |
| 8689, 8690 | 53715862 56 | | 1.00E-75 | Bacteroides fragilis YCH46 | | DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] db BAD51320.1 DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|--|---|----|-------------------|
| 8691, 8692 | 34556651 | 27 | 5.00E-17 | Wollinella succinogenes DSM 1740 | hypothetical protein WS0208 [Wollinella succinogenes DSM 1740] emb CAE09386.1 hypothetical protein [Wollinella succinogenes] | | | |
| 8693, 8694 | 6967725 | 24 | 6.00E-08 | Campylobacter jejuni subsp. jejuni NCTC 11168 | hypothetical protein Cj0248 [Campylobacter jejuni subsp. jejuni NCTC 11168] pir G81442 hypothetical protein Cj0248 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281442.1 hypothetical protein Cj0248 [Campylobacter jejuni subsp. jejuni NCTC 11168] | | | |
| 8695, 8696 | 48855460 | 25 | 9.00E-22 | Cytophaga hutchinsonii | hypothetical protein Chui02001797 [Cytophaga hutchinsonii] | | | |
| 8699, 8700 | 54023411 | 27 | 5.00E-09 | Nocardia farcinica IFM 10152 | hypothetical protein nfa14440 [Nocardia farcinica IFM 10152] dbj BAD56289.1 hypothetical protein [Nocardia farcinica IFM 10152] | | | |
| 87, 88 | 50907355 | 32 | 7.00E-16 | Oryza sativa (japonica cultivar- group) | putative guanylate binding protein [Oryza sativa (japonica cultivar-group)] dbj BAD23587.1 putative guanylate binding protein [Oryza sativa (japonica cultivar-group)] | | | |
| 8701, 8702 | 48845445 | 43 | 1.00E-28 | Geobacter metallireducens GS 15 | COG3437: Response regulator containing a CheY-like receiver domain and an HD-GYP domain [Geobacter metallireducens GS-15] | | | 2.7.3.- |
| 8703, 8704 | 42528087 | 28 | 6.00E-12 | Treponema denticola ATCC 35405 | endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405] gb AAS13104.1 endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405] | | | |
| 8707, 8708 | 21231126 | 37 | 3.00E-31 | Xanthomonas campestris pv. campestris str. ATCC 33913 | glycosyl transferase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM40967.1 glycosyl transferase [Xanthomonas campestris pv. campestris str. ATCC 33913] | | | 2.4.1.- |
| 8709, 8710 | 21673717 | 39 | 7.00E-25 | Chlorobium tepidum TLS | phosphoglycolate phosphatase [Chlorobium tepidum TLS] gb AAM72124.1 phosphoglycolate phosphatase [Chlorobium tepidum TLS] | | | 3.1.3.18 |
| 871, 872 | 53712247 | 50 | 2.00E-68 | Bacteroides fragilis YCH46 | putative oxidoreductase [Bacteroides fragilis YCH46] dbj BAD47705.1 putative oxidoreductase [Bacteroides fragilis YCH46] | | | |
| 8711, 8712 | 2314022 | 60 | 6.00E-85 | Helicobacter pylori 26695 | cysteinyI-tRNA synthetase (cysS) [Helicobacter pylori 26695] pir F64630 cysteine-tRNA ligase (EC 6.1.1.16) - Helicobacter pylori (strain 26695) ref NP_207679.1 cysteinyI-tRNA synthetase (cysS) [Helicobacter pylori 26695] sp P41259 SYC_HELPY CysteinyI-tRNA synthetase (Cysteine-tRNA ligase) (CysRS) | Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 8 of 197 of the complete genome | 91 | 6.00E-10 6.1.1.16 |
| 8713, 8714 | 54302166 | 30 | 7.00E-36 | Photobacterium profundum SS9 | hypothetical protein PBPRB0486 [Photobacterium profundum SS9] emb CAG22339.1 hypothetical protein [Photobacterium profundum] | | | 2.7.3.- |
| 8715, 8716 | 48853522 | 42 | 2.00E-35 | Cytophaga hutchinsonii | COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii] | | | 3.1.- |

| | | | | | | | | | |
|---------------|----------|----|-----------|--|--|---|----|----------|---------------|
| 8717, 8718 | 34556461 | 68 | 1.00E-107 | Wolinella succinogenes DSM 1740 | DNA GYRASE SUBUNIT B [Wolinella succinogenes DSM 1740] emb CAE09176.1 DNA GYRASE SUBUNIT B [Wolinella succinogenes] | Helicobacter hepaticus ATCC 51449 section 4 of 6 of the complete genome | 82 | 1.00E-17 | 5.99.1.3 |
| 8719, 8720 | 56461066 | 31 | 5.00E-23 | Idiomarina lithiensis L2TR | tRNA nucleotidyltransferase [Idiomarina lithiensis L2TR] gb AAV82798.1 tRNA nucleotidyltransferase [Idiomarina lithiensis L2TR] | | | | 2.7.7.19 |
| 8725, 8726 | 37912882 | 39 | 4.00E-32 | uncultured marine proteobacterium ANT32C12 | predicted methylase [uncultured marine proteobacterium ANT32C12] | | | | |
| 8727, 8728 | 5578860 | 45 | 1.00E-56 | Streptomyces coelicolor A3(2) | putative endo alpha-1,4 polygalactosaminidase [Streptomyces coelicolor A3(2)] pir T35294 probable endo alpha-1,4 polygalactosaminidase - Streptomyces coelicolor ref NP_626431.1 putative endo alpha-1,4 polygalactosaminidase [Streptomyces coelicolor A3(2)] | | | | |
| 8729, 8730 | 48858604 | 31 | 2.00E-18 | Clostridium thermocellum ATCC 27405 | COG3580: Uncharacterized protein conserved in bacteria [Clostridium thermocellum ATCC 27405] hypothetical protein BSJ40760 [Bacillus subtilis subsp. subtilis str. 168] emb CAB16113.1 yyaP [Bacillus subtilis subsp. subtilis str. 168] pir S66001 conserved hypothetical protein yyaP - Bacillus subtilis sp P37508 YYAP_BACSU Hypothetical protein yyaP db BAA05207.1 unknown [Bacillus subtilis] | | | | 3.4.24.- |
| 8731, 8732 | 16081128 | 38 | 5.00E-31 | Chloroflexus aurantiacus | COG0407: Uroporphyrinogen-III decarboxylase [Chloroflexus aurantiacus] | | | | 4.1.1.37 |
| 8733, 8734 | 34397745 | 33 | 1.00E-15 | Porphyromonas gingivalis W83 | guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [Porphyromonas gingivalis W83] ref NP_905907.1 guanosine-3',5'-bis(diphosphate) 3'- pyrophosphohydrolase [Porphyromonas gingivalis W83] hypothetical protein CPE1684 [Clostridium perfringens str. 13] db BAB81390.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | | 2.7.6.5 |
| 8735, 8736 | 18310666 | 34 | 3.00E-17 | Clostridium perfringens str. 13 | | | | | |
| 8737, 8738 | 34556647 | 40 | 1.00E-38 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0204 [Wolinella succinogenes DSM 1740] emb CAE09362.1 hypothetical protein [Wolinella succinogenes] conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_112612.1 hypothetical protein MCA0072 [Methylococcus capsulatus str. Bath] | | | | 2.7.1.13 0 |
| 8739, 8740 | 53756478 | 40 | 5.00E-22 | Methylococcus capsulatus str. Bath | | | | | |

| | | | | | | | | |
|---------------|--------------|----|----------|--|--|--|--|-------------|
| 8741, 8742 | 39996430 | 63 | 5.00E-32 | Geobacter sulfurreducens PCA | hypothetical protein GSU1328 [Geobacter sulfurreducens PCA] gb AAR34704.1 conserved hypothetical protein [Geobacter sulfurreducens PCA] | | | |
| 8745, 8746 | AAW2084 6 | 27 | 6.00E-11 | | Desc:H. pylori secreted or periplasmic protein, 12ae11404orf3. Org:Helicobacter pylori | | | |
| 8747, 8748 | 34557578 | 43 | 4.00E-63 | Wolinella succinogenes DSM 1740 | CIAB PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10293.1 CIAB PROTEIN [Wolinella succinogenes] | | | |
| 8749, 8750 | 45656989 | 50 | 2.00E-68 | Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130 | methylmalonyl-CoA mutase [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] gb AAS69712.1 methylmalonyl-CoA mutase [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] | | | |
| 875, 876 | 46324266 | 34 | 4.00E-18 | Burkholderia cepacia R1808 | hypothetical protein Bucepa03000401 [Burkholderia cepacia R1808] | | | |
| 8753, 8754 | 34557543 | 33 | 7.00E-43 | Wolinella succinogenes DSM 1740 | PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10258.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] emb CAD55552.1 NapL protein [Wolinella succinogenes] | | | |
| 8755, 8756 | 53714728 | 70 | 4.00E-47 | Bacteroides fragilis YCH46 | dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] dbj BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] | | | 2.4.1.83 |
| 8757, 8758 | 53731539 | 53 | 8.00E-40 | Methanococcus burtonii DSM 6242 | hypothetical protein Mbur03001017 [Methanococcus burtonii DSM 6242] | | | |
| 8759, 8760 | 53730423 | 39 | 2.00E-22 | Dechloromonas aromatica RCB | COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB] | | | 2.7.3.- |
| 8761, 8762 | 48846020 | 27 | 1.00E-09 | Geobacter metallireducens GS-15 | COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15] | | | |
| 8763, 8764 | 42528141 | 49 | 3.00E-77 | Treponema denticola ATCC 35405 | Fic family protein [Treponema denticola ATCC 35405] gb AAS13158.1 Fic family protein [Treponema denticola ATCC 35405] | | | |
| 8765, 8766 | 34556616 | 35 | 7.00E-38 | Wolinella succinogenes DSM 1740 | CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes] | | | 90 2.00E-10 |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|--|----------|
| 8767, 8768 | 57238514 | 43 | 3.00E-20 | Campylobacter jejuni RM1221 | DNA-binding response regulator [Campylobacter jejuni RM1221] gbIAAW36097.1] DNA-binding response regulator [Campylobacter jejuni RM1221] | | | | 2.7.-.- |
| 877, 878 | 2352096 | 45 | 4.00E-15 | Fervidobacterium islandicum | orf, similar to serine/threonine protein phosphatase [Fervidobacterium islandicum] | | | | 3.1.3.16 |
| 8771, 8772 | 32261568 | 32 | 4.00E-17 | Helicobacter hepaticus ATCC 51449 | two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] | | | | 2.7.3.- |
| 8775, 8776 | 39995927 | 44 | 6.00E-25 | Geobacter sulfurreducens PCA | hypothetical protein GSU0821 [Geobacter sulfurreducens PCA] gbIAAR34151.1] conserved hypothetical protein [Geobacter sulfurreducens PCA] | | | | |
| 8777, 8778 | 48854259 | 46 | 3.00E-65 | Cytophaga hutchinsonii | COG3550: Uncharacterized protein related to capsule biosynthesis enzymes [Cytophaga hutchinsonii] | | | | |
| 8779, 8780 | 32477010 | 60 | 6.00E-51 | Rhodopirellula baltica SH 1 | hypothetical protein RB11494 [Rhodopirellula baltica SH 1] emb CAD79157.1] conserved hypothetical protein [Pirellula sp.] | | | | |
| 8781, 8782 | 46140776 | 36 | 2.00E-36 | Dechloromonas aromatica RCB | COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Dechloromonas aromatica RCB] | | | | 1.-.- |
| 8785, 8786 | 34397071 | 29 | 5.00E-19 | Porphyromonas gingivalis W83 | TPR domain protein [Porphyromonas gingivalis W83] ref NP_905236.1 TPR domain protein [Porphyromonas gingivalis W83] | | | | |
| 8787, 8788 | 57240778 | 53 | 2.00E-73 | Campylobacter lari RM2100 | 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Campylobacter lari RM2100] gb EAL55171.1 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Campylobacter lari RM2100] | | | | 2.7.7.60 |
| 8789, 8790 | 57241023 | 42 | 5.00E-17 | Campylobacter lari RM2100 | conserved hypothetical protein TIGR00278, putative [Campylobacter lari RM2100] gb EAL54719.1] conserved hypothetical protein TIGR00278, putative [Campylobacter lari RM2100] | | | | |
| 879, 880 | 29349252 | 54 | 2.00E-86 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO78949.1] ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] | | | | 3.6.1.- |
| 8791, 8792 | 6967683 | 48 | 3.00E-25 | Campylobacter jejuni subsp. jejuni NCTC 11168 | hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281400.1 hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81437 hypothetical protein Cj0190c [Imported] - Campylobacter jejuni (strain NCTC 11168) | | | | |
| 8793, 8794 | 34558255 | 28 | 1.00E-21 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1967 [Wolinella succinogenes DSM 1740] emb CAE10970.1] hypothetical protein [Wolinella succinogenes] conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 8797, 8798 | 57240790 | 38 | 2.00E-14 | Campylobacter lari RM2100 | gb EAL55183.1] conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 8799, 8800 | 51573391 | 19 | 9.00E-11 | Borrelia garinii PBI | hypothetical protein BG0579 [Borrelia garinii PBI] ref YP_073008.1 hypothetical protein BG0579 [Borrelia garinii PBI] | | | | |

| | | | | | | | | |
|------------|----------|----|-----------|--|---|--|--|----------|
| 8801, 8802 | 48478360 | 30 | 1.00E-11 | <i>Picrophilus torridus</i> DSM 9790 | thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790] gb AAAT43873.1 thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790] | | | 2.5.1.3 |
| 8803, 8804 | 34397900 | 28 | 1.00E-09 | <i>Porphyromonas gingivalis</i> W83 | hypothetical protein PG1988 [Porphyromonas gingivalis W83] ref NP_906062.1 hypothetical protein PG1988 [Porphyromonas gingivalis W83] | | | |
| 8805, 8806 | 57238621 | 38 | 2.00E-22 | <i>Campylobacter jejuni</i> RM1221 | DNA-binding response regulator, putative [Campylobacter jejuni RM1221] gb AAW36204.1 DNA-binding response regulator, putative [Campylobacter jejuni RM1221] | | | |
| 8807, 8808 | 15612433 | 51 | 2.00E-44 | <i>Helicobacter pylori</i> J99 | LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN [Helicobacter pylori J99] gb AAD06957.1 LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN [Helicobacter pylori J99] sp Q9ZJE4 COAD_HELPJ Phosphopantetheine adenylyltransferase (Pantetheine-phosphate adenylyltransferase) (PPAT) (Dephospho-CoA pyrophosphorylase) pir C71814 lipopolysaccharide core biosynthesis protein - Helicobacter pylori (strain J99) | | | 2.7.7.3 |
| 8809, 8810 | 34557029 | 53 | 3.00E-44 | <i>Wollinella succinogenes</i> DSM 1740 | INTEGRAL MEMBRANE PROTEIN WITH KINASE ACTIVITY [Wollinella succinogenes DSM 1740] emb CAE09744.1 INTEGRAL MEMBRANE PROTEIN WITH KINASE ACTIVITY [Wollinella succinogenes] | | | 2.7.4.9 |
| 881, 882 | 29349478 | 35 | 4.00E-22 | <i>Bacteroides thetaiotaomicron</i> VPI-5482 | RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79175.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 8811, 8812 | 34557014 | 37 | 5.00E-47 | <i>Wollinella succinogenes</i> DSM 1740 | hypothetical protein WS0597 [Wollinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wollinella succinogenes] | | | |
| 8813, 8814 | 34396203 | 43 | 6.00E-48 | <i>Porphyromonas gingivalis</i> W83 | L-threonine-O-3-phosphate decarboxylase, putative [Porphyromonas gingivalis W83] ref NP_904371.1 L-threonine-O-3-phosphate decarboxylase, putative [Porphyromonas gingivalis W83] | | | 2.6.1.9 |
| 8815, 8816 | 48854595 | 30 | 5.00E-10 | <i>Cytophaga hutchinsonii</i> | hypothetical protein Chut02002797 [Cytophaga hutchinsonii] | | | |
| 8817, 8818 | 57168226 | 31 | 6.00E-23 | <i>Campylobacter coli</i> RM2228 | CMP-N-acetylneuraminic acid synthetase (neuA) [Campylobacter coli RM2228] gb EAL57269.1 CMP-N-acetylneuraminic acid synthetase (neuA) [Campylobacter coli RM2228] emb CAE73738.1 acylneuraminat cytidyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282457.1 acylneuraminat cytidyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir D81274 N-acetylneuraminat cytidyltransferase (EC 2.7.7.43) C 1311 [imported] - Campylobacter jejuni (strain NCTC 11168) | | | 2.7.7.43 |
| 8819, 8820 | 29346635 | 60 | 1.00E-100 | <i>Bacteroides thetaiotaomicron</i> VPI-5482 | GDP-fucose synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76332.1 GDP-fucose synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | 5.1.3.- |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|--|----------|
| 8821, 8822 | 29347648 | 42 | 9.00E-49 | Bacteroides thetaiotaomicron VPI-5482 | putative biotin-(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77345.1 putative biotin-(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | | 6.3.4.15 |
| 8823, 8824 | 34556663 | 44 | 2.00E-26 | Wolinella succinogenes DSM 1740 | ANTHRANILATE ISOMERASE [Wolinella succinogenes DSM 1740] emb CAE09378.1 ANTHRANILATE ISOMERASE [Wolinella succinogenes] DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | | 5.3.1.24 |
| 8825, 8826 | 34557407 | 38 | 1.00E-41 | Wolinella succinogenes DSM 1740 | | | | | 2.7.3.- |
| 8827, 8828 | 34557411 | 22 | 2.00E-18 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1025 [Wolinella succinogenes DSM 1740] emb CAE10126.1 hypothetical protein [Wolinella succinogenes] integrase-recombinase protein [Methanothermobacter thermoautotrophicus str. Delta H] gb AAB85391.1 integrase-recombinase protein [Methanothermobacter thermoautotrophicus str. Delta H] pir D69219 integrase-recombinase protein - Methanobacterium thermoautotrophicum (strain Delta H) | | | | |
| 8831, 8832 | 15678913 | 41 | 2.00E-36 | Methanothermobac ter thermoautotrophicus str. Delta H | | | | | |
| 8833, 8834 | 23121135 | 36 | 1.00E-32 | Desulfitobacterium hafniense DCB-2 | COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Desulfitobacterium hafniense DCB-2] HD-GYP domain containing protein [Clostridium acetobutylicum ATCC 824] gb AAK81572.1 HD-GYP domain containing protein [Clostridium acetobutylicum ATCC 824] pir A97348 HD-GYP domain containing protein [imported] - Clostridium acetobutylicum COG3401: Fibronectin type 3 domain-containing protein [Cytophaga hutchinsonii] | | | | |
| 8835, 8836 | 15896883 | 31 | 1.00E-19 | Clostridium acetobutylicum ATCC 824 | | | | | |
| 8837, 8838 | 48853982 | 25 | 2.00E-13 | Cytophaga hutchinsonii | | | | | |
| 8839, 8840 | 39997114 | 51 | 1.00E-50 | Geobacter sulfurreducens PCA | sensory box/GGDEF family protein [Geobacter sulfurreducens PCA] gb AAR35392.1 sensory box/GGDEF family protein [Geobacter sulfurreducens PCA] | | | | 2.7.3.- |
| 8841, 8842 | 34557317 | 28 | 5.00E-12 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0928 [Wolinella succinogenes DSM 1740] emb CAE10032.1 hypothetical protein [Wolinella succinogenes] aspartate kinase [Streptococcus thermophilus CNRZ1066] gb AAV61981.1 aspartate kinase [Streptococcus thermophilus CNRZ1066] | | | | |
| 8843, 8844 | 55822355 | 34 | 4.00E-39 | Streptococcus thermophilus CNRZ1066 | | | | | 2.7.2.4 |
| 8845, 8846 | 24217207 | 50 | 2.00E-40 | Leptospira interrogans serovar Lai str. 56601 | hypothetical protein LB146 [Leptospira interrogans serovar Lai str. 56601] gb AAN51705.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|----------------------|
| 8847, 8848 | 57242267 | 37 | 3.00E-29 | Campylobacter upsaliensis RM3195 | MutS2 family protein , putative [Campylobacter upsaliensis RM3195] gb EAL53729.1 MutS2 family protein , putative [Campylobacter upsaliensis RM3195] | | | |
| 8849, 8850 | 34557846 | 41 | 2.00E-19 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1513 [Wolinella succinogenes DSM 1740] emb CAE10561.1 conserved hypothetical protein [Wolinella succinogenes] cytochrome c biogenesis protein (ycf5) [Campylobacter lari RM2100] gb EAL55842.1 cytochrome c biogenesis protein (ycf5) [Campylobacter lari RM2100] | | | |
| 8851, 8852 | 57240528 | 32 | 6.00E-36 | Campylobacter lari RM2100 | hypothetical protein GSU2532 [Geobacter sulfurreducens PCA] gb AAR35905.1 conserved hypothetical protein [Geobacter sulfurreducens PCA] | | | |
| 8853, 8854 | 39997627 | 25 | 2.00E-08 | Geobacter sulfurreducens PCA | | | | 2.7.3.- |
| 8855, 8856 | 23126560 | 47 | 1.00E-25 | Nostoc punctiforme PCC 73102 | COG3437: Response regulator containing a CheY-like receiver domain and an HD-GYP domain [Nostoc punctiforme PCC 73102] ATP sulfurylase GTP-binding subunit/APS kinase [Pseudomonas aeruginosa PAO1] ref ZP_00137930.2 COG2895: GTPases - Sulfate adenylylate transferase subunit 1 [Pseudomonas aeruginosa UCBPP-PA14] gb AAC46387.1 ATP sulfurylase GTP-binding subunit/APS kinase [Pseudomonas aeruginosa] pir D83091 ATP sulfurylase GTP-binding subunit/APS kinase PA4442 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253132.1 ATP sulfurylase GTP-binding subunit/APS kinase [Pseudomonas aeruginosa PAO1] sp O50274 CYSN_PSEAE CysN/cysC bifunctional enzyme [includes: Sulfate adenylyltransferase subunit 1 (Sulfate adenylylate transferase) (SAT) (ATP-sulfurylase large subunit); Adenylyl- sulfate kinase (APS kinase) (ATP adenosine-5'-phosphosulfate 3'- phosphotransferase)] | | | |
| 8857, 8858 | 9950676 | 60 | 2.00E-21 | Pseudomonas aeruginosa PAO1 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860475.1 hypothetical protein HH0944 [Helicobacter hepaticus ATCC 51449] | | | 2.7.7.4 |
| 8861, 8862 | 32262494 | 67 | 1.00E-51 | Helicobacter hepaticus ATCC 51449 | | | | 3.4.13.9 |
| 8863, 8864 | 33861261 | 31 | 3.00E-14 | Prochlorococcus marinus subsp. pastoris str. CCMP1986 | putative potassium channel, VIC family [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19163.1 putative potassium channel, VIC family [Prochlorococcus marinus subsp. pastoris str. CCMP1986] | | | |
| 8867, 8868 | 23129547 | 36 | 3.00E-43 | Nostoc punctiforme PCC 73102 | COG0732: Restriction endonuclease S subunits [Nostoc punctiforme PCC 73102] | | | |
| 887, 888 | 48854835 | 77 | 3.00E-48 | Cytophaga hutchinsonii | COG0302: GTP cyclohydrolase I [Cytophaga hutchinsonii] | | | 3.1.21.3 3.5.4.16 |

| | | | | | | | | | |
|---------------|----------|----|----------|--------------------------------------|---|--|----|----------|----------|
| 8871, 8872 | 34557247 | 63 | 4.00E-62 | Wolnella succinogenes DSM 1740 | TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolnella succinogenes DSM 1740] emb CAE0962.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolnella succinogenes] | Wolnella succinogenes, complete genome; segment 3/7 | 85 | 2.00E-07 | 2.7.3.- |
| 8873, 8874 | 57238223 | 62 | 3.00E-56 | Campylobacter jejuni RM1221 | (d)Nucleoside polyphosphate hydrolase [Campylobacter jejuni RM1221] gb AAW35806.1 (d)Nucleoside polyphosphate hydrolase [Campylobacter jejuni RM1221] oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter jejuni RM1221] gb AAW35807.1 oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter jejuni RM1221] emb CAB75216.1 putative oxidoreductase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281763.1 putative oxidoreductase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81405 probable oxidoreductase Cj0580c [imported] - Campylobacter jejuni (strain NCTC 11168) | | | | 3.6.1.- |
| 8875, 8876 | 57238224 | 45 | 2.00E-33 | Campylobacter jejuni RM1221 | DNA polymerase III, beta subunit [Geobacter sulfurreducens PCA] gb AAR33336.1 DNA polymerase III, beta subunit [Geobacter sulfurreducens PCA] COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Psychrobacter sp. 273-4] ABC transporter (ATP-binding protein) [Bacillus halodurans C-125] db BAB07224.1 ABC transporter (ATP-binding protein) [Bacillus halodurans C-125] pir J84088 ABC transporter (ATP-binding protein) BH3505 [imported] - Bacillus halodurans (strain C-125) hypothetical protein MA0188 [Methanosarcina acetivorans C2A] gb AAM0364.1 hypothetical protein (multi-domain) [Methanosarcina acetivorans str. C2A] aminotransferase cobD [Clostridium tetani E88] gb AAO35324.1 aminotransferase cobD [Clostridium tetani E88] | | | | 1.-.-.- |
| 8879, 8880 | 39995112 | 46 | 6.00E-33 | Geobacter sulfurreducens PCA | | | | | 2.7.7.7 |
| 8881, 8882 | 46141215 | 70 | 3.00E-94 | Psychrobacter sp. 273-4 | | | | | 3.1.21.3 |
| 8885, 8886 | 15616067 | 44 | 1.00E-24 | Bacillus halodurans C-125 | | | | | 1.8.-.- |
| 8887, 8888 | 20089086 | 44 | 4.00E-10 | Methanosarcina acetivorans C2A | | | | | |
| 8889, 8890 | 28210443 | 33 | 2.00E-32 | Clostridium tetani E88 | | | | | 2.6.1.9 |
| 889, 890 | 48854835 | 76 | 2.00E-63 | Cytophaga hutchinsonii | | | | | 3.5.4.16 |
| 8891, 8892 | 42528086 | 38 | 4.00E-30 | Treponema denticola ATCC 35405 | | | | | 2.7.7.7 |
| 8893, 8894 | 27366536 | 31 | 2.00E-33 | Vibrio vulnificus CMCP6 | | | | | 2.7.3.- |
| 8895, 8896 | 27367375 | 49 | 8.00E-60 | Vibrio vulnificus CMCP6 | | | | | 2.7.3.- |
| 8897, 8898 | 54024734 | 39 | 8.00E-37 | Nocardia farcinica IFM 10152 | | | | | 3.1.21.3 |

| | | | | | | |
|------------|----------|----|----------|-------------------------------------|---|----------|
| 89, 90 | 15614312 | 44 | 2.00E-29 | Bacillus halodurans C-125 | DNA-3-methyladenine glycosidase [Bacillus halodurans C-125] dbj BAB05468.1 DNA-3-methyladenine glycosidase [Bacillus halodurans C-125] pir E83868 DNA-3-methyladenine glycosidase BH1749 [imported] - Bacillus halodurans [strain C-125] | 3.2.2.21 |
| 8901, 8902 | 34558460 | 55 | 4.00E-84 | Wolinella succinogenes DSM 1740 | hypothetical protein WS2184 [Wolinella succinogenes DSM 1740] emb CAE11175.1 CONSERVED HYPOTHETICAL PROTEIN [Wolinella succinogenes] | |
| 8903, 8904 | 39936981 | 52 | 1.00E-68 | Rhodopseudomonas palustris CGA009 | possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] emb CAE29361.1 possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] | 2.7.- |
| 8905, 8906 | 34558655 | 34 | 6.00E-44 | Wolinella succinogenes DSM 1740 | HYBRID SENSORY HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09370.1 HYBRID SENSORY HISTIDINE KINASE [Wolinella succinogenes] | 2.7.3.- |
| 8907, 8908 | 48856125 | 54 | 1.00E-43 | Cytophaga hutchinsonii | COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] | |
| 891, 892 | 48733625 | 46 | 1.00E-60 | Pseudomonas fluorescens PfO-1 | COG3173: Predicted aminoglycoside phosphotransferase [Pseudomonas fluorescens PfO-1] | |
| 8911, 8912 | 42524534 | 48 | 1.00E-54 | Bdellovibrio bacteriovorus HD100 | long-chain fatty-acid-CoA ligase [Bdellovibrio bacteriovorus HD100] emb CAE0907.1 long-chain fatty-acid-CoA ligase [Bdellovibrio bacteriovorus HD100] | 6.2.1.3 |
| 8915, 8916 | 31324519 | 43 | 6.00E-19 | Campylobacter coli | PtmF [Campylobacter coli] | |
| 8917, 8918 | 48860157 | 31 | 3.00E-07 | Clostridium thermocellum ATCC 27405 | COG2896: Molybdenum cofactor biosynthesis enzyme [Clostridium thermocellum ATCC 27405] | |
| 8919, 8920 | 32263209 | 36 | 1.00E-41 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861188.1 hypothetical protein HH1657 [Helicobacter hepaticus ATCC 51449] | 2.7.3.- |
| 8923, 8924 | 34558149 | 31 | 2.00E-26 | Wolinella succinogenes DSM 1740 | SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes DSM 1740] emb CAE10864.1 SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes] | |
| 8925, 8926 | 34557202 | 65 | 8.00E-70 | Wolinella succinogenes DSM 1740 | ATP PHOSPHORIBOSYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09917.1 ATP PHOSPHORIBOSYLTRANSFERASE [Wolinella succinogenes] sp Q7M9N0 HIS1_WOLSU ATP phosphoribosyltransferase [ATP-PRase] (ATP-PR) | 2.4.2.17 |
| 8927, 8928 | 15605806 | 48 | 2.00E-29 | Aquifex aeolicus VF5 | hypothetical protein aq_265 [Aquifex aeolicus VF5] gb AAC06589.1 hypothetical protein [Aquifex aeolicus VF5] pir C70324 conserved hypothetical protein aq_265 - Aquifex aeolicus | 2.7.3.- |

| | | | | | | | | | | |
|---------------|----------|----|----------|--|--|--|----------|---------|----------|--|
| 8929, 8930 | 57505466 | 50 | 1.00E-39 | Campylobacter upsaliensis RM3195 | aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195] gb EAL53077.1] aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195] | | | | 3.4.13.3 | |
| 8931, 8932 | 37222114 | 33 | 2.00E-29 | uncultured bacterium | Uvs065 [uncultured bacterium] | | | | | |
| 8933, 8934 | 40062476 | 36 | 8.00E-52 | uncultured bacterium 105 | hypothetical protein EBAC750-01A01.2 [uncultured bacterium 105] | | | | 2.7.9.2 | |
| 8935, 8936 | 28210272 | 40 | 2.00E-19 | Clostridium tetani E88 | hypothetical protein CTC00532 [Clostridium tetani E88] gb AAO35153.1] conserved protein [Clostridium tetani E88] | | | | | |
| 8937, 8938 | 57169018 | 75 | 4.00E-19 | Campylobacter coli RM2228 | Thymidylate synthase complementing protein superfamily [Campylobacter coli RM2228] gb EAL56253.1] Thymidylate synthase complementing protein superfamily [Campylobacter coli RM2228] | | | | | |
| 8939, 8940 | 16331975 | 55 | 1.00E-75 | Synechocystis sp. PCC 6803 | pyruvate oxidoreductase [Synechocystis sp. PCC 6803] dbj BAA10774.1] pyruvate oxidoreductase [Synechocystis sp. PCC 6803] pir S77082 pyruvate (flavodoxin) dehydrogenase (EC 1.2.99.-) nifJ - Synechocystis sp. (strain PCC 6803) sp P52965 NIFJ_SYNY3 Putative pyruvate-flavodoxin oxidoreductase | | | 1.2.7.1 | | |
| 8941, 8942 | 46135305 | 39 | 3.00E-24 | Anabaena variabilis ATCC 29413 | COG0395: ABC-type sugar transport system, permease component [Anabaena variabilis ATCC 29413] | | | | | |
| 8945, 8946 | 46142567 | 44 | 1.00E-26 | Methanococcoides burtonii DSM 6242 | COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242] | | | | 2.1.1.73 | |
| 8947, 8948 | 34558177 | 23 | 2.00E-11 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1882 [Wolinella succinogenes DSM 1740] emb CAE10892.1] hypothetical protein [Wolinella succinogenes] | | | | | |
| 8949, 8950 | 34557666 | 25 | 4.00E-11 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1305 [Wolinella succinogenes DSM 1740] emb CAE10381.1] hypothetical protein [Wolinella succinogenes] | | | | | |
| 895, 896 | 48855611 | 23 | 7.00E-10 | Cytophaga hutchinsonii | COG3696: Putative silver efflux pump [Cytophaga hutchinsonii] | | | | | |
| 8953, 8954 | | | | | Desulfotalea psychrophila LSV54 chromosome | | 9.00E-07 | ## | | |
| 8957, 8958 | 34557246 | 29 | 3.00E-34 | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | | | | 2.7.3.- | |
| 8961, 8962 | 51891757 | 49 | 5.00E-57 | Symbiobacterium thermophilum IAM 14863 | long-chain fatty-acid-CoA ligase [Symbiobacterium thermophilum IAM 14863] dbj BAD39604.1] long-chain fatty-acid-CoA ligase [Symbiobacterium thermophilum IAM 14863] | | | | 6.2.1.3 | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|--|---|----|----------|----------|
| 8963, 8964 | 32473996 | 42 | 7.00E-22 | Rhodopirellula baltica SH 1 | hypothetical protein RB5963 [Rhodopirellula baltica SH 1] emb CAD74532.1 hypothetical protein [Pirellula sp.] | | | | |
| 8967, 8968 | 34556798 | 61 | 8.00E-71 | Wolinella succinogenes DSM 1740 | DNA GYRASE SUBUNIT A [Wolinella succinogenes DSM 1740] emb CAE09513.1 DNA GYRASE SUBUNIT A [Wolinella succinogenes] | Campylobacter jejuni strain S3BR1 DNA gyrase subunit A (gyrA) gene, partial cds | 80 | 2.00E-15 | 5.99.1.3 |
| 8969, 8970 | 29346638 | 51 | 7.00E-93 | Bacteroides thetaiotaomicron VPI-5482 | fructose-1,6-bisphosphatase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76335.1 fructose-1,6-bisphosphatase [Bacteroides thetaiotaomicron VPI-5482] | Clostridium tetani E88, section 3 of 10 of the complete genome | 93 | 2.00E-13 | 3.1.3.11 |
| 897, 898 | 15606535 | 24 | 2.00E-09 | Aquifex aedificus VF5 | hypothetical protein aq_1332 [Aquifex aedificus VF5] gb AAC07320.1 hypothetical protein [Aquifex aedificus VF5] pir D70415 conserved | | | | |
| 8971, 8972 | 24380120 | 37 | 1.00E-14 | Streptococcus mutans UA159 | putative aspartokinase [Streptococcus mutans UA159] gb AAN59381.1 putative aspartokinase [Streptococcus mutans UA159] | | | 2.7.2.4 | |
| 8973, 8974 | 23023654 | 28 | 4.00E-09 | Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293 | COG0527: Aspartokinases [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293] | | | 2.7.2.4 | |
| 8975, 8976 | 32262428 | 60 | 9.00E-36 | Helicobacter hepaticus ATCC 51449 | ATP-dependent zinc metalloproteinase [Helicobacter hepaticus ATCC 51449] ref NP_860410.1 ATP-dependent zinc metalloproteinase [Helicobacter hepaticus ATCC 51449] | | | 3.4.24.- | |
| 8977, 8978 | 34557847 | 33 | 6.00E-20 | Wolinella succinogenes DSM 1740 | ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes DSM 1740] emb CAE10562.1 ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes] | | | 3.4.24.- | |
| 8979, 8980 | 27365382 | 30 | 4.00E-07 | Vibrio vulnificus CMCP6 | Predicted ATP-binding protein involved in virulence [Vibrio vulnificus CMCP6] gb AAO10437.1 Predicted ATP-binding protein involved in virulence [Vibrio vulnificus CMCP6] | | | | |
| 8981, 8982 | 53713068 | 32 | 4.00E-13 | Bacteroides fragilis YCH46 | hypothetical protein BF1779 [Bacteroides fragilis YCH46] dbj BAD48526.1 | | | | |
| 8983, 8984 | 34558497 | 55 | 3.00E-42 | Wolinella succinogenes DSM 1740 | PUTATIVE INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11212.1 PUTATIVE INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes] | | | 3.4.24.- | |
| 8987, 8988 | 34558447 | 47 | 2.00E-52 | Wolinella succinogenes DSM 1740 | PUTATIVE CATION-TRANSPORTING ATPASE [Wolinella succinogenes DSM 1740] emb CAE11162.1 PUTATIVE CATION-TRANSPORTING ATPASE [Wolinella succinogenes] | | | 3.6.1.- | |
| 8989, 8990 | 30721677 | 26 | 6.00E-07 | Plasmodium falciparum | phosphoprotein 300 [Plasmodium falciparum] | | | | |

| | | | | | | | | | | |
|---------------|----------|----|----------|-----|---------------------------------------|---|--|--|--|----------|
| 899, 900 | 27376391 | 33 | 3.00E-17 | 110 | Bradyrhizobium japonicum USDA | putative isopenicillin N epimerase [Bradyrhizobium japonicum USDA 110] dbj BAC46545.1 bir1280 [Bradyrhizobium japonicum USDA 110] | | | | |
| 8991, 8992 | 18310283 | 43 | 5.00E-54 | | Clostridium perfringens str. 13 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Clostridium perfringens str. 13] dbj BAB81007.1 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Clostridium perfringens str. 13] sp Q8XKU2 GPMI_CLOPE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM) | | | | 5.4.2.1 |
| 8993, 8994 | 57241727 | 47 | 2.00E-29 | | Campylobacter lari RM2100 | Iron(III) ABC transporter, ATP-binding protein [Campylobacter lari RM2100] gb EAL54397.1 iron(III) ABC transporter, ATP-binding protein [Campylobacter lari RM2100] | | | | 1.8.- |
| 8995, 8996 | 46140416 | 43 | 1.00E-23 | | Dechloromonas aromatica RCB | COG3842: ABC-type spermidine/putrescine transport systems, ATPase components [Dechloromonas aromatica RCB] | | | | 1.8.- |
| 8997, 8998 | 48853662 | 26 | 1.00E-21 | | Cytophaga hutchinsonii | COG1538: Outer membrane protein [Cytophaga hutchinsonii] | | | | |
| 9003, 9004 | 30249660 | 31 | 1.00E-25 | | Nitrosomonas europaea ATCC 19718 | hypothetical protein NE1698 [Nitrosomonas europaea ATCC 19718] emb CAD85609.1 conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] | | | | |
| 9007, 9008 | 30248800 | 32 | 9.00E-21 | | Nitrosomonas europaea ATCC 19718 | possible capK protein [Nitrosomonas europaea ATCC 19718] emb CAD84707.1 possible capK protein [Nitrosomonas europaea ATCC 19718] | | | | 6.2.1.30 |
| 9009, 9010 | 29345890 | 31 | 4.00E-38 | | Bacteroides thetaiotaomicron VPI-5482 | glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] | | | | 2.7.8.6 |
| 901, 902 | 27376391 | 34 | 6.00E-08 | | Bradyrhizobium japonicum USDA 110 | putative isopenicillin N epimerase [Bradyrhizobium japonicum USDA 110] dbj BAC46545.1 bir1280 [Bradyrhizobium japonicum USDA 110] | | | | |
| 9011, 9012 | ABG9157 | 48 | 1.00E-76 | | | Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus | | | | 2.7.7.13 |
| 9013, 9014 | ABG9157 | 33 | 2.00E-49 | | | Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus | | | | 2.7.7.13 |
| 9019, 9020 | 39997715 | 29 | 2.00E-23 | | Geobacter sulfurreducens PCA | stage II sporulation-related protein [Geobacter sulfurreducens PCA] gb AAR35993.1 stage II sporulation-related protein [Geobacter sulfurreducens PCA] | | | | |
| 9021, 9022 | 48853894 | 31 | 3.00E-27 | | Cytophaga hutchinsonii | COG0457: FOG: TPR repeat [Cytophaga hutchinsonii] | | | | |
| 9023, 9024 | 29347759 | 40 | 2.00E-36 | | Bacteroides thetaiotaomicron VPI-5482 | transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77456.1 transposase [Bacteroides thetaiotaomicron VPI-5482] | | | | |

| | | | | | | | | | |
|---------------|--------------|----|----------|---|---|--|----|----------|----------|
| 9025, 9026 | 23129857 | 33 | 1.00E-30 | Nostoc punctiforme PCC 73102 | COG3920: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102] | Methanosarcina acetivorans str. C2A, section 317 of 534 of the complete genome | 91 | 6.00E-07 | 2.7.3.- |
| 9027, 9028 | ABP6529 5 | 49 | 6.00E-17 | | Desc:Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:39. Org:Bifidobacterium longum | | | | |
| 9029, 9030 | 34556616 | 42 | 5.00E-67 | Wolfinella succinogenes DSM 1740 | CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolfinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolfinella succinogenes] | | | | |
| 903, 904 | 53714524 | 29 | 4.00E-11 | Bacteroides fragilis YCH46 | hypothetical protein BF3237 [Bacteroides fragilis YCH46] dbj BAD49982.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 9033, 9034 | 34557339 | 58 | 3.00E-33 | Wolfinella succinogenes DSM 1740 | SENSORY TRANSDUCTION REGULATOR [Wolfinella succinogenes DSM 1740] emb CAE10054.1 SENSORY TRANSDUCTION REGULATOR [Wolfinella succinogenes] | | | | |
| 9035, 9036 | 51245785 | 54 | 1.00E-36 | Desulfotalea psychrophila LSV54 | probable phosphoserine aminotransferase [Desulfotalea psychrophila LSV54] emb CAG36662.1 probable phosphoserine aminotransferase [Desulfotalea psychrophila LSV54] | | | | 2.6.1.52 |
| 9037, 9038 | 34558042 | 48 | 1.00E-63 | Wolfinella succinogenes DSM 1740 | DIHYDROPTEROATE SYNTHASE [Wolfinella succinogenes DSM 1740] emb CAE10757.1 DIHYDROPTEROATE SYNTHASE [Wolfinella succinogenes] | | | | 2.5.1.15 |
| 9039, 9040 | 53711616 | 21 | 5.00E-18 | Bacteroides fragilis YCH46 | hypothetical protein BF0325 [Bacteroides fragilis YCH46] dbj BAD47074.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 9043, 9044 | 42628871 | 38 | 8.00E-30 | Haemophilus influenzae R2846 | CQG0147: Anthranilate/para-aminobenzoate synthases component I [Haemophilus influenzae R2846] | | | | 4.1.3.- |
| 9045, 9046 | 34557248 | 37 | 1.00E-40 | Wolfinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT REGULATOR [Wolfinella succinogenes DSM 1740] emb CAE09963.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolfinella succinogenes] | | | | 2.7.3.- |
| 9047, 9048 | 15605731 | 36 | 1.00E-12 | Aquifex aeolicus VF5 | AP4A hydrolase [Aquifex aeolicus VF5] gb AAC06510.1 AP4A hydrolase [Aquifex aeolicus VF5] pir JAT0315 AP4A hydrolase - Aquifex aeolicus | | | | 3.6.1.- |
| 9049, 9050 | 34556741 | 29 | 4.00E-09 | Wolfinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolfinella succinogenes DSM 1740] emb CAE09456.1 PUTATIVE TWO-COMPONENT SENSOR [Wolfinella succinogenes] | | | | |
| 905, 906 | 46201521 | 25 | 3.00E-12 | Magnetospirillum magnetotacticum MS-1 | COG3287: Uncharacterized conserved protein [Magnetospirillum magnetotacticum MS-1] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|--|---------------|
| 9051, 9052 | 19704556 | 27 | 1.00E-21 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | hypothetical protein FN1221 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95417.1 Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | |
| 9053, 9054 | 54302555 | 55 | 3.00E-70 | Photobacterium profundum SS9 | hypothetical protein PBPR80876 [Photobacterium profundum SS9] emb CAG22748.1 hypothetical protein [Photobacterium profundum] | | | | |
| 9055, 9056 | 53691429 | 33 | 2.00E-17 | Desulfovibrio desulfuricans G20 | COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Desulfovibrio desulfuricans G20] | | | | 6.2.1.3 |
| 9057, 9058 | 51854402 | 31 | 7.00E-23 | Oryza sativa (japonica cultivar- group) | putative serine protease [Oryza sativa (japonica cultivar-group)] gb AA177386.1 putative serine protease [Oryza sativa (japonica cultivar- group)] | | | | |
| 9059, 9060 | 45520556 | 41 | 3.00E-67 | Methylobacillus flagellatus KT | COG0835: Chemotaxis signal transduction protein [Methylobacillus flagellatus KT] | | | | |
| 9061, 9062 | 53729945 | 24 | 3.00E-07 | Dechloromonas aromatica RCB | COG0835: Chemotaxis signal transduction protein [Dechloromonas aromatica RCB] | | | | |
| 9063, 9064 | 34557963 | 39 | 4.00E-27 | Wolinella succinogenes DSM 1740 | FLAVOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE10678.1 FLAVOPROTEIN [Wolinella succinogenes] | | | | |
| 9065, 9066 | 57169052 | 32 | 6.00E-19 | Campylobacter coli RM2228 | general secretory pathway protein F [Campylobacter coli RM2228] gb EAL56201.1 general secretory pathway protein F [Campylobacter coli RM2228] | | | | |
| 9067, 9068 | 28209891 | 50 | 9.00E-18 | Clostridium tetani E88 | NAD(FAD)-utilizing dehydrogenase [Clostridium tetani E88] gb AAO34772.1 NAD(FAD)-utilizing dehydrogenase [Clostridium tetani E88] | | | | |
| 9069, 9070 | 50929519 | 47 | 5.00E-27 | Oryza sativa (japonica cultivar- group) | OSJNBa0043A12.24 [Oryza sativa (japonica cultivar-group)] emb CAE02819.1 OSJNBa0043A12.24 [Oryza sativa (japonica cultivar- group)] | | | | 2.7.1.10 0 |
| 907, 908 | 57339644 | 49 | 8.00E-50 | synthetic construct Wolinella | hypothetical protein FTT0520 [synthetic construct] | | | | |
| 9073, 9074 | 34558184 | 38 | 3.00E-14 | succinogenes DSM 1740 | hypothetical protein WS1889 [Wolinella succinogenes DSM 1740] emb CAE10899.1 hypothetical protein [Wolinella succinogenes] | | | | |
| 9083, 9084 | 34558196 | 60 | 4.00E-26 | Wolinella succinogenes DSM 1740 | DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes] | | | | 2.7.7.- |
| 9085, 9086 | 51245189 | 35 | 7.00E-13 | Desulfotalea psychrophila LSV54 | hypothetical protein DP1337 [Desulfotalea psychrophila LSV54] emb CAG36086.1 unknown protein [Desulfotalea psychrophila LSV54] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|--|----------|
| 9089, 9090 | 11499619 | 29 | 4.00E-21 | Archaeoglobus fulgidus DSM 4304 uncultured | translation initiation factor eIF-2B, subunit delta (eif2BD) [Archaeoglobus fulgidus DSM 4304] gb AAB89217.1 translation initiation factor eIF-2B, subunit delta (eif2BD) [Archaeoglobus fulgidus DSM 4304] pir D69504 translation initiation factor eIF-2B, subunit delta (eif2BD) homolog - Archaeoglobus fulgidus sp O28242 E2B2_ARCFU Putative translation initiation factor eIF-2B subunit 2 (eIF-2B GDP-GTP exchange factor) | | | | |
| 909, 910 | 52550513 | 36 | 2.00E-08 | archaeon GZfos9D8 | conserved hypothetical protein [uncultured archaeon GZfos9D8] Leucyl/phenylalanyl-tRNA--protein transferase [Nitrosomonas europaea ATCC 19718] emb CAD86131.1 Leucyl/phenylalanyl-tRNA--protein transferase [Nitrosomonas europaea ATCC 19718] sp Q82ST5 LFTN_NITEU Leucyl/phenylalanyl-tRNA--protein transferase (L/F-transferase) (Leucyltransferase) (Phenylalanyltransferase) | | | | 2.3.2.6 |
| 9091, 9092 | 30250151 | 50 | 9.00E-54 | Nitrosomonas europaea ATCC 19718 | hypothetical protein Chut02001547 [Cytophaga hutchinsonii] | | | | |
| 9093, 9094 | 48855221 | 39 | 3.00E-07 | Cytophaga hutchinsonii | COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1] | | | | 2.7.3.- |
| 9097, 9098 | 46202456 | 35 | 3.00E-29 | Magnetospirillum magnetotacticum MS-1 | fructose-1,6-bisphosphatase [Campylobacter lari RM2100] gb EAL54888.1 fructose-1,6-bisphosphatase [Campylobacter lari RM2100] two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482] Signal transduction histidine kinase [Vibrio vulnificus CMCP6] gb AAO07333.1 Signal transduction histidine kinase [Vibrio vulnificus CMCP6] | | | | 3.1.3.11 |
| 9099, 9100 | 57241192 | 37 | 2.00E-30 | Campylobacter lari RM2100 | hypothetical protein BF0193 [Bacteroides fragilis YCH46] dbj BAD46942.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 91, 92 | 29349974 | 37 | 2.00E-30 | Bacteroides thetaiotaomicron VPI-5482 | hypothetical protein BF3578 [Bacteroides fragilis YCH46] dbj BAD50321.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 9101, 9102 | 27366816 | 44 | 1.00E-67 | Vibrio vulnificus CMCP6 | Autolysin sensor kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94426.1 Autolysin sensor kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] COG3279: Response regulator of the LysR/AlgR family [Microbulbifer degradans 2-40] | | | | 2.7.3.- |
| 9103, 9104 | 53711484 | 30 | 6.00E-12 | Bacteroides fragilis YCH46 | | | | | 3.1.1.61 |
| 9105, 9106 | 53714863 | 47 | 1.00E-47 | Bacteroides fragilis YCH46 | | | | | |
| 9109, 9110 | 19703565 | 41 | 5.00E-17 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | | | | | |
| 9111, 9112 | 48862014 | 45 | 3.00E-22 | Microbulbifer degradans 2-40 | | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|---|----|----------|
| 9113, 9114 | 23508673 | 28 | 2.00E-07 | Plasmodium falci-parum 3D7 | MAEBL, putative [Plasmodium falci-parum 3D7] gb AAL10509.1 erythrocyte binding protein 1 [Plasmodium falci-parum] gb AAN36066.1 MAEBL, putative [Plasmodium falci-parum 3D7] gb AAM90625.1 chimeric erythrocyte-binding protein MAEBL [Plasmodium falci-parum] | | | |
| 9115, 9116 | 54028700 | 22 | 4.00E-08 | Polaromonas sp. J5666 | COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Polaromonas sp. J5666] | | | |
| 9123, 9124 | 34558286 | 56 | 2.00E-72 | Wolinella succinogenes DSM 1740 | FLAGELLAR BASAL-BODY M-RING PROTEIN FLIF [Wolinella succinogenes DSM 1740] emb CAE11001.1 FLAGELLAR BASAL-BODY M- RING PROTEIN FLIF [Wolinella succinogenes] | | | |
| 9125, 9126 | 48836065 | 38 | 9.00E-13 | Thermobifida fusca | COG1609: Transcriptional regulators [Thermobifida fusca] | | | |
| 9127, 9128 | 34558082 | 51 | 9.00E-29 | Wolinella succinogenes DSM 1740 | LIPOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE10797.1 LIPOPROTEIN [Wolinella succinogenes] | | | |
| 9129, 9130 | 15896496 | 36 | 4.00E-40 | Clostridium acetobutylicum ATCC 824 | Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] gb AAK81185.1 Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] pir F97299 sensory transduction protein containing HD_GYP domain [Imported] - Clostridium acetobutylicum | | | |
| 913, 914 | 15678598 | 45 | 2.00E-26 | Methanothermobac- ter thermautotrophicus str. Delta H | hypothetical protein MTH570 [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85076.1 unknown [Methanothermobacter thermautotrophicus str. Delta H] pir E69175 hypothetical protein MTH570 - Methanothermobacterium thermautotrophicum (strain Delta H) | | | |
| 9133, 9134 | 52007674 | 33 | 5.00E-16 | Thiobacillus denitrificans ATCC 25259 | COG1959: Predicted transcriptional regulator [Thiobacillus denitrificans ATCC 25259] | | | |
| 9135, 9136 | 29347043 | 54 | 5.00E-39 | Bacteroides thetaiotaomicron VPI-5482 | mannose-1-phosphate guanylttransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76740.1 mannose-1-phosphate guanylttransferase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.7.7.13 |
| 9137, 9138 | 23474120 | 35 | 3.00E-39 | Desulfovibrio desulfuricans G20 | COG1061: DNA or RNA helicases of superfamily II [Desulfovibrio desulfuricans G20] | | | |
| 9139, 9140 | 23474120 | 36 | 5.00E-30 | Desulfovibrio desulfuricans G20 | COG1061: DNA or RNA helicases of superfamily II [Desulfovibrio desulfuricans G20] | | | |
| 9141, 9142 | 37678505 | 73 | 1.00E-97 | Vibrio vulnificus YJ016 | putative LPS biosynthesis protein [Vibrio vulnificus YJ016] dbj BAC93085.1 putative LPS biosynthesis protein [Vibrio vulnificus YJ016] | Vibrio vulnificus YJ016 DNA, chromosome I, complete sequence | 85 | 5.00E-10 |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|----------|
| 9143, 9144 | 34558833 | 35 | 4.00E-48 | Alvinella pompejana epibiont 7G3 | phenylalanyl-tRNA synthetase beta subunit [Alvinella pompejana epibiont 7G3] | | | 6.1.1.20 |
| 9145, 9146 | 34558357 | 51 | 7.00E-68 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-PUTATIVE Mg DEPENDENT DNase [Wolinella succinogenes DSM 1740] emb CAE11072.1 conserved hypothetical protein-PUTATIVE Mg DEPENDENT DNase [Wolinella succinogenes] | | | 3.1.21.- |
| 9147, 9148 | 34558357 | 54 | 4.00E-48 | Wolinella succinogenes DSM 1740 | conserved hypothetical protein-PUTATIVE Mg DEPENDENT DNase [Wolinella succinogenes DSM 1740] emb CAE11072.1 conserved hypothetical protein-PUTATIVE Mg DEPENDENT DNase [Wolinella succinogenes] | | | 3.1.21.- |
| 9149, 9150 | 23114483 | 37 | 3.00E-40 | Desulfotobacterium hafniense DCB-2 | COG2931: RTX toxins and related Ca2+-binding proteins [Desulfotobacterium hafniense DCB-2] | | | |
| 915, 916 | 50086533 | 40 | 6.00E-10 | Acinetobacter sp. ADP1 | hypothetical protein ACIAD3581 [Acinetobacter sp. ADP1] emb CAG70221.1 conserved hypothetical protein [Acinetobacter sp. ADP1] | | | 2.3.1.- |
| 9151, 9152 | 34557851 | 32 | 2.00E-39 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1518 [Wolinella succinogenes DSM 1740] emb CAE10566.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 9157, 9158 | 34396892 | 30 | 3.00E-13 | Porphyromonas gingivalis W83 | ISPg7, transposase [Porphyromonas gingivalis W83] ref NP_904759.1 | | | |
| 9159, 9160 | 46319318 | 48 | 5.00E-57 | Burkholderia cepacia R1808 | ISPG7, transposase [Porphyromonas gingivalis W83] COG0513: Superfamily II DNA and RNA helicases [Burkholderia cepacia R1808] | | | 2.7.7.- |
| 9161, 9162 | 34557573 | 33 | 2.00E-29 | Wolinella succinogenes DSM 1740 | SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 9163, 9164 | 23128221 | 34 | 5.00E-17 | Nostoc punctiforme PCC 73102 | COG4328: Uncharacterized protein conserved in bacteria [Nostoc punctiforme PCC 73102] | | | |
| 9165, 9166 | 34557016 | 52 | 3.00E-23 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0599 [Wolinella succinogenes DSM 1740] emb CAE09731.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 9167, 9168 | 13472325 | 31 | 3.00E-22 | Mesorhizobium loti MAFF303099 | endo-1,3-1,4-beta-glycanase [Mesorhizobium loti MAFF303099] dbj BAB49678.1 endo-1,3-1,4-beta-glycanase [Mesorhizobium loti MAFF303099] | | | 3.2.1.- |
| 9169, 9170 | 23103201 | 50 | 2.00E-53 | Azotobacter vinelandii | COG2871: Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrF [Azotobacter vinelandii] | | | 1.6.5.- |
| 917, 918 | 21241362 | 50 | 1.00E-76 | Xanthomonas axonopodis pv. citri str. 306 | dipeptidyl peptidase IV [Xanthomonas axonopodis pv. citri str. 306] gb AAM35480.1 dipeptidyl peptidase IV [Xanthomonas axonopodis pv. citri str. 306] | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|------------|---|--|--|----|------------------|
| 9173, 9174 | 34556562 | 80 | 2.00E-97 | 1740 | Wolinella succinogenes DSM | PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes DSM 1740] emb CAE09277.1 PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes] | | | |
| 9177, 9178 | 15669248 | 31 | 4.00E-11 | 2661 | Methanocaldococcus jannaschii DSM | capsular polysaccharide biosynthesis protein M [Methanocaldococcus jannaschii DSM 2661] gb AAB99063.1 capsular polysaccharide biosynthesis protein M [Methanocaldococcus jannaschii DSM 2661] pir B64432 capsular polysaccharide biosynthesis protein M homolog - Methanocaldococcus jannaschii sp Q58459 YA59_METJA Hypothetical glycosyl transferase MJ1059 | | | 2.4.1.- |
| 9179, 9180 | 50591112 | 27 | 2.00E-09 | 89/1591 | Streptococcus suis | COG0438: Glycosyltransferase [Streptococcus suis 89/1591] | | | 2.-.-.- |
| 9185, 9186 | AAW9853 | 56 | 1.00E-76 | | | Desc:H. pylori GHPO 1479 protein. Org:Helicobacter pylori | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6 | 95 | 4.00E-08 1.8.-.- |
| 9189, 9190 | 46130289 | 56 | 1.00E-32 | 7942 | Synechococcus elongatus PCC | COG0517: FOG: CBS domain [Synechococcus elongatus PCC 7942] | | | 2.7.3.- |
| 919, 920 | 48853693 | 54 | 7.00E-38 | | Cytophaga hutchinsonii | COG1801: Uncharacterized conserved protein [Cytophaga hutchinsonii] | | | |
| 9193, 9194 | 45683694 | 41 | 1.00E-31 | BNC1 | Mesorhizobium sp. | COG0438: Glycosyltransferase [Mesorhizobium sp. BNC1] | | | |
| 9197, 9198 | 45508536 | 39 | 3.00E-20 | ATCC 29413 | Anabaena variabilis | COG0535: Predicted Fe-S oxidoreductases [Anabaena variabilis ATCC 29413] gb AA93025.1 NifX2 | | | |
| 9201, 9202 | 20807566 | 29 | 1.00E-17 | MB4 | Thermoanaerobacter tengcongensis | Diguanylate cyclase/phosphodiesterase domain 1 (GGDEF) [Thermoanaerobacter tengcongensis MB4] gb AAM2434.1 Diguanylate cyclase/phosphodiesterase domain 1 (GGDEF) [Thermoanaerobacter tengcongensis MB4] | | | 2.7.3.- |
| 9207, 9208 | 57168029 | 42 | 3.00E-24 | RM2228 | Campylobacter coli | ADP-heptose-lps heptosyltransferase II (rfaf) [Campylobacter coli RM2228] gb EAL57072.1 ADP-heptose-lps heptosyltransferase II (rfaf) [Campylobacter coli RM2228] | | | |
| 9209, 9210 | 48833897 | 39 | 5.00E-09 | MC-1 | Magnetococcus sp. | COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1] | | | |
| 921, 922 | 21241377 | 50 | 2.00E-31 | | Xanthomonas axonopodis pv. citri str. 306 | endonuclease [Xanthomonas axonopodis pv. citri str. 306] gb AAM35495.1 endonuclease [Xanthomonas axonopodis pv. citri str. 306] | | | 3.2.2.23 |
| 9211, 9212 | 48853603 | 46 | 2.00E-52 | | Cytophaga hutchinsonii | COG0809: S-adenosylmethionine tRNA-ribosyltransferase-isomerase (queuine synthetase) [Cytophaga hutchinsonii] | | | 5.-.-.- |

| | | | | | | | | |
|---------------|----------|----|-----------|---|--|--|--|----------|
| 9213, 9214 | 9948626 | 51 | 1.00E-71 | Pseudomonas aeruginosa PAO1 | conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pfr B83326 conserved hypothetical protein PA2566 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_251256.1 hypothetical protein PA2566 [Pseudomonas aeruginosa PAO1] | | | 1.6.99.3 |
| 9215, 9216 | 32261568 | 40 | 2.00E-45 | Helicobacter hepaticus ATCC 51449 | two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] | | | 2.7.3.- |
| 9217, 9218 | 57168343 | 33 | 5.00E-44 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56825.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | |
| 9219, 9220 | 53712708 | 36 | 2.00E-42 | Bacteroides fragilis YCH46 | hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46] related to two-component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila Lsv54] emb CAG37842.1 related to two- component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila Lsv54] | | | 2.7.3.- |
| 9221, 9222 | 51246965 | 38 | 1.00E-37 | Desulfotalea psychrophila Lsv54 | biotin synthetase [Clostridium perfringens str. 13] dbj BAB81250.1 biotin synthetase [Clostridium perfringens str. 13] | | | 2.8.1.6 |
| 9225, 9226 | 18310526 | 44 | 4.00E-18 | Clostridium perfringens str. 13 | COG0536: Predicted GTPase [Cytophaga hutchinsonii] hypoxanthine-guanine phosphoribosyltransferase [Bacteroides thetataomicron VPI-5482] gb AAO79491.1 hypoxanthine-guanine phosphoribosyltransferase [Bacteroides thetataomicron VPI-5482] | | | 2.4.2.8 |
| 9227, 9228 | 48853834 | 77 | 1.00E-102 | Cytophaga hutchinsonii | COG0587: DNA polymerase III, alpha subunit [Mesorhizobium sp. BNC1] | | | 2.7.7.7 |
| 9229, 9230 | 29349794 | 53 | 9.00E-50 | Bacteroides thetataomicron VPI-5482 | sensory box sensor histidine kinase/response regulator [Dehalococcoides ethenogenes 195] gb AAW39739.1 sensory box sensor histidine kinase/response regulator [Dehalococcoides ethenogenes 195] SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | 2.7.3.- |
| 923, 924 | 45684496 | 37 | 1.00E-21 | Mesorhizobium sp. BNC1 | SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes] | | | 2.7.3.- |
| 9231, 9232 | 57234234 | 39 | 6.00E-24 | Dehalococcoides ethenogenes 195 | hypothetical protein lpp0207 [Legionella pneumophila str. Paris] emb CAH11354.1 hypothetical protein [Legionella pneumophila str. Paris] | | | 2.7.3.- |
| 9233, 9234 | 34557573 | 35 | 6.00E-13 | Wolinella succinogenes DSM 1740 | | | | |
| 9235, 9236 | 34558157 | 44 | 8.00E-16 | Legionella pneumophila str. Paris | | | | |
| 9239, 9240 | 54296182 | 33 | 1.00E-27 | Paris | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|--|----------|
| 9245, 9246 | 29608580 | 31 | 3.00E-18 | Streptomyces avermitilis MA-4680 | hypothetical protein [Streptomyces avermitilis MA-4680] ref NP_826099.1 hypothetical protein SAV4922 [Streptomyces avermitilis MA-4680] | | | | |
| 9247, 9248 | 34557912 | 40 | 5.00E-38 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1588 [Wolinella succinogenes DSM 1740] emb CAE10027.1 conserved hypothetical protein [Wolinella succinogenes] two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] gb AAO79283.1 two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] | | | | |
| 925, 926 | 29349586 | 27 | 1.00E-11 | Bacteroides thetaitaomicron VPI-5482 | | | | | |
| 9251, 9252 | 34557353 | 34 | 6.00E-35 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10068.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | 2.7.3.- |
| 9253, 9254 | 34558157 | 29 | 6.00E-18 | Wolinella succinogenes DSM 1740 | SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes] | | | | 2.7.3.- |
| 9255, 9256 | 57506022 | 57 | 1.00E-29 | Campylobacter upsaliensis RM3195 | chemotaxis regulatory protein Cj1118c [Campylobacter upsaliensis RM3195] upsaliensis RM3195] | | | | 2.7.3.- |
| 9257, 9258 | 37913015 | 45 | 2.00E-37 | uncultured marine alpha proteobacterium HOT2C01 | predicted sugar fermentation stimulation protein [uncultured marine alpha proteobacterium HOT2C01] | | | | |
| 9261, 9262 | 29655162 | 32 | 3.00E-21 | Coxiella burnetii RSA 493 | hypothetical protein CBU1877 [Coxiella burnetii RSA 493] gb AAO91388.1 conserved domain protein [Coxiella burnetii RSA 493] | | | | |
| 9263, 9264 | 38637724 | 38 | 4.00E-11 | Cupriavidus necator | putative integrase/recombinase [Cupriavidus necator] gb AAP85812.1 putative integrase/recombinase [Ralstonia eutropha] | | | | |
| 9265, 9266 | 34556591 | 49 | 2.00E-31 | Wolinella succinogenes DSM 1740 | PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE09306.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes] | | | | 4.2.1.70 |
| 9267, 9268 | 34556593 | 33 | 8.00E-09 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0145 [Wolinella succinogenes DSM 1740] emb CAE09308.1 conserved hypothetical protein [Wolinella succinogenes] sp Q7MST9 TRMB_WOLSU tRNA (guanine-N(7))-methyltransferase (tRNA(m7G46)-methyltransferase) | | | | 2.1.1.- |
| 9269, 9270 | 34556592 | 33 | 8.00E-26 | Wolinella succinogenes DSM 1740 | PUTATIVE FIBRONECTIN DOMAIN-CONTAINING LIPOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE09307.1 PUTATIVE FIBRONECTIN DOMAIN-CONTAINING LIPOPROTEIN [Wolinella succinogenes] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|--|----|----------|----------|
| 927, 928 | 48862188 | 36 | 3.00E-09 | Microbulbifer degradans 2-40 | COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Microbulbifer degradans 2-40] | | | | |
| 9273, 9274 | 19703530 | 26 | 4.00E-13 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | hypothetical protein FN0185 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94391.1 Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] | | | | |
| 9275, 9276 | 57168392 | 37 | 3.00E-23 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56874.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | | |
| 9277, 9278 | 34556741 | 22 | 2.00E-10 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09456.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | | |
| 9279, 9280 | 15823603 | 35 | 9.00E-35 | Sphaerotilus natans | putative RNA polymerase associated protein [Sphaerotilus natans] | | | | 2.7.7.- |
| 9281, 9282 | 48860351 | 48 | 9.00E-52 | Clostridium thermocellum ATCC 27405 | COG2206: HD-GYP domain [Clostridium thermocellum ATCC 27405] | | | | |
| 9283, 9284 | 34558426 | 67 | 7.00E-80 | Wolinella succinogenes DSM 1740 | CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes DSM 1740] emb CAE11141.1 CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 1/6 | 81 | 1.00E-23 | 6.3.5.5 |
| 9285, 9286 | 29348936 | 63 | 1.00E-85 | Bacteroides thetaiotaomicron VPI-5482 | alpha-1,2-mannosidase [Bacteroides thetaiotaomicron VPI-5482] gb AAC78633.1 alpha-1,2-mannosidase [Bacteroides thetaiotaomicron VPI- 5482] | Bacteroides thetaiotaomicron VPI-5482, section 18 of 21 of the complete genome | 83 | 5.00E-07 | |
| 9287, 9288 | 53712180 | 31 | 2.00E-07 | Bacteroides fragilis YCH46 | hypothetical protein BF0887 [Bacteroides fragilis YCH46] dbj BAD47638.1 hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 9289, 9290 | 57167668 | 49 | 3.00E-59 | Campylobacter coli RM2228 | DNA repair protein RecN, putative [Campylobacter coli RM2228] gb EAL57454.1 DNA repair protein RecN, putative [Campylobacter coli RM2228] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 | 93 | 2.00E-09 | |
| 929, 930 | 48856028 | 46 | 1.00E-37 | Cytophaga hutchinsonii | COG1057: Nicotinic acid mononucleotide adenyltransferase (Cytophaga hutchinsonii) | | | | 2.7.7.18 |
| 9291, 9292 | 57241121 | 41 | 9.00E-39 | Campylobacter lari RM2100 | DNA repair protein RecN, putative [Campylobacter lari RM2100] gb EAL54817.1 DNA repair protein RecN, putative [Campylobacter lari RM2100] | | | | |

| | | | | | | | | | |
|----------------------|----------------------|----------|----------------------|--|---|--|--|--|---------------|
| 9293, 9294 | 57505945 AAY7460 | 32 | 7.00E-07 | Campylobacter upsaliensis RM3195 | hypothetical protein CUPA0081 [Campylobacter upsaliensis gb EAL52535.1 hypothetical protein CUPA0081 [Campylobacter upsaliensis RM3195] | | | | |
| 9295, 9296 | 4 | 45 | 3.00E-78 | | Desc:Neisseria meningitidis ORF 164 protein sequence SEQ ID NO:682. Org:Neisseria meningitidis | | | | 6.2.1.3 |
| 9297, 9298 | 53758726 | 39 | 4.00E-30 | Methylococcus capsulatus str. Bath | oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath] ref YP_113360.1 oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath] | | | | |
| 9299, 9300 | 34558271 | 72 | 2.00E-94 | Wolinella succinogenes DSM 1740 | DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10986.1 DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes] | | | | |
| 93, 9303, 9304 | 45357832 56315748 | 39 34 | 1.00E-30 3.00E-26 | Methanococcus maripaludis S2 Azoarcus sp. EBN1 | hypothetical protein MMP0269 [Methanococcus maripaludis S2] emb CAF29825.1 conserved hypothetical protein [Methanococcus maripaludis S2] conserved hypothetical protein [Azoarcus sp. EBN1] | | | | |
| 9305, 9306 | 57240361 | 37 | 3.00E-12 | Campylobacter lari RM2100 | conserved hypothetical protein [Campylobacter lari gb EAL55475.1 conserved hypothetical protein [Campylobacter lari RM2100] | | | | |
| 9309, 9310 | 34763472 | 63 | 2.00E-75 | Fusobacterium nucleatum subsp. vincentii ATCC 49256 | Fe-S OXIDOREDUCTASE (1.8.-.-) [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23990.1 Fe-S OXIDOREDUCTASE (1.8.-.-) [Fusobacterium nucleatum subsp. vincentii ATCC 49256] | | | | 1.8.-.- |
| 9311, 9312 | 34555560 | 35 | 2.00E-54 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | | |
| 9313, 9314 | 9655294 | 32 | 7.00E-13 | Vibrio cholerae O1 blovar eltor str. N16961 | conserved hypothetical protein [Vibrio cholerae O1 blovar eltor str. N16961] ref NP_230490.1 hypothetical protein VC0842 [Vibrio cholerae O1 blovar eltor str. N16961] gb AAK20799.1 unknown [Vibrio cholerae] gb AAK20769.1 unknown [Vibrio cholerae] pir G82273 conserved hypothetical protein VC0842 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | | |
| 9315, 9316 | 53735933 | 41 | 6.00E-52 | Crocospaera watsonii WH 8501 | COG2202: FOG: PAS/PAC domain [Crocospaera watsonii WH 8501] | | | | |
| 9317, 9318 | 34557196 | 53 | 4.00E-44 | Wolinella succinogenes DSM 1740 | LIPID A DISACCHARIDE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE09911.1 LIPID A DISACCHARIDE SYNTHASE [Wolinella succinogenes] | | | | 2.4.1.18 2 |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|----------|
| 9319, 9320 | 37679818 | 39 | 2.00E-12 | Vibrio vulnificus YJ016 | ATP-dependent DNA ligase [Vibrio vulnificus YJ016] dbj BAC94398.1 ATP-dependent DNA ligase [Vibrio vulnificus YJ016] | | | 6.5.1.1 |
| 9321, 9322 | 57240881 | 37 | 3.00E-32 | Campylobacter lari RM2100 | molybdenum cofactor biosynthesis protein [Campylobacter lari RM2100] gb EAL55274.1 molybdenum cofactor biosynthesis protein [Campylobacter lari RM2100] | | | |
| 9323, 9324 | 34396573 | 35 | 5.00E-07 | Porphyromonas gingivalis W83 | hypothetical protein PG0439 [Porphyromonas gingivalis W83] ref NP_904740.1 hypothetical protein PG0439 [Porphyromonas gingivalis W83] | | | |
| 9325, 9326 | 28195134 | 48 | 2.00E-31 | Agrobacterium tumefaciens | OphA [Agrobacterium tumefaciens] | | | |
| 9327, 9328 | 27807025 | 50 | 1.00E-40 | ubiquinone | NADH dehydrogenase flavoprotein 2 (24kD) [ubiquinone] [NADH-ubiquinone reductase 24 kDa mitochondrial] [Bos taurus] sp P04394 NUHM_BOVIN NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor (Polypeptide II) pir B30113 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) 24K chain precursor - bovine gb AAA87358.1 NADH-ubiquinone reductase 24 kDa subunit [Bos taurus] | | | 1.6.5.3 |
| 9329, 9330 | 27365565 | 38 | 1.00E-36 | Vibrio vulnificus CMCP6 | Transcriptional regulator [Vibrio vulnificus CMCP6] ref NP_934898.1 transcriptional regulator [Vibrio vulnificus YJ016] gb AAO10820.1 Transcriptional regulator [Vibrio vulnificus CMCP6] gb AAK31574.1 transcriptional regulator [Vibrio vulnificus] dbj BAC94869.1 transcriptional regulator [Vibrio vulnificus YJ016] | | | 2.7.3.- |
| 9331, 9332 | 52548588 | 28 | 4.00E-16 | uncultured archaeon GZfos17F1 | FOG TPR repeat [uncultured archaeon GZfos17F1] | | | |
| 9333, 9334 | 53714264 | 40 | 3.00E-37 | Bacteroides fragilis YCH46 | folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46] | | | 6.3.2.17 |
| 9335, 9336 | 21673114 | 27 | 1.00E-15 | Chlorobium tepidum TLS | hypothetical protein CT0275 [Chlorobium tepidum TLS] gb AAM71521.1 hypothetical protein [Chlorobium tepidum TLS] | | | |
| 9339, 9340 | 46140415 | 53 | 5.00E-41 | Dechloromonas aromatica RCB | COG2360: Leu/Phe-tRNA-protein transferase [Dechloromonas aromatica RCB] | | | 2.3.2.6 |
| 9341, 9342 | 52549555 | 34 | 3.00E-13 | uncultured archaeon GZfos27G5 | transposase [uncultured archaeon GZfos27G5] | | | |
| 9343, 9344 | 34557172 | 35 | 1.00E-42 | Wolinella succinogenes DSM 1740 | SENSORY PROTEIN, CONTAINING EAL-DOMAIN [Wolinella succinogenes DSM 1740] emb CAE09887.1 SENSORY PROTEIN, CONTAINING EAL-DOMAIN [Wolinella succinogenes] | | | |
| 9345, 9346 | 56707343 | 41 | 6.00E-19 | Francisella tularensis subsp. tularensis Schu 4 | Acetyltransferase [Francisella tularensis subsp. tularensis Schu 4] emb CAG44810.1 Acetyltransferase [Francisella tularensis subsp. tularensis] | | | 2.3.1.12 |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|---------------|--|--|
| 9347, 9348 | 37519796 | 28 | 2.00E-11 | Gloeobacter violaues PCC 7421 | hypothetical protein glr0227 [Gloeobacter violaceus PCC 7421] dbj BAC88168.1 glr0227 [Gloeobacter violaceus PCC 7421] | | | |
| 9349, 9350 | 15607034 | 38 | 9.00E-16 | Aquifex aeolicus VF5 | hypothetical protein aq_2067 [Aquifex aeolicus VF5] gb AAC07822.1 hypothetical protein [Aquifex aeolicus VF5] pir C70477 conserved hypothetical protein aq_2067 - Aquifex aeolicus | | | |
| 935, 936 | 18977094 | 57 | 3.00E-56 | Pyrococcus furius DSM 3638 | alkyl hydroperoxide reductase subunit c [Pyrococcus furius DSM 3638] gb AAL80846.1 alkyl hydroperoxide reductase subunit c [Pyrococcus furius DSM 3638] | 1.6.4.- | | |
| 9353, 9354 | 37527191 | 38 | 4.00E-23 | Photorhabdus luminescens subsp. laumondii TTO1 | hypothetical protein plu3313 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15687.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] | 2.7.3.- | | |
| 9355, 9356 | 34558184 | 30 | 1.00E-24 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1889 [Wolinella succinogenes DSM 1740] emb CAE10899.1 hypothetical protein [Wolinella succinogenes] | | | |
| 9357, 9358 | 34556947 | 41 | 4.00E-19 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0526 [Wolinella succinogenes DSM 1740] emb CAE09662.1 hypothetical protein [Wolinella succinogenes] | | | |
| 9363, 9364 | 34557494 | 45 | 8.00E-27 | Wolinella succinogenes DSM 1740 | PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes DSM 1740] emb CAE10209.1 PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes] | 6.3.4.6 | | |
| 9365, 9366 | 53713853 | 28 | 1.00E-09 | Bacteroides fragilis YCH46 | hypothetical protein BF2562 [Bacteroides fragilis YCH46] dbj BAD49311.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |
| 9367, 9368 | 34557273 | 45 | 1.00E-25 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0881 [Wolinella succinogenes DSM 1740] emb CAE09988.1 hypothetical protein [Wolinella succinogenes] | 2.7.1.14 8 | | |
| 9369, 9370 | 32262467 | 41 | 3.00E-17 | Helicobacter hepaticus ATCC 51449 | hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449] ref NP_860448.1 hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449] | | | |
| 937, 938 | 15669750 | 44 | 7.00E-56 | Methanocaldococ us jannaschii DSM 2661 | aspartyl-tRNA synthetase (aspS) [Methanocaldococcus jannaschii DSM 2661] gb AAB99575.1 aspartyl-tRNA synthetase (aspS) [Methanocaldococcus jannaschii DSM 2661] pir B64494 aspartate-tRNA ligase (EC 6.1.1.12) - Methanocaldococcus jannaschii sp Q58950 SYD_METJA Aspartyl-tRNA synthetase (Aspartate-tRNA ligase) (AspRS) | 6.1.1.12 | | |
| 9371, 9372 | 57506092 | 36 | 2.00E-22 | Campylobacter upsallensis RM3195 | site-specific recombinase, phage integrase family, putative [Campylobacter upsallensis RM3195] gb EAL52368.1 site-specific recombinase, phage integrase family, putative [Campylobacter upsallensis RM3195] | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|--|--|----|-----------|----------|
| 9381, 9382 | 57505780 | 49 | 7.00E-44 | Campylobacter upsaliensis RM3195 | Phosphoglycolate phosphatase [Campylobacter upsaliensis RM3195] gb EAL52841.1 Phosphoglycolate phosphatase [Campylobacter upsaliensis RM3195] | | | 3.1.3.18 | |
| 9383, 9384 | 34557641 | 54 | 3.00E-32 | Wolinella succinogenes DSM 1740 | MEMBRANE-BOUND LYTC MUREIN TRANSGLYCOSYLASE C [Wolinella succinogenes DSM 1740] emb CAE10356.1 MEMBRANE-BOUND LYTC MUREIN TRANSGLYCOSYLASE C [Wolinella succinogenes] | | | 3.2.1.- | |
| 9385, 9386 | 57237342 | 44 | 1.00E-18 | Campylobacter jejuni RM1221 | transcription elongation factor GreA [Campylobacter jejuni RM1221] gb AAW34925.1 transcription elongation factor GreA [Campylobacter jejuni RM1221] emb CAB72754.1 transcription elongation factor [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281480.1 transcription elongation factor [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81447 transcription elongation factor Cj0287c [imported] - Campylobacter jejuni (strain NCTC 11168) sp Q9PIK9 GRE_A_CAMJE Transcription elongation factor greA (Transcript cleavage factor greA) | | | | |
| 9387, 9388 | 9654693 | 44 | 6.00E-27 | Vibrio cholerae O1 biovar eltor str. N16961 | methyl-accepting chemotaxis protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229938.1 methyl-accepting chemotaxis protein [Vibrio cholerae O1 biovar eltor str. N16961] pir F82342 methyl-accepting chemotaxis protein VC0282 [imported] - Vibrio cholerae (strain N16961 serogroup O1) | | | 2.7.3.- | |
| 9389, 9390 | 16799970 | 53 | 1.00E-37 | Listeria innocua Clip11262 | hypothetical protein lin0897 [Listeria innocua Clip11262] emb CAC96129.1 lin0897 [Listeria innocua] pir A11544 conserved hypothetical protein lin0897 [Imported] - Listeria innocua (strain Clip11262) | | | | |
| 939, 940 | 46114100 | 34 | 9.00E-25 | Exiguobacterium sp. 255-15 | COG2357: Uncharacterized protein conserved in bacteria [Exiguobacterium sp. 255-15] | | | | |
| 9395, 9396 | 53711901 | 60 | 9.00E-93 | Bacteroides fragilis YCH46 | threonine synthase [Bacteroides fragilis YCH46] dbj BAD47359.1 threonine synthase [Bacteroides fragilis YCH46] | | | 4.2.99.2 | |
| 9397, 9398 | 48853586 | 68 | 7.00E-73 | Cytophaga hutchinsonii | COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga hutchinsonii] | Buchnera aphidicola str. Sg (Schizaphis graminum) section 47 of 57 of the complete genome | 86 | 7.00E-123 | 3.4.21.5 |
| 9399, 9400 | 53682950 | 27 | 2.00E-12 | Desulfotobacterium hafnense DCB-2 | COG1506: Dipeptidyl aminopeptidases/acylaminoacyl-peptidases [Desulfotobacterium hafnense DCB-2] | | | | |
| 9403, 9404 | 53712001 | 33 | 8.00E-37 | Bacteroides fragilis YCH46 | DNA polymerase III alpha subunit [Bacteroides fragilis YCH46] dbj BAD47459.1 DNA polymerase III alpha subunit [Bacteroides fragilis YCH46] | | | | 2.7.7.7 |

| | | | | | | | | |
|--------------------------------|----------|----|-----------|---|--|--|--|----------|
| 9407, 9408 | 33594842 | 59 | 1.00E-98 | Bordetella parapertussis 12822 | putative asparagine synthetase [Bordetella parapertussis 12822] emb CAE39864.1 putative asparagine synthetase [Bordetella parapertussis] | | | 6.3.5.4 |
| 9409, 9410, 9411, 942 | 6968464 | 40 | 2.00E-30 | Campylobacter jejuni subsp. jejuni NCTC 11168 | possible purine/pyrimidine phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81305 probable purine/pyrimidine phosphoribosyltransferase Cj1028c [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282178.1 possible purine/pyrimidine phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] | | | |
| 9411, 942 | 48864233 | 42 | 6.00E-20 | Microbulbifer degradans 2-40 | COG0845: Membrane-fusion protein [Microbulbifer degradans 2-40] | | | |
| 9411, 9412 | 57241187 | 52 | 1.00E-73 | Campylobacter lari RM2100 | glutamyl-tRNA synthetase [Campylobacter lari RM2100] gb EAL54883.1 glutamyl-tRNA synthetase [Campylobacter lari RM2100] | | | 6.1.1.17 |
| 9415, 9416 | 34558436 | 45 | 2.00E-57 | Wolinella succinogenes DSM 1740 | FERROCHELATASE LIKE PROTEIN, HemH [Wolinella succinogenes DSM 1740] emb CAE11151.1 FERROCHELATASE LIKE PROTEIN, HemH [Wolinella succinogenes] sp Q7M7P9 HEMZ_WOLSU Ferrochelatase (Protoheme ferro-lyase) (Heme synthetase) | | | 4.99.1.1 |
| 9417, 9418 | 46142296 | 60 | 1.00E-106 | Methanococcoides burtonii DSM 6242 | COG4804: Uncharacterized conserved protein [Methanococcoides burtonii DSM 6242] | | | |
| 9421, 9422 | 42523963 | 29 | 7.00E-17 | Bdellovibrio bacteriovorus HD100 | hypothetical protein Bc2538 [Bdellovibrio bacteriovorus HD100] emb CAE80336.1 hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100] | | | |
| 9423, 9424 | 34556564 | 51 | 3.00E-75 | Wolinella succinogenes DSM 1740 | PUTATIVE OXIDOREDUCTASE [Wolinella succinogenes DSM 1740] emb CAE09279.1 PUTATIVE OXIDOREDUCTASE [Wolinella succinogenes] | | | 1.-.- |
| 9425, 9426 | 11500024 | 28 | 4.00E-19 | Archaeoglobus fulgidus DSM 4304 | spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine- binding protein:(potD) [Archaeoglobus fulgidus DSM 4304] | | | |
| 9427, 9428 | 18976874 | 33 | 9.00E-11 | Pyrococcus furius DSM 3638 | iron(III) dicitrate transport system permease protein fece [Pyrococcus furius DSM 3638] gb AAL80626.1 iron(III) dicitrate transport system permease protein fece [Pyrococcus furius DSM 3638] | | | |
| 9429, 9430 | 15644626 | 43 | 4.00E-55 | Thermotoga maritima MSB8 | transketolase, N-terminal subunit [Thermotoga maritima MSB8] | | | 2.2.1.1 |
| 943, 944 | 53713329 | 30 | 7.00E-30 | Bacteroides fragilis YCH46 | putative two-component system sensor histidine kinase [Bacteroides fragilis YCH46] dbj BAD48787.1 putative two-component system sensor histidine kinase [Bacteroides fragilis YCH46] | | | 2.7.3.- |
| 9431, 9432 | 34557407 | 43 | 1.00E-35 | Wolinella succinogenes DSM 1740 | DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] | | | 2.7.3.- |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|----|-------------------|
| 9433, 9434 | 34557728 | 34 | 7.00E-19 | Wolinella succinogenes DSM 1740 | CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wolinella succinogenes DSM 1740] emb CAE10443.1 CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wolinella succinogenes] | | | |
| 9437, 9438 | 57169066 | 26 | 2.00E-23 | Campylobacter coli RM2228 | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56215.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | |
| 9439, 9440 | 48860369 | 31 | 2.00E-19 | Clostridium thermocellum ATCC 27405 | COG4585: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405] | | | 2.7.3.- |
| 9443, 9444 | 34557809 | 68 | 2.00E-85 | Wolinella succinogenes DSM 1740 | ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10524.1 ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wolinella succinogenes] | Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 4/6 | 82 | 2.00E-09 1.8.-.- |
| 9445, 9446 | 57285504 | 56 | 2.00E-30 | Staphylococcus aureus subsp. aureus COL | type I restriction-modification system, S subunit, EcoA family, putative [Staphylococcus aureus subsp. aureus COL] ref NP_373643.1 probable restriction modification system specificity subunit [Staphylococcus aureus subsp. aureus N315] db BAB56594.1 probable restriction modification system specificity subunit [Staphylococcus aureus subsp. aureus Mu50] pir B89808 hypothetical protein hsdS [imported] - Staphylococcus aureus (strain N315) db BAB41621.1 probable restriction modification system specificity subunit [Staphylococcus aureus subsp. aureus N315] ref NP_370956.1 probable restriction modification system specificity subunit [Staphylococcus aureus subsp. aureus Mu50] ref YP_185367.1 type I restriction-modification system, S subunit, EcoA family, putative [Staphylococcus aureus subsp. aureus COL] | Desc:Staphylococ- cus aureus contig SEQ ID #546. Org:Staphylococcus aureus | 87 | 5.00E-10 3.1.21.3 |
| 9447, 9448 | 48855054 | 50 | 3.00E-22 | Cytophaga hutchinsonii | COG0491: Zn-dependent hydrolases, including glyoxylases [Cytophaga hutchinsonii] | | | 3.1.2.6 |
| 945, 946 | 15678643 | 45 | 4.00E-53 | Methanothermobac- ter thermautotrophicus str. Delta H | adenylosuccinate synthetase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85121.1 adenylosuccinate synthetase [Methanothermobacter thermautotrophicus str. Delta H] pir G69181 adenylosuccinate synthetase - Methanothermobacterium thermautotrophicum (strain Delta H) sp Q26712 PURA_METTH Adenylosuccinate synthetase (IMP-aspartate ligase) (AdSS) (AMPSase) | | | 6.3.4.4 |
| 9453, 9454 | 34557754 | 45 | 1.00E-65 | Wolinella succinogenes DSM 1740 | TRANSCRIPTIONAL REGULATOR (NIFA FAMILY) [Wolinella succinogenes DSM 1740] emb CAE10469.1 TRANSCRIPTIONAL REGULATOR (NIFA FAMILY) [Wolinella succinogenes] | | | 2.7.3.9 |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|---------------|--|--|
| 9455, 9456 | 46142296 | 74 | 3.00E-74 | Methanococcoides burtonii DSM 6242 | COG4804: Uncharacterized conserved protein [Methanococcoides burtonii] DSM 6242] | | | |
| 9457, 9458 | 34557246 | 27 | 8.00E-34 | Wolinella succinogenes DSM 1740 | SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] embiCAE09961.1] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes] | 2.7.3.- | | |
| 9459, 9460 | 34557573 | 49 | 6.00E-75 | Wolinella succinogenes DSM 1740 | SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] embiCAE10288.1] SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes] | 2.7.3.- | | |
| 9461, 9462 | 57241121 | 43 | 9.00E-41 | Campylobacter lari RM2100 | DNA repair protein RecN, putative [Campylobacter lari RM2100] gb[EAL54817.1] DNA repair protein RecN, putative [Campylobacter lari RM2100] | | | |
| 9463, 9464 | 57505936 | 27 | 2.00E-13 | Campylobacter upsallensis RM3195 | hypothetical protein CUPA0072 [Campylobacter upsallensis RM3195] gb[EAL52526.1] hypothetical protein CUPA0072 [Campylobacter upsallensis RM3195] | 2.1.1.11 3 | | |
| 9465, 9466 | 20089049 | 28 | 5.00E-15 | Methanosarcina acetivorans C2A | hypothetical protein MA0151 [Methanosarcina acetivorans C2A] gb/AAM03604.1] predicted protein [Methanosarcina acetivorans str. C2A] | | | |
| 9467, 9468 | 45524150 | 63 | 6.00E-81 | Crocospaera watsonii WH 8501 | COG0674: Pyruvate:ferredoxin oxidoreductase and related 2- oxoacid:ferredoxin oxidoreductases, alpha subunit [Crocospaera watsonii WH 8501] | 1.2.7.1 | | |
| 9469, 9470 | 53731591 | 48 | 5.00E-27 | Methanococcoides burtonii DSM 6242 | COG0784: FOG: CheY-like receiver [Methanococcoides burtonii DSM 6242] putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482] gb/AAO77165.1] putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482] | 2.7.3.- | | |
| 947, 948 | 29347468 | 49 | 1.00E-50 | Bacteroides thetaitotaomicron VPI-5482 | EXBDITOLR FAMILY TRANSPORT PROTEIN [Wolinella succinogenes DSM 1740] embiCAE09656.1] EXBDITOLR FAMILY TRANSPORT PROTEIN [Wolinella succinogenes] | 2.5.1.1 | | |
| 9471, 9472 | 34556941 | 46 | 1.00E-26 | Wolinella succinogenes DSM 1740 | Glu-tRNA amidotransferase (gatB) [Methanocaldococcus jannaschii DSM 2661] gb/AA097995.1] Glu-tRNA amidotransferase (gatB) [Methanocaldococcus jannaschii DSM 2661] sp Q60325 GATE_METJA Glutaryl-tRNA(Gln) amidotransferase subunit E (Glu-ADT subunit E) p f C64302 hypothetical protein MJ0019 - Methanococcus jannaschii hypothetical protein BT4316 [Bacteroides thetaiotaomicron VPI-5482] gb/AAO79421.1] conserved hypothetical protein [Bacteroides thetaitotaomicron VPI-5482] | 6.3.5.- | | |
| 9473, 9474 | 15668190 | 37 | 2.00E-42 | Methanocaldococ us jannaschii DSM 2661 | prespore protein MF12 [Dictyostellium discoideum] | | | |
| 9475, 9476 | 29349724 | 31 | 8.00E-16 | Bacteroides thetaitotaomicron VPI-5482 | | | | |
| 9477, 9478 | 7595998 | 33 | 3.00E-07 | Dictyostellium discoideum | | | | |

| | | | | | | | | | |
|------------|----------|----|----------|------------------------------------|--|--|--|--|----------|
| 9479, 9480 | 15606976 | 32 | 8.00E-18 | Aquifex aeolicus VF5 | hypothetical protein aq_1980 [Aquifex aeolicus VF5] gb AAC07760.1 hypothetical protein [Aquifex aeolicus VF5] pir A70470 conserved hypothetical protein aq_1980 - Aquifex aeolicus | | | | |
| 9481, 9482 | 45527937 | 31 | 7.00E-30 | Crocospaera watsonii WH 8501 | COG0471: Di- and tricarboxylate transporters [Crocospaera watsonii WH 8501] | | | | |
| 9485, 9486 | 1197006 | 50 | 8.00E-56 | Bacteroides fragilis | unknown protein [Bacteroides fragilis] gb AAA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 [Transposon TN4551] | | | | |
| 9487, 9488 | 53756727 | 22 | 6.00E-16 | Methylococcus capsulatus str. Bath | conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_115226.1 hypothetical protein MCA2832 [Methylococcus capsulatus str. Bath] | | | | |
| 9489, 9490 | 48845594 | 21 | 3.00E-12 | Geobacter metallireducens GS | COG1538: Outer membrane protein [Geobacter metallireducens GS-15] | | | | |
| 949, 950 | 32041369 | 37 | 3.00E-40 | Pseudomonas aeruginosa UCBPP-PA14 | COG1864: DNA/RNA endonuclease G, NUC1 [Pseudomonas aeruginosa UCBPP-PA14] | | | | |
| 9491, 9492 | 53711426 | 34 | 3.00E-26 | Bacteroides fragilis YCH46 | hypothetical protein BF0135 [Bacteroides fragilis YCH46] dbj BAD46884.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 9493, 9494 | 18309802 | 32 | 6.00E-24 | Clostridium perfringens str. 13 | hypothetical protein CPE0820 [Clostridium perfringens str. 13] dbj BAB80526.1 conserved hypothetical protein [Clostridium perfringens str. 13] | | | | |
| 9495, 9496 | 34557163 | 37 | 2.00E-24 | Wollinella succinogenes DSM 1740 | PUTATIVE PHOSPHATE ABC TRANSPORTER [Wollinella succinogenes DSM 1740] emb CAE09878.1 PUTATIVE PHOSPHATE ABC TRANSPORTER [Wollinella succinogenes] | | | | |
| 9499, 9500 | 34557678 | 36 | 4.00E-46 | Wollinella succinogenes DSM 1740 | hypothetical protein WS1317 [Wollinella succinogenes DSM 1740] emb CAE10393.1 conserved hypothetical protein [Wollinella succinogenes] | | | | |
| 95, 96 | 53731382 | 62 | 9.00E-67 | Methanococcus burtonii DSM 6242 | COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Methanococcus burtonii DSM 6242] | | | | 3.1.21.3 |
| 9503, 9504 | 34557782 | 43 | 5.00E-31 | Wollinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes] | | | | 2.7.3.- |
| 9509, 9510 | 34558486 | 31 | 2.00E-18 | Wollinella succinogenes DSM 1740 | POLYPEPTIDE DEFORMYLASE PDF FORMYL METHIONINE DEFORMYLASE [Wollinella succinogenes DSM 1740] emb CAE11201.1 POLYPEPTIDE DEFORMYLASE PDF FORMYL METHIONINE DEFORMYLASE [Wollinella succinogenes] sp Q7M7M2 DEF_WOLSU Peptide deformylase (PDF) (Polypeptide deformylase) | | | | 3.5.1.88 |

| | | | | | | | | |
|---------------|----------------------|----------|----------------------|---|--|--|--|----------------|
| 951, 952 | 30018489 | 60 | 5.00E-99 | Bacillus cereus ATCC 14579 | 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579] gb AAP07321.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579] | | | 1.13.11. 27 |
| 9511, 9512 | | | | | conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228] | | | |
| 9513, 9514 | 57169064 53714701 | 34 48 | 2.00E-20 2.00E-51 | Campylobacter coli RM2228 Bacteroides fragilis YCH46 | histidyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD50159.1 histidyl-tRNA synthetase [Bacteroides fragilis YCH46] | | | 6.1.1.21 |
| 9515, 9516 | | | | Bacteroides thetataoamicron VPI-5482 | histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76947.1 histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI- 5482] sp Q8A6N7 SYH_BACTN Histidyl-tRNA synthetase (Histidine--tRNA ligase) (HisRS) | | | 6.1.1.21 |
| 9517, 9518 | 29347250 | 70 | 1.00E-66 | Wolnella succinogenes DSM 1740 | conserved hypothetical protein-SAM dependent methyltransferases [Wolnella succinogenes DSM 1740] emb CAE10924.1 conserved hypothetical protein-SAM dependent methyltransferases [Wolnella succinogenes] | | | 2.1.1.52 |
| 9521, 9522 | 34558209 57236932 | 42 43 | 6.00E-44 6.00E-46 | Campylobacter jejuni RM1221 | cytochrome c551 peroxidase [Campylobacter jejuni RM1221] gb AAW34515.1 cytochrome c551 peroxidase [Campylobacter jejuni RM1221] | | | 1.11.1.5 |
| 9523, 9524 | | | | Pseudomonas syringae pv. syringae B728a | COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Pseudomonas syringae pv. syringae B728a] | | | |
| 9525, 9526 | 46142516 | 54 | 9.00E-67 | Methanococcoides burtonii DSM 6242 | COG0399: Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis [Methanococcoides burtonii DSM 6242] | | | |
| 9527, 9528 | | | | Wolnella succinogenes DSM 1740 | FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolnella succinogenes DSM 1740] emb CAE09765.1 FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolnella succinogenes] | | | |
| 9529, 9530 | 34557050 48833354 | 49 28 | 4.00E-25 1.00E-19 | Magnetococcus sp. MC-1 | COG1309: Transcriptional regulator [Magnetococcus sp. MC-1] | | | |
| 9531, 9532 | 52006058 | 23 | 1.00E-08 | Thiobacillus denitrificans ATCC 25259 | COG2128: Uncharacterized conserved protein [Thiobacillus denitrificans ATCC 25259] | | | |
| 9533, 9534 | | | | Wolnella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolnella succinogenes DSM 1740] emb CAE10068.1 GGDEF FAMILY PROTEIN [Wolnella succinogenes] | | | |
| 9535, 9536 | 34557353 53714372 | 34 26 | 3.00E-38 5.00E-10 | Bacteroides fragilis YCH46 | hypothetical protein BF5085 [Bacteroides fragilis YCH46] dbj BAD49830.1 hypothetical protein [Bacteroides fragilis YCH46] | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|---|---|--|--|--|---------------|
| 9537, 9538 | 56421836 | 44 | 1.00E-48 | Geobacillus kaustophilus HTA426 | transposase [Geobacillus kaustophilus HTA426] ref YP_148757.1 transposase [Geobacillus kaustophilus HTA426] ref YP_146188.1 transposase [Geobacillus kaustophilus HTA426] dbj BAD77586.1 transposase [Geobacillus kaustophilus HTA426] dbj BAD77189.1 transposase [Geobacillus kaustophilus HTA426] dbj BAD74620.1 transposase [Geobacillus kaustophilus HTA426] | | | | |
| 9539, 9540 | 45658394 | 33 | 4.00E-12 | Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 | hypothetical protein LIC12553 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711308.1 hypothetical protein LA1128 [Leptospira interrogans serovar Lai str. 56601] gb AAAN48327.1 unknown protein [Leptospira interrogans serovar lai str. 56601] gb AAS71117.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | | |
| 9541, 9542 | 53713469 | 37 | 1.00E-17 | Bacteroides fragilis YCH46 | putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46] | | | | 3.6.1.- |
| 9543, 9544 | 27367788 | 56 | 4.00E-48 | Vibrio vulnificus CMCP6 | 3,4-dihydroxy-2-butanone 4-phosphate synthase [Vibrio vulnificus CMCP6] ref NP_936316.1 3,4-dihydroxy-2-butanone 4-phosphate synthase [Vibrio vulnificus YJ016] gb AAO08305.1 3,4-dihydroxy-2-butanone 4-phosphate synthase [Vibrio vulnificus CMCP6] sp Q7MFR0 RIBB_VIBVY 3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase) sp Q8D485 RIBB_VIBVU 3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase) dbj BAC96286.1 3,4-dihydroxy-2-butanone 4-phosphate synthase [Vibrio vulnificus YJ016] | | | | 3.5.4.25 |
| 9547, 9548 | 23015349 | 53 | 3.00E-68 | Magnetospirillum magnetotacticum MS-1 | COG1032: Fe-S oxidoreductase [Magnetospirillum magnetotacticum MS-1] | | | | 1.97.1.4 |
| 9549, 9550 | 34556398 | 51 | 4.00E-52 | Wolinella succinogenes DSM 1740 | PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE11113.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes] | | | | 4.2.1.70 |
| 955, 956 | 32476719 | 46 | 7.00E-64 | Rhodopirella baltica SH 1 | putative oxidoreductase [Rhodopirella baltica SH 1] emb CAD77091.1 putative oxidoreductase [Pirella sp.] | | | | 1.-.-.- |
| 9553, 9554 | 34556517 | 48 | 7.00E-19 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0063 [Wolinella succinogenes DSM 1740] emb CAE09232.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 9555, 9556 | 57167724 | 43 | 4.00E-31 | Campylobacter coli RM2228 | 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228] gb EAL57510.1 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228] | | | | |
| 9557, 9558 | 53713881 | 50 | 1.00E-47 | Bacteroides fragilis YCH46 | 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [Bacteroides fragilis YCH46] dbj BAD49339.1 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [Bacteroides fragilis YCH46] | | | | 2.7.1.14 8 |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|----------|----------|
| 9559, 9560 | 57240278 | 28 | 7.00E-20 | Campylobacter lari RM2100 | probable transcription regulator Cj0571 [Campylobacter lari RM2100] gb EAL55392.1 probable transcription regulator Cj0571 [Campylobacter lari RM2100] | | | |
| 9565, 9566 | 20806611 | 25 | 7.00E-15 | Thermoanaerobact er tengcongensis MB4 | Transcriptional regulator [Thermoanaerobacter tengcongensis MB4] gb AAM23386.1 Transcriptional regulator [Thermoanaerobacter tengcongensis MB4] | | | |
| 9567, 9568 | 48854159 | 36 | 7.00E-28 | Cytophaga hutchinsonii | COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii] deoxyguanosinetriphosphate triphosphohydrolase [Pseudomonas aeruginosa PAO1] pir H83505 deoxyguanosinetriphosphate triphosphohydrolase PA1124 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_249815.1 deoxyguanosinetriphosphate triphosphohydrolase [Pseudomonas aeruginosa PAO1] sp Q9J4L1 DGTP_PSEAE Probable deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase) | | 3.1.1.24 | |
| 9569, 9570 | 9947043 | 53 | 3.00E-45 | Pseudomonas aeruginosa PAO1 | PHOSPHOENOLPYRUVATE SYNTHASE [Wolinnella succinogenes DSM 1740] emb CAE09937.1 PHOSPHOENOLPYRUVATE SYNTHASE [Wolinnella succinogenes] | | | 3.1.5.1 |
| 9571, 9572 | 34557222 | 61 | 2.00E-83 | Wolinnella succinogenes DSM 1740 | COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family [Burkholderia cepacia R1808] | | | 2.7.9.2 |
| 9573, 9574 | 46321918 | 61 | 4.00E-47 | Burkholderia cepacia R1808 | GDP-mannose pyrophosphorylase homolog [Actinobacillus actinomycetemcomitans] | | | 5.2.1.8 |
| 9575, 9576 | 7592813 | 49 | 2.00E-77 | Actinobacillus actinomycetemcom itans | ExsB protein [Chlorobium tepidum TLS] gb AAM71774.1 ExsB protein [Chlorobium tepidum TLS] | | | 2.7.7.22 |
| 9577, 9578 | 21673367 | 59 | 7.00E-49 | Chlorobium tepidum TLS | ABC transporter [Bacillus licheniformis ATCC 14580] gb AAU21793.1 ABC transporter [Bacillus licheniformis ATCC 14580] ref YP_089831.1 YbaE [Bacillus licheniformis ATCC 14580] gb AAU39138.1 YbaE [Bacillus licheniformis DSM 13] | | | 1.8.-.- |
| 9579, 9580 | 52078640 | 49 | 3.00E-64 | Bacillus licheniformis ATCC 14580 | hypothetical protein ECA1089 [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG74000.1 hypothetical protein [Erwinia carotovora subsp. atroseptica SCRI1043] | | | |
| 9581, 9582 | 50120029 | 21 | 3.00E-07 | Erwinia carotovora subsp. atroseptica SCRI1043 | hypothetical protein WS0453 [Wolinnella succinogenes DSM 1740] emb CAE09595.1 hypothetical protein [Wolinnella succinogenes] | | | |
| 9583, 9584 | 34556880 | 27 | 1.00E-10 | Wolinnella succinogenes DSM 1740 | PREDICTED TRANSCRIPTIONAL REGULATOR [Wolinnella succinogenes DSM 1740] emb CAE10254.1 PREDICTED TRANSCRIPTIONAL REGULATOR [Wolinnella succinogenes] | | | |
| 9585, 9586 | 34557539 | 45 | 2.00E-24 | Wolinnella succinogenes DSM 1740 | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|--|-------------|----------|
| 9587, 9588 | 34556543 | 62 | 2.00E-71 | Wolinella succinogenes DSM 1740 | PUTATIVE PHOSPHOHYDROLASE [Wolinella succinogenes DSM 1740] emb CAE09258.1 PUTATIVE PHOSPHOHYDROLASE [Wolinella succinogenes] sp Q7MAQ8 HIS2_WOLSU Histidine biosynthesis bifunctional protein hisIE [includes: Phosphoribosyl-AMP cyclohydrolase (PRA-CH); Phosphoribosyl-ATP pyrophosphatase (PRA-PH)] | | | 3.5.4.19 |
| 959, 960 | 48854559 | 50 | 3.00E-38 | Cytophaga hutchinsonii | COG1162: Predicted GTPases [Cytophaga hutchinsonii] | | | |
| 9591, 9592 | 47569586 | 25 | 2.00E-17 | Bacillus cereus G9241 | sporulation kinase [Bacillus cereus G9241] gb EAL12142.1 sporulation kinase [Bacillus cereus G9241] | | | 2.7.3.- |
| 9593, 9594 | 34557851 | 39 | 2.00E-49 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1518 [Wolinella succinogenes DSM 1740] emb CAE10566.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 9595, 9596 | 32262690 | 44 | 6.00E-46 | Helicobacter hepaticus ATCC 51449 | transaldolase [Helicobacter hepaticus ATCC 51449] ref NP_860671.1 transaldolase [Helicobacter hepaticus ATCC 51449] | | | 2.2.1.2 |
| 9597, 9598 | 1197006 | 54 | 1.00E-60 | Bacteroides fragilis Wolinella succinogenes DSM 1740 | unknown protein [Bacteroides fragilis] gb AA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 [Transposon TN4551] | Vibrio vulnificus CMCP6 chromosome I section 9 of 11 of the complete sequence | 85 2.00E-09 | |
| 9601, 9602 | 34556843 | 39 | 1.00E-41 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0414 [Wolinella succinogenes DSM 1740] emb CAE09558.1 conserved hypothetical protein [Wolinella succinogenes] | | | 2.7.3.- |
| 9603, 9604 | 48833864 | 47 | 7.00E-30 | Magnetococcus sp. MC-1 | COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Magnetococcus sp. MC-1] | | | 2.7.3.- |
| 9607, 9608 | 23501737 | 66 | 8.00E-37 | Brucella suis 1330 | ribulose-phosphate 3-epimerase [Brucella suis 1330] gb AAN29779.1 ribulose-phosphate 3-epimerase [Brucella suis 1330] | | | 5.1.3.1 |
| 9611, 9612 | 23127382 | 26 | 6.00E-12 | Nostoc punctiforme PCC 73102 | COG0419: ATPase involved in DNA repair [Nostoc punctiforme PCC 73102] | | | 3.1.11.- |
| 9615, 9616 | 48844618 | 42 | 3.00E-55 | Geobacter metallireducens GS-15 | COG2902: NAD-specific glutamate dehydrogenase [Geobacter metallireducens GS-15] | | | 1.4.1.2 |
| 9621, 9622 | 34557571 | 58 | 5.00E-85 | Wolinella succinogenes DSM 1740 | GLUTAMATE SYNTHASE, LARGE SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10286.1 GLUTAMATE SYNTHASE, LARGE SUBUNIT [Wolinella succinogenes] | | | 1.4.1.13 |
| 9623, 9624 | 57238620 | 47 | 6.00E-38 | Campylobacter jejuni RM1221 | ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221] gb AAW36203.1 ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221] | | | 2.7.7.60 |

| | | | | | | | | |
|---------------|----------|----|----------|--|---|--|--|-----------|
| 9625, 9626 | 57240551 | 61 | 1.00E-80 | Campylobacter lari RM2100 | conserved hypothetical integral membrane protein [Campylobacter lari RM2100] gb EAL55665.1 conserved hypothetical integral membrane protein [Campylobacter lari RM2100] | | | |
| 9627, 9628 | 57242456 | 27 | 8.00E-13 | Campylobacter upsaliensis RM3195 | probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195] gb EAL53524.1 probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195] | | | |
| 9629, 9630 | 34558270 | 37 | 2.00E-14 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1982 [Wolinella succinogenes DSM 1740] emb CAE10985.1 hypothetical protein [Wolinella succinogenes] transcriptional regulator YtrA [Bacillus licheniformis ATCC 14580] gb AAU24683.1 transcriptional regulator YtrA [Bacillus licheniformis ATCC 14580] ref YP_092738.1 YtrA [Bacillus licheniformis ATCC 14580] gb AAU42045.1 YtrA [Bacillus licheniformis DSM 13] hypothetical protein PBPR80876 [Photobacterium profundum SS9] emb CAG22748.1 hypothetical protein [Photobacterium profundum] | | | |
| 9631, 9632 | 52081530 | 46 | 1.00E-14 | Bacillus licheniformis ATCC 14580 | hypothetical protein wblA [imported] - Vibrio cholerae dbj BAA33632.1 probable beta-D-galactoside 2-alpha-L-fucosyl transferase [Vibrio cholerae] hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4] gb AAM25797.1 hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4] | | | 2.4, 1.69 |
| 9633, 9634 | 11282475 | 39 | 9.00E-56 | Thermoanaerobact er tengcongensis MB4 | ABC transporter, ATP-binding protein [Methanosarcina acetivorans C2A] gb AAM07031.1 ABC transporter, ATP-binding protein [Methanosarcina acetivorans str. C2A] | | | 1.8, -- |
| 9635, 9636 | 20809022 | 24 | 2.00E-08 | Methanosarcina acetivorans C2A | pxo1-13 [Bacillus anthracis] gb AAD32317.1 pxo1-13 [Bacillus anthracis] pir E55992 hypothetical protein pxo1-13 - Bacillus anthracis virulence plasmid pXO1 | | | |
| 9637, 9638 | 20092476 | 42 | 5.00E-31 | Bacillus anthracis Wolinella succinogenes DSM 1740 | SULFATE ADENYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10944.1 SULFATE ADENYLTRANSFERASE [Wolinella succinogenes] | | | 2.7, 7.4 |
| 9639, 9640 | 10956260 | 29 | 1.00E-17 | Acinetobacter sp. ADP1 | cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyrinic acid synthase | | | 3, --, -- |
| 9641, 9642 | 34558229 | 46 | 8.00E-46 | Wolinella succinogenes DSM 1740 | MOLYBDENUM-PTERIN-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10827.1 MOLYBDENUM-PTERIN-BINDING PROTEIN [Wolinella succinogenes] | | | |
| 9645, 9646 | 50084270 | 53 | 8.00E-68 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96234.1 site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | |
| 9647, 9648 | 34558112 | 47 | 8.00E-20 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | | | | |
| 9649, 9650 | 46580167 | 22 | 2.00E-08 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|---------------|
| 965, 966 | 39996205 | 63 | 4.00E-69 | Geobacter sulfurreducens PCA | long-chain-fatty-acid-CoA ligase, putative [Geobacter sulfurreducens PCA] gb AAR34429.1 long-chain-fatty-acid-CoA ligase, putative [Geobacter sulfurreducens PCA] | | | 6.2.1.3 |
| 9651, 9652 | 48831352 | 31 | 2.00E-17 | Magnetococcus sp. MC-1 | COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] | | | |
| 9653, 9654 | 42524060 | 47 | 1.00E-38 | Bdellovibrio bacteriovorus HD100 | adenylate cyclase [Bdellovibrio bacteriovorus HD100] emb CAE80433.1 adenylate cyclase [Bdellovibrio bacteriovorus HD100] | | | 4.6.1.1 |
| 9655, 9656 | 48853682 | 31 | 2.00E-09 | Cytophaga hutchinsonii | COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Cytophaga hutchinsonii] | | | 2.3.1.51 |
| 9657, 9658 | 46118958 | 48 | 6.00E-41 | Crocospaera watsonii WH 8501 | COG2081: Predicted flavoproteins [Crocospaera watsonii WH 8501] | | | |
| 9659, 9660 | 46578435 | 38 | 2.00E-60 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94502.1 methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | 2.7.3.- |
| 9661, 9662 | 47779389 | 52 | 2.00E-63 | uncultured gamma proteobacterium eBACHOT4E07 | predicted HsdM [uncultured gamma proteobacterium eBACHOT4E07] PANTOTHENATE METABOLISM FLAVOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE11060.1 PANTOTHENATE METABOLISM FLAVOPROTEIN [Wolinella succinogenes] | | | 2.1.1.72 |
| 9663, 9664 | 34558345 | 43 | 3.00E-24 | succinogenes DSM 1740 | | | | 6.3.2.5 |
| 9665, 9666 | 46579872 | 28 | 1.00E-27 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | glutamyl-tRNA reductase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS95939.1 glutamyl-tRNA reductase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | 1.2.1.- |
| 9667, 9668 | 56964394 | 31 | 6.00E-15 | Bacillus clausii KSM-K16 | uroporphyrinogen III cosynthase [Bacillus clausii KSM-K16] dbj BAD65164.1 uroporphyrinogen III cosynthase [Bacillus clausii KSM-K16] | | | 4.2.1.75 |
| 9669, 9670 | 34557978 | 38 | 2.00E-57 | Wolinella succinogenes DSM 1740 | PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10693.1 PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes] | | | 2.3.2.- |
| 967, 968 | 23128197 | 45 | 3.00E-75 | Nostoc punctiforme PCC 73102 | COG1505: Serine proteases of the peptidase family S9A [Nostoc punctiforme PCC 73102] | | | 3.4.21.2 6 |
| 9671, 9672 | 32263303 | 55 | 2.00E-25 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861282.1 hypothetical protein HH1751 [Helicobacter hepaticus ATCC 51449] | | | 3.1.-.- |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|----|------------------|
| 9673, 9674 | 29345875 | 56 | 1.00E-35 | Bacteroides thetaiotaomicron VPI-5482 | dTDP-4-dehydrohamnose reductase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75572.1 dTDP-4-dehydrohamnose reductase [Bacteroides thetaiotaomicron VPI-5482] | | | 1.1.1.13 3 |
| 9675, 9676 | 45250013 | 66 | 2.00E-47 | Aneurinibacillus thermoaerophilus | dTDP-glucose 4,6-dehydratase [Aneurinibacillus thermoaerophilus] | | | 4.2.1.46 |
| 9677, 9678 | 56461438 | 63 | 6.00E-72 | Idiomarina loihlensis L2TR | Glutamate dehydrogenase [Idiomarina loihlensis L2TR] gb AAV83170.1 Glutamate dehydrogenase [Idiomarina loihlensis L2TR] | | 87 | 5.00E-07 1.4.1.4 |
| 9679, 9680 | 57242734 | 45 | 8.00E-48 | Campylobacter upsaliensis RM3195 | response regulator, putative [Campylobacter upsaliensis RM3195] gb EAL53447.1 response regulator, putative [Campylobacter upsaliensis RM3195] | | 93 | 2.00E-09 2.7.3.- |
| 9681, 9682 | 57240513 | 41 | 3.00E-33 | Campylobacter lari RM2100 | signal-transducing protein, histidine kinase, putative [Campylobacter lari RM2100] gb EAL55627.1 signal-transducing protein, histidine kinase, putative [Campylobacter lari RM2100] | | | 2.7.3.- |
| 9683, 9684 | 16326479 | 44 | 2.00E-18 | Rhizobium leguminosarum bv. trifolii | ImpC [Rhizobium leguminosarum bv. trifolii] | | | |
| 9685, 9686 | 34557419 | 35 | 1.00E-22 | Wolinella succinogenes DSM 1740 | PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes] | | | 2.7.3.- |
| 9687, 9688 | 34556574 | 25 | 1.00E-10 | Wolinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09289.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] | | | |
| 9689, 9690 | 29346464 | 26 | 3.00E-17 | Bacteroides thetaiotaomicron VPI-5482 | ATP-dependent helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76161.1 ATP-dependent helicase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 969, 970 | 48893318 | 33 | 3.00E-38 | Trichodesmium erythraeum IMS101 | COG0474: Cation transport ATPase [Trichodesmium erythraeum IMS101] | | | 3.6.3.- |
| 9691, 9692 | 34557601 | 40 | 2.00E-20 | Wolinella succinogenes DSM 1740 | hypothetical protein WS1236 [Wolinella succinogenes DSM 1740] emb CAE10316.1 hypothetical protein [Wolinella succinogenes] | | | 2.7.7.7 |
| 9693, 9694 | 18254491 | 33 | 4.00E-09 | Pectobacterium chrysanthemi | invertase [Pectobacterium chrysanthemi] | | | |
| 9695, 9696 | 34557638 | 65 | 3.00E-97 | Wolinella succinogenes DSM 1740 | QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes] | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|-------------|----------|
| 9697, 9698 | 57240463 | 56 | 7.00E-61 | Campylobacter lari RM2100 | aspartate carbamoyltransferase [Campylobacter lari RM2100] gb EAL55577.1 aspartate carbamoyltransferase [Campylobacter lari RM2100] | | | 2.1.3.2 |
| 9699, 9700 | 34558267 | 54 | 5.00E-76 | Wolinnella succinogenes DSM 1740 | PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinnella succinogenes DSM 1740] emb CAE10982.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinnella succinogenes] | | | 4.2.1.70 |
| 9705, 9706 | 50745174 | 33 | 3.00E-18 | Gallus gallus | PREDICTED: similar to L-glutono-gamma-lactone oxidase precursor [Gallus gallus] | | | 1.1.3.8 |
| 9707, 9708 | 54311293 | 37 | 1.00E-21 | Xenopus laevis | Unknown (protein for MGC:86416) [Xenopus laevis] | | | 1.1.3.8 |
| 9709, 9710 | 57241815 | 34 | 1.00E-18 | Campylobacter lari RM2100 | signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54233.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100] | | | 2.7.3.- |
| 971, 972 | 48853467 | 59 | 1.00E-45 | Cytophaga hutchinsonii | COG1473: Metal-dependent amidase/aminoacylase/carboxypeptidase [Cytophaga hutchinsonii] | | | 3.5.1.14 |
| 9711, 9712 | 6978030 | 44 | 3.00E-51 | Desulfovibrio gigas | putative Sol [Desulfovibrio gigas] | | | |
| 9713, 9714 | 57240664 | 25 | 7.00E-12 | Campylobacter lari RM2100 | probable periplasmic protein Cj1621 [Campylobacter lari RM2100] gb EAL55057.1 probable periplasmic protein Cj1621 [Campylobacter lari RM2100] | | | |
| 9715, 9716 | 34558196 | 57 | 7.00E-46 | Wolinnella succinogenes DSM 1740 | DNA PRIMASE PROTEIN [Wolinnella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinnella succinogenes] | Wolinnella succinogenes, complete genome; segment 6/7 | 91 3.00E-07 | 2.7.7.- |
| 9719, 9720 | 21398586 | 32 | 1.00E-31 | Bacillus anthracis str. A2012 | EAL, Domain of unknown function 2 [Bacillus anthracis str. A2012] | | | 2.7.3.- |
| 9721, 9722 | 28850485 | 38 | 2.00E-40 | Pseudomonas syringae pv. tomato str. DC3000 | type I site-specific deoxyribonuclease, HsdR family [Pseudomonas syringae pv. tomato str. DC3000] ref NP_789870.1 type I site-specific deoxyribonuclease, HsdR family [Pseudomonas syringae pv. tomato str. DC3000] | | | 3.1.21.3 |
| 9723, 9724 | 48858979 | 43 | 5.00E-18 | Clostridium thermocellum ATCC 27405 | hypothetical protein Chte02001700 [Clostridium thermocellum ATCC 27405] | | | |
| 9725, 9726 | 15896339 | 32 | 8.00E-17 | Clostridium acetobutylicum ATCC 824 | NtrC family transcriptional regulator, ATPase domain fused to two PAS domains [Clostridium acetobutylicum ATCC 824] gb AAK81028.1 NtrC family transcriptional regulator, ATPase domain fused to two PAS domains [Clostridium acetobutylicum ATCC 824] pir A97280 ntrC family transcription regulator, ATPase domain fused to two PAS domains CAC3088 [imported] - Clostridium acetobutylicum | | | |
| 9727, 9728 | 48864065 | 47 | 1.00E-29 | Microbulifer degradans 2-40 | COG0328: Ribonuclease HI [Microbulifer degradans 2-40] | | | 3.1.26.4 |

| | | | | | | | | |
|---------------|----------|----|-----------|--|---|---|-------------|----------|
| 9729, 9730 | 34556614 | 57 | 1.00E-69 | Wolinella succinogenes DSM 1740 | CARBOXYNORSPERMIDINE DECARBOXYLASE (NSPC) [Wolinella succinogenes DSM 1740] emb CAE09329.1 CARBOXYNORSPERMIDINE DECARBOXYLASE (NSPC) [Wolinella succinogenes] | | | 4.1.1.- |
| 973, 974 | 23125101 | 35 | 1.00E-12 | Nostoc punctiforme PCC 73102 | COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Nostoc punctiforme PCC 73102] | | | |
| 9731, 9732 | 34556768 | 70 | 1.00E-103 | Wolinella succinogenes DSM 1740 | DIAMINOPELMATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes DSM 1740] emb CAE09483.1 DIAMINOPELMATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes] putative carbonate dehydratase, cynT [Parachlamydia sp. UWE25] emb CAF23782.1 putative carbonate dehydratase, cynT [Parachlamydia sp. UWE25] | | | 4.1.1.20 |
| 9733, 9734 | 46446692 | 42 | 6.00E-39 | Parachlamydia sp. UWE25 | | | | 4.2.1.1 |
| 9735, 9736 | 34557590 | 28 | 2.00E-10 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10305.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes] | | | |
| 9737, 9738 | 57506236 | 62 | 3.00E-67 | Campylobacter upsaliensis RM3195 | malate:quinone oxidoreductase, putative [Campylobacter upsaliensis RM3195] gb EAL52259.1 malate:quinone oxidoreductase, putative [Campylobacter upsaliensis RM3195] | Campylobacter [ejuni subsp. [ejuni] NCTC 11168 complete genome; segment 2/6 | 85 2.00E-10 | 1.1.99.1 |
| 9739, 9740 | 34557590 | 30 | 7.00E-17 | Wolinella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10305.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes] | | | |
| 9743, 9744 | 48856925 | 27 | 2.00E-19 | Cytophaga hutchinsonii | COG1309: Transcriptional regulator [Cytophaga hutchinsonii] | | | |
| 9745, 9746 | 33637041 | 67 | 1.00E-95 | Geobacillus stearothermophilus | glucose-1-phosphate thymidyltransferase [Geobacillus stearothermophilus] SPERMIDINE SYNTHASE SPEE [Wolinella succinogenes DSM 1740] emb CAE11142.1 SPERMIDINE SYNTHASE SPEE [Wolinella succinogenes] sp Q7M7Q6 SPEE_WOLSU Spermidine synthase (Putrescine aminopropyltransferase) (SPDSY) | | | 2.7.7.24 |
| 9749, 9750 | 34558427 | 23 | 3.00E-12 | Wolinella succinogenes DSM 1740 | | | | |
| 9751, 9752 | 48839535 | 28 | 2.00E-24 | Methanosarcina barkeri str. fusaro | COG2202: FOG: PAS/PAC domain [Methanosarcina barkeri str. fusaro] HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] emb CAE80147.1 HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] | | | 2.7.3.- |
| 9757, 9758 | 42523774 | 27 | 1.00E-13 | Bdellovibrio bacteriovorus HD100 | | | | |
| 9765, 9766 | 48855616 | 30 | 9.00E-09 | Cytophaga hutchinsonii | COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii] | | | |

| | | | | | | | | |
|---------------|----------|----|----------|--|--|--|--|----------|
| 9769, 9770 | 51892702 | 54 | 3.00E-77 | Symbiobacterium thermophilum IAM 14863 | putative 4-hydroxybenzoate decarboxylase [Symbiobacterium thermophilum IAM 14863] dbj BAD40549.1 putative 4-hydroxybenzoate decarboxylase [Symbiobacterium thermophilum IAM 14863] | | | 4.1.1.- |
| 977, 978 | 23098370 | 55 | 3.00E-37 | Oceanobacillus ihayensis HTE831 | hypothetical protein OB0915 [Oceanobacillus ihayensis HTE831] dbj BAC12871.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831] | | | |
| 9771, 9772 | 2984569 | 35 | 2.00E-20 | Aquifex aeolicus VF5 | putative protein [Aquifex aeolicus VF5] ref NP_046416.1 hypothetical protein aq_aa25 [Aquifex aeolicus VF5] sp O66416 YZ25_AQUAE Hypothetical protein AA25 | | | |
| 9773, 9774 | 48856863 | 44 | 1.00E-48 | Cytophaga hutchinsonii | COG1073: Hydrolases of the alpha/beta superfamily [Cytophaga hutchinsonii] | | | 3.1.1.5 |
| 9775, 9776 | 56961907 | 40 | 1.00E-34 | Bacillus clausii KSM-K16 | 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase [Bacillus clausii KSM-K16] dbj BAD62668.1 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase [Bacillus clausii KSM-K16] | | | 2.7.7.60 |
| 9777, 9778 | 34555655 | 38 | 2.00E-16 | Wolnella succinogenes DSM 1740 | PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes DSM 1740] emb CAE09280.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes] emb CAD23185.1 putative transcriptional regulator protein [Wolnella succinogenes] | | | |
| 9779, 9780 | 34555981 | 30 | 3.00E-19 | Wolnella succinogenes DSM 1740 | hypothetical protein WS0562 [Wolnella succinogenes DSM 1740] emb CAE09696.1 conserved hypothetical protein [Wolnella succinogenes] | | | |
| 9783, 9784 | 57238505 | 37 | 2.00E-16 | Campylobacter jejuni RM1221 | hypothetical protein CJE1655 [Campylobacter jejuni RM1221] gb AAW36088.1 conserved hypothetical protein [Campylobacter jejuni RM1221] | | | |
| 9785, 9786 | 34397173 | 32 | 5.00E-18 | Porphyromonas gingivalis W83 | ribonucleotide reductase [Porphyromonas gingivalis W83] ref NP_905338.1 ribonucleotide reductase [Porphyromonas gingivalis W83] | | | 1.17.4.1 |
| 9789, 9790 | 48846630 | 50 | 2.00E-75 | Geobacter metallireducens GS-15 | COG1086: Predicted nucleoside-diphosphate sugar epimerases [Geobacter metallireducens GS-15] | | | 4.2.1.- |
| 979, 980 | 23098370 | 58 | 2.00E-32 | Oceanobacillus ihayensis HTE831 | hypothetical protein OB0915 [Oceanobacillus ihayensis HTE831] dbj BAC12871.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831] | | | |
| 9793, 9794 | 56962744 | 53 | 6.00E-73 | Bacillus clausii KSM-K16 | chaperone protein HtpG [Bacillus clausii KSM-K16] dbj BAD63509.1 chaperone protein HtpG [Bacillus clausii KSM-K16] | | | |
| 9795, 9796 | 28211154 | 56 | 3.00E-58 | Clostridium tetani E88 | putative histidine decarboxylase [Clostridium tetani E88] gb AAO36035.1 putative histidine decarboxylase [Clostridium tetani E88] | | | 4.1.1.15 |

| | | | | | | | | | |
|---------------|----------|----|----------|--|--|--|----|----------|----------|
| 9797, 9798 | 18311483 | 29 | 3.00E-17 | Clostridium perfringens str. 13 | leucine aminopeptidase [Clostridium perfringens str. 13] dbj BAB82207.1 leucine aminopeptidase [Clostridium perfringens str. 13] sp Q8XHI3 AMPA_CLOPE Probable cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) | | | | 3.4.11.1 |
| 9799, 9800 | 32261675 | 45 | 2.00E-59 | Helicobacter hepaticus ATCC 51449 | conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_959659.1 hypothetical protein HH0128 [Helicobacter hepaticus ATCC 51449] | Alvinella pompejana epibiont 6C6 fosmid clone 6C6, complete sequence | 87 | 2.00E-09 | 6.3.2.15 |
| 9801, 9802 | 48782408 | 35 | 2.00E-35 | Burkholderia fungorum LB400 | COG0207: Thymidylate synthase [Burkholderia fungorum LB400] | | | | 2.1.1.45 |
| 9805, 9806 | 48863829 | 33 | 1.00E-21 | Microbulbifer degradans 2-40 | COG3769: Predicted hydrolase (HAD superfamily) [Microbulbifer degradans 2-40] | | | | |
| 9807, 9808 | 39995248 | 22 | 6.00E-08 | Geobacter sulfurreducens PCA | hypothetical protein GSU0137 [Geobacter sulfurreducens PCA] gb AAR33472.1 hypothetical protein GSU0137 [Geobacter sulfurreducens PCA] | | | | |
| 981, 982 | 53714045 | 50 | 1.00E-55 | Bacteroides fragilis YCH46 | putative transcriptional regulator for phosphate uptake [Bacteroides fragilis YCH46] dbj BAD49503.1 putative transcriptional regulator for phosphate uptake [Bacteroides fragilis YCH46] | | | | |
| 9811, 9812 | 56542586 | 36 | 2.00E-10 | Zymomonas mobilis subsp. mobilis ZM4 | conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_161851.1 hypothetical protein ZMO0116 [Zymomonas mobilis subsp. mobilis ZM4] | | | | |
| 9817, 9818 | 51243917 | 44 | 4.00E-26 | Desulfotalea psychrophila LSV54 | related to pyruvate formate-lyase activating enzyme [Desulfotalea psychrophila LSV54] emb CAG34794.1 related to pyruvate formate-lyase activating enzyme [Desulfotalea psychrophila LSV54] | | | | 1.97.1.4 |
| 9821, 9822 | 48854003 | 27 | 8.00E-12 | Cytophaga hutchinsonii | hypothetical protein Chuf02003091 [Cytophaga hutchinsonii] | | | | |
| 9823, 9824 | 51891413 | 31 | 2.00E-16 | Symbiobacterium thermophilum IAM 14863 | transposase [Symbiobacterium thermophilum IAM 14863] dbj BAD39260.1 transposase [Symbiobacterium thermophilum IAM 14863] | | | | |
| 9825, 9826 | 57167713 | 49 | 3.00E-33 | Campylobacter coli RM2228 | probable proteinase Cj0701 [Campylobacter coli RM2228] gb EAL57499.1 probable proteinase Cj0701 [Campylobacter coli RM2228] | | | | 3.4.-- |
| 9827, 9828 | 51594858 | 35 | 8.00E-18 | Yersinia pseudotuberculosis IP 32953 | hypothetical protein YPTB0506 [Yersinia pseudotuberculosis IP 32953] emb CAH19746.1 conserved hypothetical protein [Yersinia pseudotuberculosis IP 32953] | | | | |
| 9829, 9830 | 23128114 | 37 | 7.00E-25 | Nostoc punctiforme PCC 73102 | hypothetical protein Npun02002480 [Nostoc punctiforme PCC 73102] | | | | |

| | | | | | | | | | |
|---------------|----------|----|----------|--|---|---|----|----------|----------|
| 983, 984 | 48854219 | 74 | 4.00E-70 | Cytophaga hutchinsonii | COG1117: ABC-type phosphate transport system, ATPase component [Cytophaga hutchinsonii] | Mycobacterium smegmatis Inorganic phosphate transporter operon, complete sequence, PhoU (phoU) gene, complete cds; and unknown genes | 90 | 2.00E-08 | 1.8.- |
| 9831, 9832 | 48766646 | 39 | 3.00E-30 | Rhodospirillum rubrum | COG2902: NAD-specific glutamate dehydrogenase [Rhodospirillum rubrum] | | | | 1.4.1.2 |
| 9833, 9834 | 1197006 | 55 | 3.00E-43 | Bacteroides fragilis | unknown protein [Bacteroides fragilis] gb AA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551) | Vibrio vulnificus CMCP6 chromosome I section 9 of 11 of the complete sequence | 85 | 1.00E-09 | |
| 9835, 9836 | 48853319 | 29 | 3.00E-09 | Cytophaga hutchinsonii | hypothetical protein Chut02003935 [Cytophaga hutchinsonii] | | | | |
| 9837, 9838 | 48855703 | 33 | 1.00E-09 | Cytophaga hutchinsonii | COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii] | | | | 2.7.3.- |
| 9845, 9846 | 48855010 | 56 | 7.00E-29 | Cytophaga hutchinsonii | COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii] | | | | 3.2.1.4 |
| 9847, 9848 | 48855010 | 62 | 8.00E-84 | Cytophaga hutchinsonii | COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii] | | | | 3.2.1.4 |
| 9849, 9850 | 34558823 | 53 | 3.00E-76 | Alvinella pompejana epibiont 7G3 | MutS2 family protein [Alvinella pompejana epibiont 7G3] | | | | |
| 9851, 9852 | 53613159 | 43 | 7.00E-16 | Azotobacter vinelandii | COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Azotobacter vinelandii] | | | | |
| 9853, 9854 | 34557032 | 31 | 5.00E-17 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0616 [Wolinella succinogenes DSM 1740] emb CAE09747.1 conserved hypothetical protein [Wolinella succinogenes] | | | | |
| 9857, 9858 | 47459024 | 39 | 2.00E-11 | Mycoplasma mobile 163K | protoporphyrinogen oxidase [Mycoplasma mobile 163K] gb AAT27675.1 protoporphyrinogen oxidase [Mycoplasma mobile 163K] methionyl-tRNA synthetase [Thermococcus kodakaraensis] ref YP_183462.1 methionyl-tRNA synthetase [Thermococcus kodakaraensis] | | | | 2.1.1.- |
| 9859, 9860 | 57159308 | 54 | 1.00E-76 | Thermococcus kodakaraensis | | | | | 6.1.1.10 |

| | | | | | | | | |
|---------------|----------|----|----------|---|---|---|----|----------|
| 9861, 9862 | 28210338 | 57 | 1.00E-89 | Clostridium tetani E88 | fructose-1,6-bisphosphatase [Clostridium tetani E88] fructose-1,6-bisphosphatase [Clostridium tetani E88] | | | 3.1.3.11 |
| 9863, 9864 | 46578435 | 38 | 2.00E-55 | Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough | methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gblAAS94502.1 methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] | | | 2.7.3.- |
| 9867, 9868 | 20808761 | 31 | 3.00E-13 | Thermoanaerobacter tengcongensis MB4 | SAM-dependent methyltransferases [Thermoanaerobacter tengcongensis MB4] gblAAM25536.1 SAM-dependent methyltransferases [Thermoanaerobacter tengcongensis MB4] | | | 2.1.1.- |
| 9873, 9874 | 15678362 | 42 | 2.00E-37 | Methanothermobacter thermautotrophicus str. Delta H | perosamine synthetase [Methanothermobacter thermautotrophicus str. Delta H] gblAAB84840.1 perosamine synthetase [Methanothermobacter thermautotrophicus str. Delta H] pir H69142 perosamine synthetase - Methanobacterium thermoautotrophicum (strain Delta H) | Methanobacterium thermoautotrophicum from bases 264585 to 276866 (section 24 of 148) of the complete genome | 91 | 4.00E-10 |
| 9875, 9876 | 48855342 | 58 | 2.00E-72 | Cytophaga hutchinsonii | COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii] | | | 3.4.- |
| 9877, 9878 | 52144139 | 38 | 6.00E-21 | Bacillus cereus ZK | cardiolipin synthetase [Bacillus cereus ZK] gblAAU19158.1 cardiolipin synthetase [Bacillus cereus ZK] | | | 2.7.8.- |
| 9879, 9880 | 24214122 | 34 | 9.00E-36 | Leptospira interrogans serovar Lai str. 56601 | Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gblAAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601] | | | 3.4.11.- |
| 9881, 9882 | | | | | | | | |
| 9883, 9884 | 48861156 | 26 | 3.00E-18 | Microbulbifer degradans 2-40 | hypothetical protein Mdeg02003535 [Microbulbifer degradans 2-40] | | | |
| 9887, 9888 | 34557204 | 45 | 4.00E-56 | Wolinella succinogenes DSM 1740 | hypothetical protein WS0806 [Wolinella succinogenes DSM 1740] emb CAE09919.1 conserved hypothetical protein [Wolinella succinogenes] | | | |
| 9889, 9890 | 53691858 | 50 | 7.00E-72 | Desulfovibrio desulfuricans G20 | hypothetical protein Ddes02000066 [Desulfovibrio desulfuricans G20] | | | |
| 989, 990 | 53761461 | 49 | 8.00E-49 | Ralstonia eutropha JMP134 | COG5526: Uncharacterized conserved protein [Ralstonia eutropha JMP134] | | | |
| 9893, 9894 | 34557685 | 34 | 4.00E-40 | Wolinella succinogenes DSM 1740 | HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10400.1 HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes] | | | |

| | | | | | | | | | |
|---------------|-----------|----|----------|---|--|--|--|----------|--|
| 9897, 9898 | 40062562 | 38 | 8.00E-07 | uncultured bacterium 159 | | FG-GAP repeat protein [uncultured bacterium 159] | Coxiella burnetii strain RSA 493, section 1 of 7 of the complete genome | 4.00E-11 | |
| 9899, 9900 | 34556661 | 48 | 5.00E-54 | Wolinella succinogenes DSM 1740 | | PUTATIVE FRUCTOSE-1,6-BISPHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE09376.1 PUTATIVE FRUCTOSE-1,6- BISPHOSPHATASE [Wolinella succinogenes] | | 3.1.3.11 | |
| 99, 100 | 4902890 | 29 | 3.00E-16 | Streptococcus pneumoniae | | galactosyl transferase [Streptococcus pneumoniae] | | 2.4.1.- | |
| 9901, 9902 | 48859134 | 29 | 8.00E-18 | Clostridium thermocellum ATCC 27405 | | COG0507: ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member [Clostridium thermocellum ATCC 27405] | | 3.1.11.5 | |
| 9903, 9904 | 23474422 | 29 | 4.00E-17 | Desulfovibrio desulfuricans G20 | | COG0840: Methyl-accepting chemotaxis protein [Desulfovibrio desulfuricans G20] | | | |
| 9905, 9906 | 48858423 | 41 | 4.00E-31 | Clostridium thermocellum ATCC 27405 | | COG2206: HD-GYP domain [Clostridium thermocellum ATCC 27405] | | | |
| 9909, 9910 | 29347707 | 56 | 5.00E-76 | Bacteroides thetaiotaomicron VPI-5482 | | putative reverse transcriptase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77404.1 putative reverse transcriptase [Bacteroides thetaiotaomicron VPI-5482] | | 2.7.7.49 | |
| 991, 992 | 53713337 | 63 | 4.00E-50 | Bacteroides fragilis YCH46 | | putative GTP-binding protein [Bacteroides fragilis YCH46] db BAD48795.1 putative GTP-binding protein [Bacteroides fragilis YCH46] | | | |
| 9913, 9914 | 345558118 | 26 | 7.00E-07 | Wolinella succinogenes DSM 1740 | | HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10833.1 HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes] | | | |
| 9917, 9918 | 34556786 | 43 | 2.00E-58 | Wolinella succinogenes DSM 1740 | | PUTATIVE PROCESSING PROTEASE [Wolinella succinogenes DSM 1740] emb CAE09501.1 PUTATIVE PROCESSING PROTEASE [Wolinella succinogenes] | | 3.4.-.- | |
| 9919, 9920 | 34556712 | 46 | 4.00E-36 | Wolinella succinogenes DSM 1740 | | GLUTAMYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE09427.1 GLUTAMYL-TRNA SYNTHETASE [Wolinella succinogenes] | | 6.1.1.17 | |
| 9921, 9922 | 488595902 | 35 | 2.00E-15 | Trichodesmium erythraeum IMS101 | | COG2755: Lysophospholipase L1 and related esterases [Trichodesmium erythraeum IMS101] | | | |
| 9925, 9926 | 53713488 | 38 | 9.00E-43 | Bacteroides fragilis YCH46 | | two-component system sensor histidine kinase [Bacteroides fragilis YCH46] db BAD48946.1 two-component system sensor histidine kinase [Bacteroides fragilis YCH46] | | 2.7.3.- | |
| 9927, 9928 | 48853682 | 33 | 1.00E-26 | Cytophaga hutchinsonii | | COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Cytophaga hutchinsonii] | | 2.3.1.51 | |

| | | | | | | | | |
|-------|----------|----|----------|---|--|--|--|----------|
| 9929, | 23506369 | 31 | 6.00E-10 | Francisella tularensis subsp. novicida | galactose epimerase [Francisella tularensis subsp. novicida] | | | 5.1.3.2 |
| 9930, | | | | | | | | |
| 9933, | 48855702 | 43 | 4.00E-40 | Cytophaga hutchinsonii | COG3279: Response regulator of the LysR/AlgR family [Cytophaga hutchinsonii] | | | 2.7.-.- |
| 9934 | | | | | | | | |
| 9935, | | | | Wolinella succinogenes DSM 1740 | NADH-UBIQUINONE OXIDOREDUCTASE, NQO3 SUBUNIT NQO3 [Wolinella succinogenes DSM 1740] emb CAE09618.1 NADH-UBIQUINONE OXIDOREDUCTASE, NQO3 SUBUNIT NQO3 [Wolinella succinogenes] | | | 1.6.5.3 |
| 9936 | 34556903 | 49 | 1.00E-59 | Bacteroides thetaiotaomicron VPI-5482 | topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 9937, | | | | | | | | 5.99.1.- |
| 9938 | 29348988 | 53 | 1.00E-90 | Bacteroides thetaiotaomicron VPI-5482 | gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] | | | |
| 9939, | | | | Bacteroides thetaiotaomicron | putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | 2.5.1.1 |
| 9940 | 29347468 | 47 | 2.00E-25 | VPI-5482 | gb AAO77165.1 putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482] | | | |
| | | | | | | | | |
| 9941, | | | | Geobacillus kaustophilus HTA426 | type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426] | | | |
| 9942 | 56418878 | 59 | 2.00E-86 | Wolinella succinogenes DSM 1740 | db BAD74628.1 type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426] | | | 2.1.1.72 |
| 9943, | | | | | | | | |
| 9944 | 34557807 | 31 | 1.00E-14 | Wolinella succinogenes DSM 1740 | SIGNAL-TRANSDUCING PROTEIN, HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE10522.1 SIGNAL-TRANSDUCING PROTEIN, HISTIDINE KINASE [Wolinella succinogenes] | | | 2.7.3.- |
| 9945, | | | | Helicobacter hepaticus ATCC 35061 | conserved hypothetical protein [Helicobacter hepaticus ATCC 35061] | | | |
| 9946 | 32263209 | 37 | 9.00E-20 | 51449 | ref NP_861188.1 hypothetical protein HH1657 [Helicobacter hepaticus ATCC 35061] | | | 2.7.3.- |
| | | | | | | | | |
| 9947, | | | | Wolinella succinogenes DSM 1740 | UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE GLMU [Wolinella succinogenes DSM 1740] emb CAE11088.1 UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE GLMU [Wolinella succinogenes] | | | |
| 9948 | 34558373 | 66 | 9.00E-79 | 1740 | | | | |
| 9949, | | | | Bacteroides fragilis YCH46 | putative GTPase [Bacteroides fragilis YCH46] | | | |
| 9950 | 53711977 | 50 | 6.00E-78 | YCH46 | GTPase [Bacteroides fragilis YCH46] | | | 3.6.1.- |
| | | | | | | | | |
| 995, | | | | Leptospira interrogans serovar Copenhageni str. | hypothetical protein LIC13227 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714224.1 hypothetical protein LA4044 [Leptospira interrogans serovar Lai str. 56601] gb AA51242.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] | | | |
| 996 | 45659049 | 44 | 4.00E-25 | Flocruz L1-130 | gb AA571772.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] | | | |

| | | | | | | | | | | |
|---------------|--------------|----|-----------|---------------|---|--|---|----|----------|--|
| 9951, 9952 | 15669198 | 23 | 2.00E-11 | 2661 | Methanocaldococcus jannaschii DSM | phosphate transport system regulatory protein (phoU) [Methanocaldococcus jannaschii DSM 2661] gb AAB9901.1.1 phosphate transport system regulatory protein (phoU) [Methanocaldococcus jannaschii DSM 2661] pir H64425 phosphate transport system regulatory protein homolog - [Methanococcus jannaschii sp Q58415 PHOU_METJA Phosphate transport system protein phoU homolog | | | | |
| 9953, 9954 | 48893217 | 45 | 3.00E-16 | 16 | Trichodesmium erythraeum IMS101 | COG3914: Predicted O-linked N-acetylglucosamine transferase, SPINDLY family [Trichodesmium erythraeum IMS101] | | | | |
| 9963, 9964 | ABP7392 2 | 45 | 7.00E-53 | | | Desc:Candida albicans essential protein SEQ ID NO 7759. Org:Candida albicans | | | 4.2.1.36 | |
| 9965, 9966 | 34557622 | 64 | 1.00E-106 | 1740 | Wollinella succinogenes DSM | PREPROTEIN TRANSLOCASE SECA SUBUNIT [Wollinella succinogenes DSM 1740] emb CAE10337.1 PREPROTEIN TRANSLOCASE SECA SUBUNIT [Wollinella succinogenes] | Wollinella succinogenes, complete genome; segment 4/7 | 86 | 5.00E-11 | |
| 9967, 9968 | 34556981 | 30 | 4.00E-24 | 1740 | Wollinella succinogenes DSM | hypothetical protein WS0562 [Wollinella succinogenes DSM 1740] emb CAE09696.1 conserved hypothetical protein [Wollinella succinogenes] | | | | |
| 9969, 9970 | 21673298 | 42 | 2.00E-43 | 1740 | Chlorobium tepidum TLS | ubiquinone/menaquinone biosynthesis methyltransferase [Chlorobium tepidum TLS] gb AAM71705.1 ubiquinone/menaquinone biosynthesis methyltransferase [Chlorobium tepidum TLS] sp Q8KF69 UBIE_CHLTE Menaquinone biosynthesis methyltransferase ubiE | | | 2.1.1.- | |
| 997, 998 | 21242456 | 41 | 2.00E-25 | 306 | Xanthomonas axonopodis pv. citri str. 306 | general stress protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM36574.1 general stress protein [Xanthomonas axonopodis pv. citri str. 306] | | | | |
| 9971, 9972 | 23473540 | 36 | 1.00E-31 | G20 | Desulfovibrio desulfuricans G20 | COG0463: Glycosyltransferases involved in cell wall biogenesis [Desulfovibrio desulfuricans G20] | | | 2.4.1.83 | |
| 9973, 9974 | 30250106 | 33 | 8.00E-10 | 19718 | Nitrosomonas europaea ATCC | SAM (and some other nucleotide) binding motif [Nitrosomonas europaea ATCC 19718] emb CAD86083.1 SAM (and some other nucleotide) binding motif [Nitrosomonas europaea ATCC 19718] | | | | |
| 9975, 9976 | 53712362 | 42 | 3.00E-20 | YCH46 | Bacteroides fragilis YCH46 | hypothetical protein BF1070 [Bacteroides fragilis YCH46] dbj BAD47820.1 conserved hypothetical protein [Bacteroides fragilis YCH46] | | | | |
| 9977, 9978 | 54301960 | 45 | 2.00E-11 | profundum SS9 | Photobacterium profundum SS9 | hypothetical protein PBPR80280 [Photobacterium profundum SS9] emb CAG22153.1 hypothetical protein [Photobacterium profundum] | | | | |
| 9979, 9980 | 53712694 | 36 | 5.00E-09 | YCH46 | Bacteroides fragilis YCH46 | putative ferric aerobactin receptor [Bacteroides fragilis YCH46] dbj BAD48152.1 putative ferric aerobactin receptor [Bacteroides fragilis YCH46] | | | | |

| | | | | | | | | |
|---------------|----------|----|----------|---|--|--|--|----------|
| 9983, 9984 | 34557269 | 60 | 3.00E-85 | Wollinella succinogenes DSM 1740 | ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes] | | | 3.6.1.- |
| 9985, 9986 | 57237984 | 52 | 5.00E-61 | Campylobacter jejuni RM1221 | tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] gb AAW35567.1 tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] | | | 4.2.1.70 |
| 9987, 9988 | 57242490 | 56 | 7.00E-72 | Campylobacter upsaliensis RM3195 | Mg chelatase-related protein [Campylobacter upsaliensis RM3195] gb EAL53558.1 Mg chelatase-related protein [Campylobacter upsaliensis RM3195] | | | |
| 9989, 9990 | 6967683 | 51 | 1.00E-32 | Campylobacter jejuni subsp. jejuni NCTC 11168 | hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281400.1 hypothetical protein Cj0190c [Campylobacter jejuni/ subsp. jejuni NCTC 11168] pir E81437 hypothetical protein Cj0190c [Imported] - Campylobacter jejuni (strain NCTC 11168) | | | |
| 999, 1000 | 48853385 | 46 | 1.00E-18 | Cytophaga hutchinsonii | hypothetical protein Chut02003884 [Cytophaga hutchinsonii] | | | |
| 9991, 9992 | 23130537 | 39 | 3.00E-37 | Nostoc punctiforme PCC 73102 | COG0778: Nitroreductase [Nostoc punctiforme PCC 73102] | | | |
| 9993, 9994 | 34556638 | 60 | 1.00E-26 | Wollinella succinogenes DSM 1740 | ABC TRANSPORTER, ATP-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09353.1 ABC TRANSPORTER, ATP-BINDING PROTEIN [Wollinella succinogenes] | | | 1.8.- |
| 9995, 9996 | 34556560 | 44 | 4.00E-60 | Wollinella succinogenes DSM 1740 | GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes] | | | |

WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising

(a) a nucleic acid sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues,

wherein the nucleic acid encodes at least one polypeptide having an enzymatic activity, or encodes a polypeptide or peptide capable of generating an antibody that binds specifically to a polypeptide having a sequence comprising any of the even numbered SEQ ID NO:s in the sequence listing, including from SEQ ID NO:2 through SEQ ID NO:26,898;

(b) a nucleic acid sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897,

wherein the nucleic acid encodes a polypeptide having an activity as set forth in Table 3, or encodes a polypeptide or peptide capable of generating an antibody that binds specifically to a polypeptide having a sequence comprising any of the even numbered SEQ ID NO:s in the sequence listing, including from SEQ ID NO:2 through SEQ ID NO:26,898,

and the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes,

and optionally the nucleic acid is at least about 20, 30, 40, 50, 60, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript; and

(c) a nucleic acid sequence complementary to (a) or (b).

2. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897.

3. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, or the full length of a gene or a transcript.

4. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence comprises a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897.

5. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence encodes a polypeptide having a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897.

6. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

7. The isolated or recombinant nucleic acid of claim 6, wherein the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

8. The isolated or recombinant nucleic acid of claim 1, wherein at least one enzymatic activity is one of the enzymatic activities described in Table 1, Table 2 or Table 3.

9. The isolated or recombinant nucleic acid of claim 1, wherein the protein is a structural or binding protein.

10. The isolated or recombinant nucleic acid of claim 8, wherein the enzymatic activity comprises aldolase, alpha-galactosidase, amidase, secondary amidase, amylase, catalase, dehalogenase, endoglucanase, epoxide hydrolase, or esterase activity.

11. The isolated or recombinant nucleic acid of claim 8, wherein the enzymatic activity comprises an activity in the carotenoid pathway.

12. The isolated or recombinant nucleic acid of claim 8, wherein the enzymatic activity comprises hydrolase, glucosidase, glycosidase, intein, isomerase, laccase, lipase, or monooxygenase activity.

13. The isolated or recombinant nucleic acid of claim 8, wherein the enzymatic activity comprises nitroreductase, nitrilase, P450 enzyme, pectate lyase, phosphatase, phospholipase, phytase, polymerase or xylanase activity.

14. The isolated or recombinant nucleic acid of claim 1, wherein the enzyme or protein is thermostable or thermotolerant.

15. The isolated or recombinant nucleic acid of claim 14, wherein the polypeptide retains enzyme activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C, or, the polypeptide retains enzyme activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C.

16. An isolated or recombinant nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, and the nucleic acid encodes a polypeptide having enzyme activity or encodes a protein.

17. The isolated or recombinant nucleic acid of claim 16, wherein the nucleic acid is at least about 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript.

18. The isolated or recombinant nucleic acid of claim 16, wherein the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

19. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein, wherein the probe comprises at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500 or more consecutive bases of a sequence comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID

listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, wherein the probe identifies the nucleic acid by binding or hybridization.

20. The nucleic acid probe of claim 19, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

21. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, wherein the probe comprises a nucleic acid comprising at least about 10 consecutive residues of a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

22. The nucleic acid probe of claim 21, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

23. An amplification primer pair for amplifying a nucleic acid encoding a polypeptide having an enzymatic activity or encoding a protein, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence as set forth in claim 1 or claim 16, or a subsequence thereof.

24. The amplification primer pair of claim 23, wherein a member of the amplification primer pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40 or more consecutive bases of the sequence.

25. An amplification primer pair, wherein the amplification primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 42, 33, 34, 35 or more residues of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 42, 33, 34, 35 or more residues of the complementary strand of the first member.

26. An enzyme-encoding or protein-encoding nucleic acid generated by amplification of a polynucleotide using an amplification primer pair as set forth in claim 23 or claim 25.

27. The enzyme-encoding or protein-encoding nucleic acid of claim 26, wherein the amplification is by polymerase chain reaction (PCR).

28. The enzyme-encoding or protein-encoding nucleic acid of claim 26, wherein the nucleic acid generated by amplification of a gene library.

29. The enzyme-encoding or protein-encoding nucleic acid of claim 28, wherein the gene library is an environmental library.

30. An isolated or recombinant polypeptide having an enzymatic activity or encoding a protein encoded by a nucleic acid as set forth in claim 26.

31. A method of amplifying a nucleic acid encoding a polypeptide having an enzymatic activity or encoding a protein comprising amplification of a template nucleic acid with an amplification primer pair capable of amplifying a nucleic acid sequence as set forth in claim 1 or claim 16, or a subsequence thereof.

32. An expression cassette comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 16.

33. A vector comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 16.

34. A cloning vehicle comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 16, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

35. The cloning vehicle of claim 34, wherein the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector.

36. A bacterial artificial chromosome (BAC), a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC) or a mammalian artificial chromosome (MAC) comprising a sequence as set forth in claim 1 or claim 16.

37. A transformed cell comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 16.

38. A transformed cell comprising an expression cassette as set forth in claim 32.

39. The transformed cell of claim 38, wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

40. A transgenic non-human animal comprising a sequence as set forth in claim 1 or claim 16.

41. The transgenic non-human animal of claim 40, wherein the animal is a mouse, a goat, a rabbit, a sheep, a pig, a cow or a rat.

42. A transgenic plant comprising a sequence as set forth in claim 1 or claim 16.

43. The transgenic plant of claim 42, wherein the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

44. A transgenic seed comprising a sequence as set forth in claim 1 or claim 16.

45. The transgenic seed of claim 44, wherein the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

46. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 16, or a subsequence thereof.

47. The antisense oligonucleotide of claim 46, wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

48. A method of inhibiting the translation of an enzyme-encoding or protein-encoding message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 16.

49. A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of a sequence as set forth in claim 1 or claim 16, wherein optionally the RNAi is an siRNA or an miRNA molecule.

50. The double-stranded inhibitory RNA (RNAi) molecule of claim 49, wherein the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length, wherein optionally the RNAi is an siRNA or an miRNA molecule.

51. A method of inhibiting the expression of an enzyme or a protein in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of a sequence as set forth in claim 1 or claim 16, wherein optionally the RNAi is an siRNA or an miRNA molecule.

52. An isolated or recombinant polypeptide (i) having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or complete sequence identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898, over a region of at least about 20, 30, 40, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700 or more residues, wherein optionally the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or, (ii) encoded by a nucleic acid having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, over a region of at least about 20, 30, 40, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700 or more residues, or encoded by a nucleic acid capable of hybridizing under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897.

53. The isolated or recombinant polypeptide of claim 52, wherein the sequence identity is over a region of at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or is 100% sequence identity.

54. The isolated or recombinant polypeptide of claim 52, wherein the sequence identity is over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050 or more residues, or the full length of an enzyme.

55. The isolated or recombinant polypeptide of claim 52, wherein the polypeptide has a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898.

56. The isolated or recombinant polypeptide of claim 52, wherein the polypeptide has an enzymatic activity or encodes a protein.

57. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises aldolase, alpha-galactosidase, amidase, secondary amidase, amylase, catalase, dehalogenase, endoglucanase, epoxide hydrolase, or esterase activity.

58. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises an activity in the carotenoid pathway.

59. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises hydrolase, glucosidase, glycosidase, intein, isomerase, laccase, lipase, or monooxygenase activity.

60. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises nitroreductase, nitrilase, P450 enzyme, pectate lyase, phosphatase, phospholipase, phytase, polymerase or xylanase activity.

61. The isolated or recombinant polypeptide of claim 56, wherein the enzyme or the protein is thermostable or thermotolerant.

62. The isolated or recombinant polypeptide of claim 61, wherein the polypeptide retains enzymatic activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 95°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or, the polypeptide retains enzymatic activity after exposure to a temperature in the range from between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more.

63. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 52 and lacking a signal sequence or a prepro sequence.

64. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 52 and having a heterologous signal sequence or a heterologous prepro sequence.

65. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein.

66. The isolated or recombinant polypeptide of claim 61, wherein thermotolerance comprises retention of at least half of the specific activity of the enzyme at 37°C after being heated to an elevated temperature.

67. The isolated or recombinant polypeptide of claim 61, wherein thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature.

68. The isolated or recombinant polypeptide of claim 52, wherein the polypeptide comprises at least one glycosylation site.

69. The isolated or recombinant polypeptide of claim 68, wherein the glycosylation is an N-linked glycosylation.

70. The isolated or recombinant polypeptide of claim 68, wherein the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

71. The isolated or recombinant polypeptide of claim 56, wherein the polypeptide retains an enzymatic activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0.

72. The isolated or recombinant polypeptide of claim 56, wherein the polypeptide retains an enzymatic activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.

73. A protein preparation comprising a polypeptide as set forth in claim 52, wherein the protein preparation comprises a liquid, a solid or a gel.

74. A heterodimer comprising a polypeptide as set forth in claim 52 and a second domain.

75. The heterodimer of claim 74, wherein the second domain is a polypeptide and the heterodimer is a fusion protein.

76. The heterodimer of claim 74, wherein the second domain is an epitope or a tag.
77. A homodimer comprising a polypeptide as set forth in claim 52.
78. An immobilized polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 52, or a subsequence thereof.
79. The immobilized polypeptide of claim 78, wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.
80. An array comprising an immobilized polypeptide as set forth in claim 52.
81. An array comprising an immobilized nucleic acid as set forth in claim 1 or claim 16.
82. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 52.
83. The isolated or recombinant antibody of claim 82, wherein the antibody is a monoclonal or a polyclonal antibody.
84. A hybridoma comprising an antibody that specifically binds to a polypeptide as set forth in claim 52.
85. A method of isolating or identifying a polypeptide with an enzymatic activity or encoding a protein comprising the steps of:
- (a) providing an antibody as set forth in claim 82;
 - (b) providing a sample comprising polypeptides; and

(c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having enzymatic activity or encoding a protein.

86. A method of making an anti-enzyme or anti-protein antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 or claim 16 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-enzyme or anti-protein antibody.

87. A method of making an anti-enzyme or anti-protein antibody comprising administering to a non-human animal a polypeptide as set forth in claim 52 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-enzyme or anti-protein antibody.

88. A method of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises a sequence as set forth in claim 1 or claim 16; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

89. The method of claim 88, further comprising transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide.

90. A method for identifying a polypeptide having an enzyme activity or encoding a protein comprising the following steps:

(a) providing a polypeptide as set forth in claim 52;

(b) providing an enzyme substrate; and

(c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having an enzyme activity or encoding a protein.

91. A method for identifying an enzyme or protein substrate comprising the following steps:

- (a) providing a polypeptide as set forth in claim 52;
- (b) providing a test substrate; and
- (c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as an enzyme or protein substrate.

92. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

- (a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has a sequence as set forth in claim 1 or claim 16;
- (b) providing a test compound;
- (c) contacting the polypeptide with the test compound; and
- (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

93. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

- (a) providing a polypeptide as set forth in claim 52;
- (b) providing a test compound;
- (c) contacting the polypeptide with the test compound; and
- (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

94. A method for identifying a modulator of an enzyme activity comprising the following steps:

- (a) providing a polypeptide as set forth in claim 56;
- (b) providing a test compound;
- (c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the enzyme, wherein a change in the enzyme activity

measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the enzyme activity.

95. The method of claim 94, wherein the enzyme activity is measured by providing an enzyme substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product.

96. The method of claim 95, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of an enzyme activity.

97. The method of claim 95, wherein an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of an enzyme activity.

98. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence as set forth in claim 52, a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16.

99. The computer system of claim 98, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

100. The computer system of claim 99, wherein the sequence comparison algorithm comprises a computer program that indicates polymorphisms.

101. The computer system of claim 98, further comprising an identifier that identifies one or more features in said sequence.

102. A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 52; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16.

103. A method for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 52; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16; and (b) identifying one or more features in the sequence with the computer program.

104. A method for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 52 or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16; and (b) determining differences between the first sequence and the second sequence with the computer program.

105. The method of claim 104, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

106. The method of claim 104, further comprising an identifier that identifies one or more features in a sequence.

107. The method of claim 104, comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

108. A method for isolating or recovering a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein from an environmental sample comprising the steps of:

(a) providing an amplification primer pair as set forth in claim 23 or claim 25;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein from an environmental sample.

109. The method of claim 108, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, or a subsequence thereof.

110. A method for isolating or recovering a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising a sequence as set forth in claim 1 or claim 16, or a subsequence thereof;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein from an environmental sample.

111. The method of claim 108 or claim 110, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample.

112. The method of claim 111, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

113. A method of generating a variant of a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein comprising the steps of:

(a) providing a template nucleic acid comprising a sequence as set forth in claim 1 or claim 16; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid.

114. The method of claim 113, further comprising expressing the variant nucleic acid to generate a variant enzyme or protein polypeptide.

115. The method of claim 113, wherein the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR) and a combination thereof.

116. The method of claim 113, wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

117. The method of claim 113, wherein the method is iteratively repeated until an enzyme or protein having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced.

118. The method of claim 117, wherein the variant enzyme or protein polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature.

119. The method of claim 117, wherein the variant enzyme or protein polypeptide has increased glycosylation as compared to the enzyme or protein encoded by a template nucleic acid.

120. The method of claim 117, wherein the variant enzyme or protein polypeptide has an enzyme activity under a high temperature, wherein the enzyme encoded by the template nucleic acid is not active under the high temperature.

121. The method of claim 113, wherein the method is iteratively repeated until an enzyme or protein coding sequence having an altered codon usage from that of the template nucleic acid is produced.

122. The method of claim 113, wherein the method is iteratively repeated until an enzyme or protein gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

123. A method for modifying codons in a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein comprising a sequence as set forth in claim 1 or claim 16; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented

in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

124. A method for modifying codons in a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein comprising a sequence as set forth in claim 1 or claim 16; and,

(b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding an enzyme or a protein.

125. A method for modifying codons in a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, comprising a sequence as set forth in claim 1 or claim 16; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

126. A method for modifying a codon in a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein to decrease its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein comprising a sequence as set forth in claim 1 or claim 16; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell.

127. The method of claim 125, wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

128. A method for producing a library of nucleic acids encoding a plurality of modified enzyme or protein active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, or a subsequence thereof, and the nucleic acid encodes an enzyme or protein active site or an enzyme or protein substrate binding site;

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified enzyme or protein active sites or substrate binding sites.

129. The method of claim 128, comprising mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, Gene Site Saturation Mutagenesis (GSSM), or a synthetic ligation reassembly (SLR).

130. The method of claim 128, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR) and a combination thereof.

131. The method of claim 128, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

132. A method for making a small molecule comprising the following steps:

- (a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises an enzyme encoded by a nucleic acid comprising a sequence as set forth in claim 1 or claim 16;
- (b) providing a substrate for at least one of the enzymes of step (a); and
- (c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

133. A method for modifying a small molecule comprising the following steps:

(a) providing an enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence as set forth in claim 1 or claim 16;

(b) providing a small molecule; and

(c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the enzyme, thereby modifying a small molecule by an enzymatic reaction.

134. The method of claim 133, comprising a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the enzyme.

135. The method of claim 133, further comprising a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions.

136. The method of claim 135, further comprising the step of testing the library to determine if a particular modified small molecule which exhibits a desired activity is present within the library.

137. The method of claim 136, wherein the step of testing the library further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

138. A method for determining a functional fragment of an enzyme comprising the steps of:

(a) providing an enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16; and

(b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for an enzyme activity, thereby determining a functional fragment of an enzyme.

139. The method of claim 138, wherein the enzyme activity is measured by providing an enzyme substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

140. A method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps:

(a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid comprising a sequence as set forth in claim 1 or claim 16;

(b) culturing the modified cell to generate a plurality of modified cells;

(c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and,

(d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis.

141. The method of claim 140, wherein the genetic composition of the cell is modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene.

142. The method of claim 141, further comprising selecting a cell comprising a newly engineered phenotype.

143. The method of claim 142, further comprising culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

144. An isolated or recombinant signal sequence (signal peptide) consisting of a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1

to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44, 1 to 45, 1 to 46, or 1 to 47, of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898.

145. A chimeric polypeptide comprising at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 144, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

146. The chimeric polypeptide of claim 145, wherein the heterologous polypeptide or peptide is not an enzyme.

147. The chimeric polypeptide of claim 145, wherein the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or an enzyme catalytic domain (CD).

148. An isolated or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 144, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

149. A method of increasing thermotolerance or thermostability of a enzyme polypeptide, the method comprising glycosylating an enzyme, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16, thereby increasing thermotolerance or thermostability of the enzyme.

150. A method for overexpressing a recombinant enzyme in a cell comprising expressing a vector comprising a nucleic acid sequence as set forth in claim 1 or claim 16, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

151. A method of making a transgenic plant comprising the following steps:

(a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 16, thereby producing a transformed plant cell;

(b) producing a transgenic plant from the transformed cell.

152. The method as set forth in claim 151, wherein the step (a) further comprises introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts.

153. The method as set forth in claim 152, wherein the step (a) comprises introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment or by using an *Agrobacterium tumefaciens* host.

154. A method of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps:

(a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 16;

(b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

155. A method for decreasing the amount of a compound in a composition comprising the following steps:

(a) providing a polypeptide having an enzyme activity or encoding a protein as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16;

(b) providing a composition comprising the compound; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the enzyme hydrolyzes, breaks up or otherwise processes the compound in the composition.

156. The method as set forth in claim 155, wherein the composition comprises an animal food or feed.

157. A drink or beverage comprising at least one polypeptide as set forth in claim 52.

158. The drink or beverage of claim 157, wherein the drink or beverage is a food or feed supplement.

159. A food, a feed or a nutritional supplement comprising a polypeptide as set forth in claim 52.

160. A method for utilizing an enzyme or protein as a nutritional supplement in an animal diet, the method comprising:

preparing a nutritional supplement containing an enzyme or protein comprising at least thirty contiguous amino acids of a polypeptide as set forth in claim 52; and

administering the nutritional supplement to the animal.

161. The method of claim 160, wherein the animal is a human.

162. The method of claim 160, wherein the animal is a ruminant or a monogastric animal.

163. The method of claim 160, wherein the enzyme or protein is prepared by expression of a polynucleotide encoding the enzyme or protein in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal.

164. The method of claim 163, wherein the organism is selected from the group consisting of a *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

165. An edible enzyme delivery matrix comprising a thermostable recombinant enzyme or protein having a sequence as set forth in claim 56.

166. A method for delivering an enzyme or protein supplement to an animal, the method comprising:

preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and thermostable recombinant enzyme or protein having a sequence as set forth in claim 56, wherein the pellets readily disperse the enzyme or protein contained therein into aqueous media, and administering the edible enzyme delivery matrix to the animal.

167. The method of claim 166, wherein the granulate edible carrier comprises a carrier selected from the group consisting of a grain germ, a grain germ that is spent of oil, a hay, an alfalfa, a timothy, a soy hull, a sunflower seed meal and a wheat midd.

168. The method of claim 166, wherein the granulate edible carrier comprises grain germ that is spent of oil.

169. The method of claim 166, wherein the enzyme is glycosylated to provide thermostability at pelletizing conditions.

170. The method of claim 166, wherein the delivery matrix is formed by pelletizing a mixture comprising a grain germ and an enzyme or protein.

171. The method of claim 166, wherein the pelletizing conditions include application of steam.

172. The method of claim 166, wherein the pelletizing conditions comprise application of a temperature in excess of about 80°C for about 5 minutes and the

enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

173. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having an enzyme activity and a signal sequence, wherein the nucleic acid comprises a sequence as set forth in claim 1.

174. The isolated or recombinant nucleic acid of claim 173, wherein the signal sequence is derived from another enzyme.

175. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having an enzyme activity or encoding a protein, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence as set forth in claim 1.

176. A pharmaceutical composition comprising a polypeptide as set forth in claim 52.

177. The pharmaceutical composition of claim 176 formulated as an edible delivery agent.

178. The pharmaceutical composition of claim 177, wherein the formulation comprises a tablet, a gel, a capsule or a gellab.

179. The pharmaceutical composition of claim 177, wherein the formulation comprises a lotion, a spray or a gel.

180. A method for delivering an enzyme or protein supplement to an animal, the method comprising:

- (a) providing a cell that recombinantly generates a polypeptide as set forth in claim 56, and
- (b) administering the cell or the recombinantly generated polypeptide to the animal.

181. The method as claim 180, wherein the cell is a plant cell, a bacterial cell, a yeast cell, an insect cell or an animal cell.

182. The method of claim 181, wherein the cell is selected from the group consisting of a *Schizosaccharomyces* sp., *Saccharomyces* sp., *Pichia* sp., *Escherichia* sp., *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

183. The method of claim 182, wherein the cell is *Saccharomyces pombe*.

184. The method of claim 182, wherein the cell is *Saccharomyces cerevisiae*.

185. The method of claim 182, wherein the cell is *Pichia pastoris*.

186. The method of claim 182, wherein the cell is *Escherichia coli*.

187. The method of claim 182, wherein the cell is *Bacillus cereus*.

188. A composition comprising an encapsulated formulation comprising at least one polypeptide as set forth in claim 56.

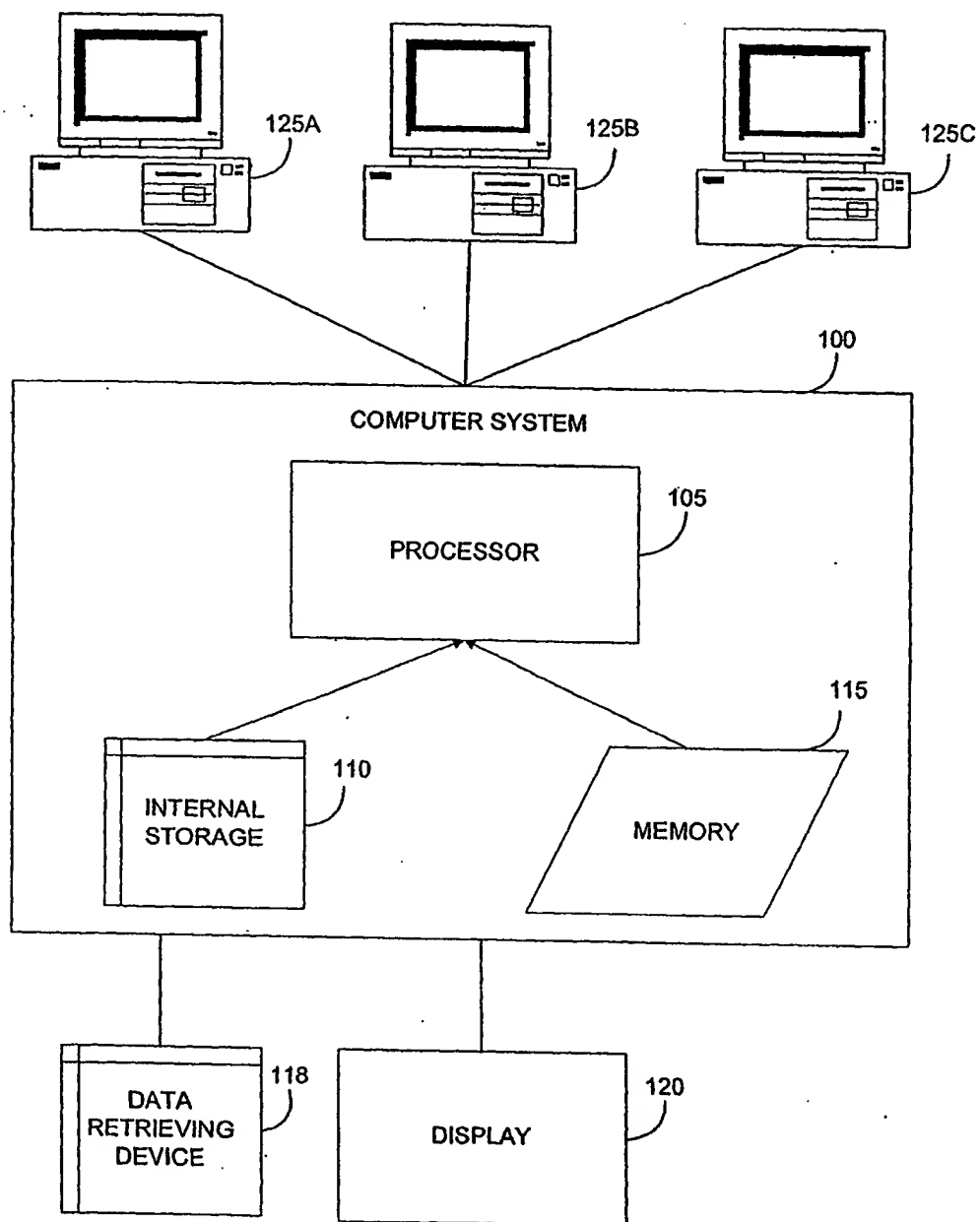


FIGURE 1

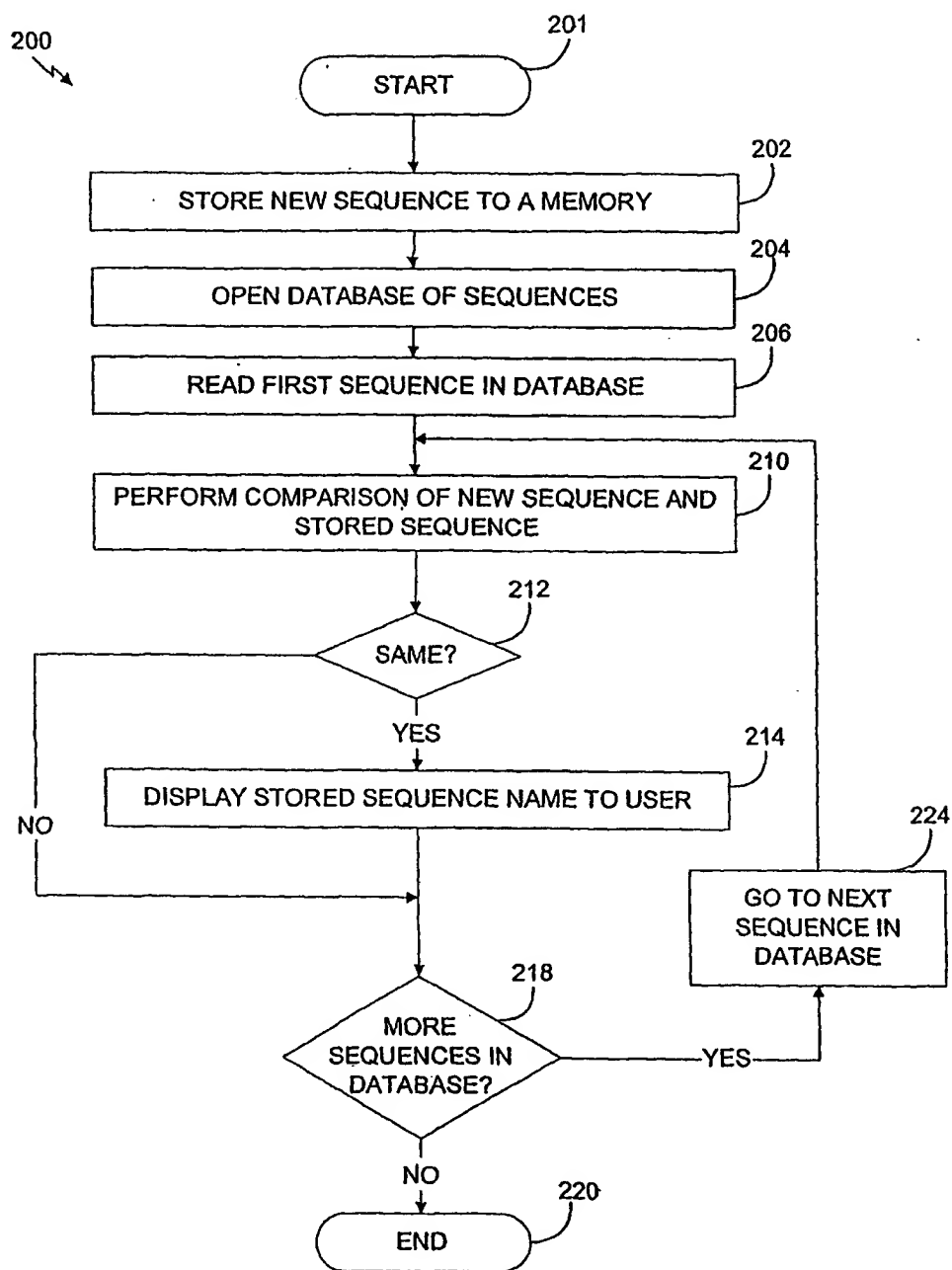


FIGURE 2

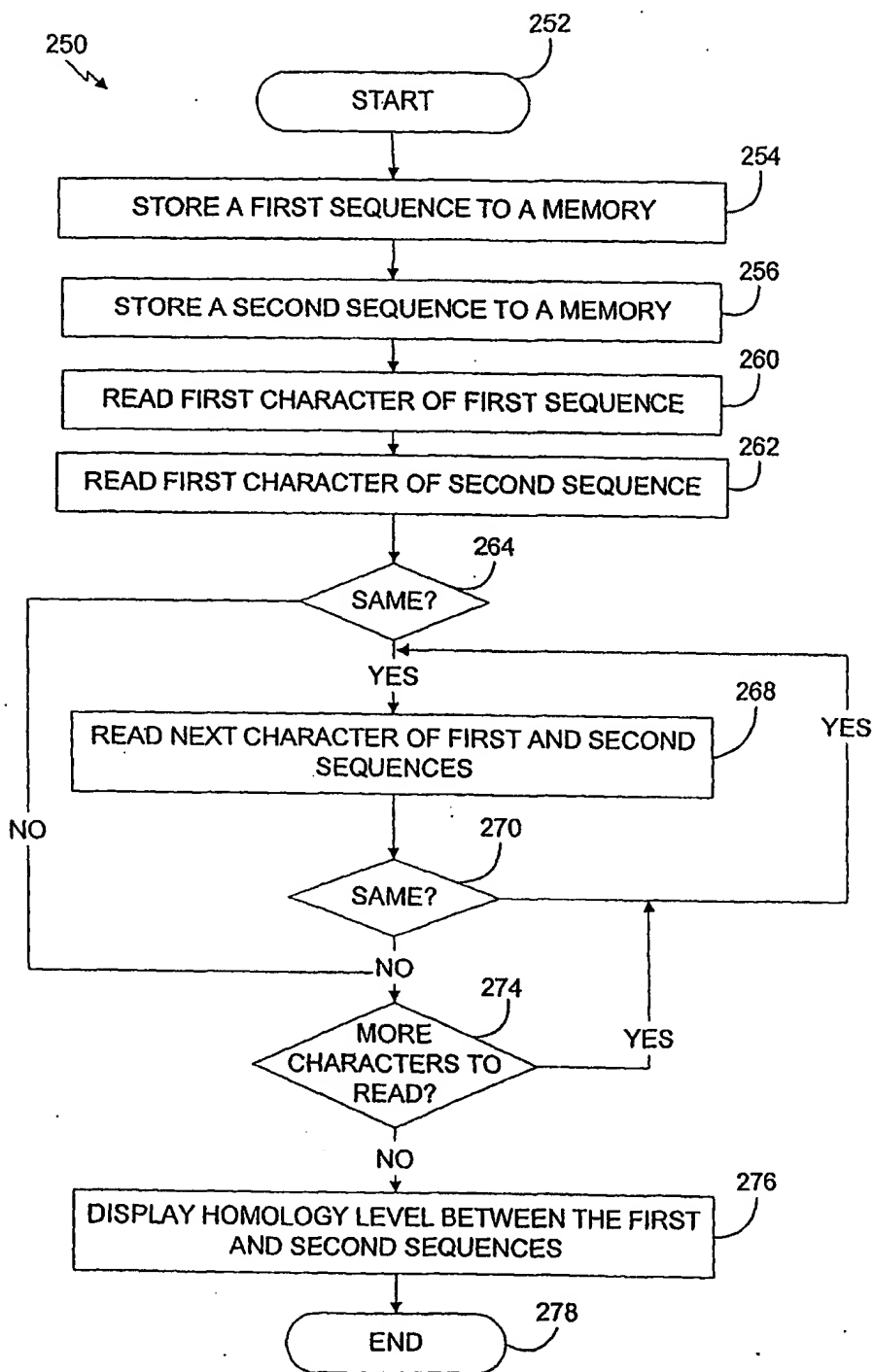


FIGURE 3

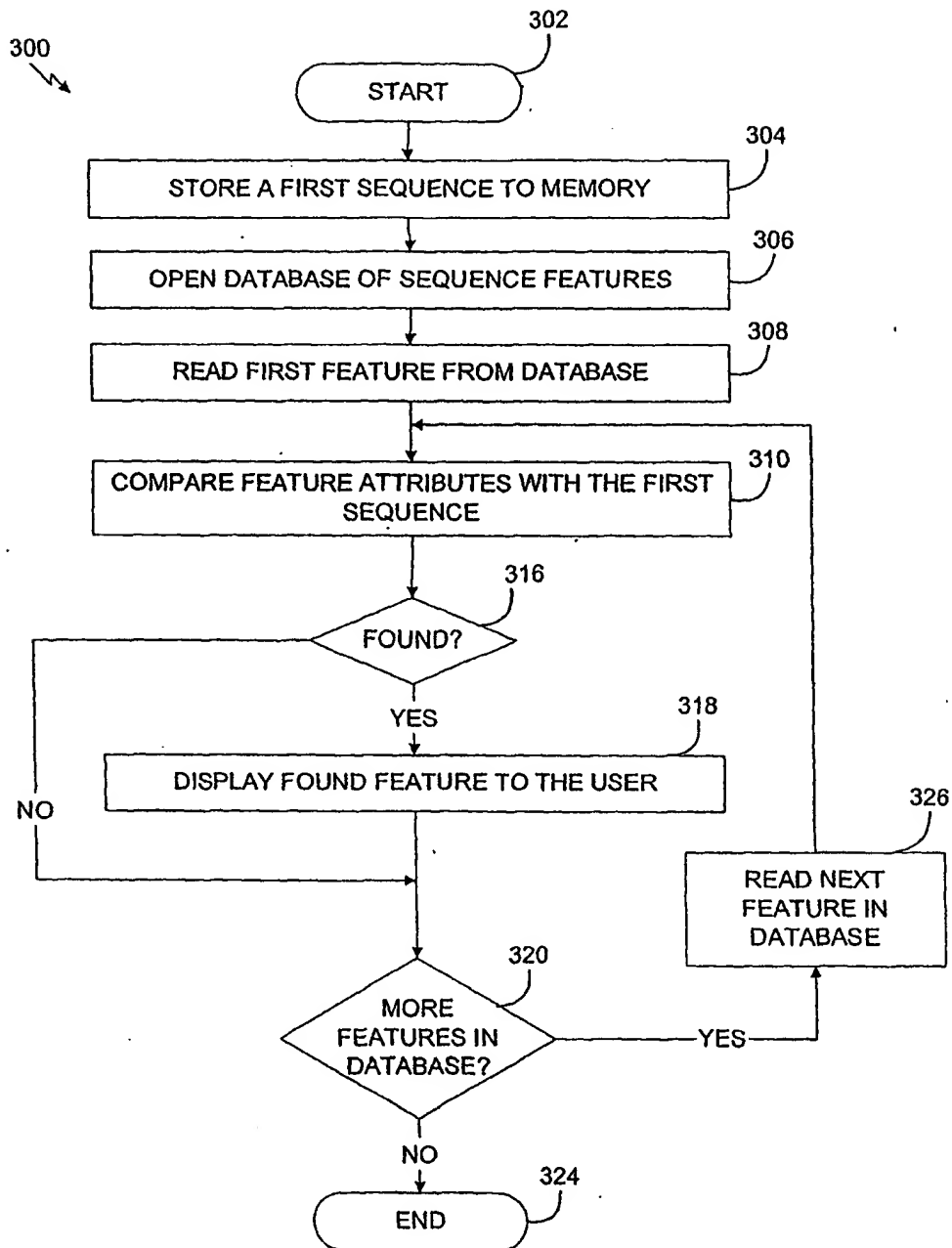


FIGURE 4